Package 'MultiAssayExperiment'

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Title Software for the integration of multi-omics experiments in Bioconductor

Version 1.38.0

Description Harmonize data management of multiple experimental assays performed on an overlapping set of specimens. It provides a familiar Bioconductor user experience by extending concepts from SummarizedExperiment, supporting an open-ended mix of standard data classes for individual assays, and allowing subsetting by genomic ranges or rownames. Facilities are provided for reshaping data into wide and long formats for adaptability to graphing and downstream analysis.

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URL http://waldronlab.io/MultiAssayExperiment/

BugReports https://github.com/waldronlab/MultiAssayExperiment/issues

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Contents

MultiAssayExperiment-package . . . 3
ExperimentList . . . 4
ExperimentList-class . . . 5
hasAssay . . . 7
HDF5MultiAssayExperiment . . . 8
listToMap . . . 9
MatchedAssayExperiment-class . . . 10
miniACC . . . 11
MultiAssayExperiment . . . 12
MultiAssayExperiment-class . . . 14
MultiAssayExperiment-helpers . . . 18
MultiAssayExperiment-methods . . . 25
MultiAssayExperimentToMAF . . . 28
prepMultiAssay . . . 28
reexports . . . 30
subsetBy . . . 30
upsetSamples . . . 34

Index **36**

`MultiAssayExperiment-package` *MultiAssayExperiment: Build an integrative multi-assay container*

Description

MultiAssayExperiment allows the manipulation of related multiassay datasets with partially overlapping samples, associated metadata at the level of an entire study, and at the level of the "biological unit". The biological unit may be a patient, plant, yeast strain, etc.

Details

The package hierarchy of information:

- study
- experiments
- samples

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See Also

Useful links:

- http://waldronlab.io/MultiAssayExperiment/
- Report bugs at https://github.com/waldronlab/MultiAssayExperiment/issues

ExperimentList *Represent multiple experiments as a List-derivative* ExperimentList

Description

The ExperimentList class can contain several different types of data. The only requirements for an ExperimentList class are that the objects contained have the following set of methods: dim, [, dimnames

Usage

```
ExperimentList(...)
```

Arguments

...	A named list class object

Value

A ExperimentList class object of experiment data

Examples

```
## Create an empty ExperimentList instance
ExperimentList()

## Create array matrix and AnnotatedDataFrame to create an ExpressionSet class
arraydat <- matrix(data = seq(101, length.out = 20), ncol = 4,
    dimnames = list(
        c("ENST00000294241", "ENST00000355076",
        "ENST00000383706","ENST00000234812", "ENST00000383323"),
        c("array1", "array2", "array3", "array4")
    ))

colDat <- data.frame(slope53 = rnorm(4),
    row.names = c("array1", "array2", "array3", "array4"))

## SummarizedExperiment constructor
exprdat <- SummarizedExperiment::SummarizedExperiment(arraydat,
    colData = colDat)

## Create a sample methylation dataset
methyldat <- matrix(data = seq(1, length.out = 25), ncol = 5,
    dimnames = list(
        c("ENST00000355076", "ENST00000383706",
          "ENST00000383323", "ENST00000234812", "ENST00000294241"),
        c("methyl1", "methyl2", "methyl3",
          "methyl4", "methyl5")
    ))
```

```
## Create a sample RNASeqGene dataset
rnadat <- matrix(
    data = sample(c(46851, 5, 19, 13, 2197, 507,
        84318, 126, 17, 21, 23979, 614), size = 20, replace = TRUE),
    ncol = 4,
    dimnames = list(
        c("XIST", "RPS4Y1", "KDM5D", "ENST00000383323", "ENST00000234812"),
        c("samparray1", "samparray2", "samparray3", "samparray4")
    ))

## Create a mock RangedSummarizedExperiment from a data.frame
rangedat <- data.frame(chr="chr2", start = 11:15, end = 12:16,
    strand = c("+", "-", "+", "*", "."),
    samp0 = c(0,0,1,1,1), samp1 = c(1,0,1,0,1), samp2 = c(0,1,0,1,0),
    row.names = c(paste0("ENST", "00000", 135411:135414), "ENST00000383323"))

rangeSE <- SummarizedExperiment::makeSummarizedExperimentFromDataFrame(rangedat)

## Combine to a named list and call the ExperimentList constructor function
assayList <- list(Affy = exprdat, Methyl450k = methyldat, RNASeqGene = rnadat,
                GISTIC = rangeSE)

## Use the ExperimentList constructor
ExpList <- ExperimentList(assayList)
```

`ExperimentList-class` *ExperimentList - A container for multi-experiment data*

Description

The `ExperimentList` class is a container that builds on the `SimpleList` with additional checks for consistency in experiment names and length. It contains a `SimpleList` of experiments with sample identifiers. One element present per experiment performed.

Convert from `SimpleList` or `list` to the multi-experiment data container. When using the **mergeReplicates** method, additional arguments are passed to the given `simplify` function argument (e.g., `na.rm = TRUE`)

Usage

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

## S4 method for signature 'ExperimentList'
isEmpty(x)

## S4 method for signature 'ExperimentList'
dimnames(x)

## S4 method for signature 'ExperimentList'
```

```
colnames(x, do.NULL = TRUE, prefix = "col")

## S4 method for signature 'ExperimentList'
rownames(x, do.NULL = TRUE, prefix = "row")

## S4 method for signature 'ExperimentList'
mergeReplicates(x, replicates = list(), simplify = BiocGenerics::mean, ...)

## S4 method for signature 'ANY,missing'
assay(x, i, withDimnames = TRUE, ...)

## S4 method for signature 'ExperimentList'
assays(x, withDimnames = TRUE, ...)

## S4 method for signature 'ExperimentList,missing'
assay(x, i, withDimnames = TRUE, ...)

## S4 method for signature 'ExperimentList,numeric'
assay(x, i, withDimnames = TRUE, ...)

## S4 method for signature 'ExperimentList,character'
assay(x, i, withDimnames = TRUE, ...)
```

Arguments

object, x	An ExperimentList object
do.NULL, prefix	See ?base::rownames for a description of these arguments.
replicates	mergeReplicates: A list or LogicalList where each element represents a sample and a vector of repeated measurements for the sample
simplify	A function for merging columns where duplicates are indicated by replicates
...	Additional arguments. See details for more information.
i	A scalar character or integer index
withDimnames	logical (default TRUE) whether to return dimension names

Value

An ExperimentList class object

Methods (by generic)

- show(ExperimentList): Show method for ExperimentList class
- isEmpty(ExperimentList): check for zero length across all experiments
- dimnames(ExperimentList): Get the dimension names for an ExperimentList using CharacterList
- colnames(ExperimentList): Get the column names for an ExperimentList as a CharacterList slightly more efficiently
- rownames(ExperimentList): Get the row names for an ExperimentList as a CharacterList slightly more efficiently

- mergeReplicates(ExperimentList): Apply the mergeReplicates method on the ExperimentList elements
- assay(x = ANY, i = missing): Obtain the specified assay with a numeric or character reference
- assays(ExperimentList): Get the assay data from each element in the ExperimentList

coercion

Convert a list or S4 List to an ExperimentList using the as() function.

In the following example, x is either a list or List:

```
as(x, "ExperimentList")
```

Examples

```
ExperimentList()
```

---

hasAssay *Checking assay method for any class*

Description

The hasAssay function is intended for developers who would like to include new classes into a MultiAssayExperiment instance. It checks the methods tables of the assay function for the specified class of the argument.

Usage

```
hasAssay(object)
```

Arguments

object	A MultiAssayExperiment or named list object instance

Value

A logical value indicating method availability

Examples

```
lst <- structure(list(), .Names=character())
hasAssay(lst)
```

HDF5MultiAssayExperiment *Save a MultiAssayExperiment class object to HDF5 and Rds files*

Description

This function takes a MultiAssayExperiment object and uses the assays functionality to obtain data matrices out of the experiments. These are then saved into the .h5 file format. This function relies heavily on the HDF5Array package whose installation is required before use. saveHDF5MultiAssayExpeirment preserves the classes contained in the ExperimentList with the exception of matrix which is converted to HDF5Matrix. Internal SummarizedExperiment assays are converted to HDF5-backed assays as in HDF5Array::saveHDF5SummarizedExperiment. SummarizedExperiment objects with multiple i-th assays will have the first assay take precedence and others assays will be dropped with a warning. If the first assay in a SummarizedExperiment contains an array, the array is preserved in the process of saving and loading the HDF5-backed MultiAssayExperiment.

Usage

```
saveHDF5MultiAssayExperiment(
  x,
  dir = "h5_mae",
  prefix = NULL,
  replace = FALSE,
  chunkdim = NULL,
  level = NULL,
  as.sparse = NA,
  verbose = NA
)

loadHDF5MultiAssayExperiment(dir = "h5_mae", prefix = NULL)
```

Arguments

x	A MultiAssayExperiment object or derivative
dir	The path (as a single string) to the directory where to save the HDF5-based MultiAssayExperiment object or to load it from. When saving, the directory will be created if it doesn't already exist. If the directory already exists and no prefix is specified and replace is set to TRUE, then it's replaced with an empty directory.
prefix	An optional prefix to add to the names of the files created inside dir. This allows saving more than one object in the same directory. When the prefix is NULL, the name of the x input MultiAssayExperiment is used. To avoid the default setting use an empty character string i.e., "". An underscore (_) is appended to the prefix when provided; therefore, typical inputs should be words, e.g., "test".
replace	When no prefix is specified, should a pre-existing directory be replaced with a new empty one? The content of the pre-existing directory will be lost!

chunkdim, level	The dimensions of the chunks and the compression level to use for writing the assay data to disk. Passed to the internal calls to writeHDF5Array. See ?writeHDF5Array for more information.
as.sparse	Whether the assay data should be flagged as sparse or not. If set to NA (the default), then the specific as.sparse value to use for each assay is determined by calling is_sparse() on them. Passed to the internal calls to writeHDF5Array. See ?writeHDF5Array for more information and an IMPORTANT NOTE.
verbose	Set to TRUE to make the function display progress. In the case of saveHDF5MultiAssayExperiment(), verbose is set to NA by default, in which case verbosity is controlled by DelayedArray.verbose.block.processing option. Setting verbose to TRUE or FALSE overrides the option.

Value

- saveHDF5MultiAssayExperiment: saves an Rds and h5 file to a directory from the input MultiAssayExperiment
- loadHDF5MultiAssayExperiment: a MultiAssayExperiment object loaded from a folder as saved by saveHDF5MultiAssayExperiment

Examples

```
data("miniACC")

testDir <- file.path(tempdir(), "test_mae")

saveHDF5MultiAssayExperiment(
    miniACC, dir = testDir, verbose = TRUE, replace = TRUE
)

## inspect the files in the dir
list.files(testDir)

loadHDF5MultiAssayExperiment(
    dir = testDir
)

## remove example files
unlink(testDir, recursive = TRUE)
```

---

listToMap *Convert map from data.frame or DataFrame to list and vice versa*

Description

The mapToList function provides a convenient way of reordering a data.frame to a list. The listToMap function does the opposite by taking a list and converting it to DataFrame.

Usage

```
listToMap(listmap, fill = TRUE)

mapToList(dfmap, assayCol = "assay")
```

Arguments

listmap	A named list object containing DataFrames with "primary" and "colname" columns
fill	logical(1) Whether to fill the map with an empty DataFrame when empty elements are present in the input list
dfmap	A data.frame or DataFrame object with identifiers in the first column
assayCol	A character vector of length one indicating the assay names column

Value

A DataFrame class object of names

A list object of DataFrames for each assay

Functions

- listToMap(): The inverse of the listToMap operation

Examples

```
example("MultiAssayExperiment")

## Create a sampleMap from a list using the listToMap function
sampMap <- listToMap(maplist)

## The inverse operation is also available
maplist <- mapToList(sampMap)
```

MatchedAssayExperiment-class

MatchedAssayExperiment - A matched-samples MultiAssayExperiment class

---

Description

This class supports the use of matched samples where an equal number of observations per biological unit are present in all assays.

Usage

```
MatchedAssayExperiment(...)
```

Arguments

...	Either a single MultiAssayExperiment or the components to create a valid MultiAssayExperiment

Value

A MatchedAssayExperiment object

Functions

- MatchedAssayExperiment(): Construct a MatchedAssayExperiment class from MultiAssayExperiment

See Also

MultiAssayExperiment

Examples

```
data("miniACC")
acc <- as(miniACC, "MatchedAssayExperiment")
acc
```

---

miniACC *Adrenocortical Carcinoma (ACC) MultiAssayExperiment*

Description

A MultiAssayExperiment object providing a reduced version of the TCGA ACC dataset for all 92 patients. RNA-seq, copy number, and somatic mutations are included only for genes whose proteins are included in the reverse-phase protein array. The MicroRNA-seq dataset is also included, with infrequently expressed microRNA removed. Clinical, pathological, and subtype information are provided by colData(miniACC), and some additional details are provided by metadata(miniACC).

Usage

```
data("miniACC")
```

Format

A MultiAssayExperiment with 5 experiments, providing:

RNASeq2GeneNorm RNA-seq count data: an ExpressionSet with 198 rows and 79 columns

gistict Reccurent copy number lesions identified by GISTIC2: a SummarizedExperiment with 198 rows and 90 columns

RPPAArray Reverse Phase Protein Array: an ExpressionSet with 33 rows and 46 columns. Rows are indexed by genes, but protein annotations are available from featureData(miniACC[["RPPAArray"]]). The source of these annotations is noted in abstract(miniACC[["RPPAArray"]])

Mutations Somatic mutations: a `matrix` with 223 rows and 90 columns. 1 for any kind of non-silent mutation, zero for silent (synonymous) or no mutation.

miRNASeqGene microRNA sequencing: an `ExpressionSet` with 471 rows and 80 columns. Rows not having at least 5 counts in at least 5 samples were removed.

Author(s)

Levi Waldron <lwaldron.research@gmail.com>

Source

https://github.com/waldronlab/multiassayexperiment-tcga

References

Zheng S *et al.*: Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell 2016, 29:723-736.

Examples

```
data("miniACC")
metadata(miniACC)
colnames(colData(miniACC))
table(miniACC$vital_status)
longForm(
    miniACC["MAPK3", , ],
    colDataCols = c("vital_status", "days_to_death")
)

wideFormat(
    miniACC["MAPK3", , ],
    colDataCols = c("vital_status", "days_to_death")
)
```

`MultiAssayExperiment` *Construct an integrative representation of multi-omic data with* `MultiAssayExperiment`

Description

The constructor function for the MultiAssayExperiment combines multiple data elements from the different hierarchies of data (study, experiments, and samples). It can create instances where neither a `sampleMap` or a `colData` set is provided. Please see the MultiAssayExperiment API documentation for more information.

Usage

```
MultiAssayExperiment(
  experiments = ExperimentList(),
  colData = S4Vectors::DataFrame(),
 sampleMap = S4Vectors::DataFrame(assay = factor(), primary = character(), colname =
    character()),
  metadata = list(),
  drops = list()
)
```

Arguments

experiments	A list or ExperimentList of all combined experiments
colData	A DataFrame or data.frame of characteristics for all biological units
sampleMap	A DataFrame or data.frame of assay names, sample identifiers, and colname samples
metadata	An optional argument of "ANY" class (usually list) for content describing the experiments
drops	A list of unmatched information (included after subsetting)

Value

A MultiAssayExperiment object that can store experiment and phenotype data

colData

The colData input can be either DataFrame or data.frame with subsequent coercion to DataFrame. The rownames in the colData must match the colnames in the experiments if no sampleMap is provided.

experiments

The experiments input can be of class SimpleList or list. This input becomes the ExperimentList. Each element of the input list or List must be named, rectangular with two dimensions, and have dimnames.

sampleMap

The sampleMap can either be input as DataFrame or data.frame with eventual coercion to DataFrame. The sampleMap relates biological units and biological measurements within each assay. Each row in the sampleMap is a single such link. The standard column names of the sampleMap are "assay", "primary", and "colname". Note that the "assay" column is a factor corresponding to the names of each experiment in the ExperimentList. In the case where these names do not match between the sampleMap and the experiments, the documented experiments in the sampleMap take precedence and experiments are dropped by the harmonization procedure. The constructor function will generate a sampleMap in the case where it is not provided and this method may be a 'safer' alternative for creating the MultiAssayExperiment (so long as the rownames are identical in the colData, if provided). An empty sampleMap may produce empty experiments if the levels of the "assay" factor in the sampleMap do not match the names in the ExperimentList.

See Also

MultiAssayExperiment

Examples

```
## Run the example ExperimentList
example("ExperimentList")

## Create sample maps for each experiment
exprmap <- data.frame(
    primary = c("Jack", "Jill", "Barbara", "Bob"),
    colname = c("array1", "array2", "array3", "array4"),
    stringsAsFactors = FALSE)

methylmap <- data.frame(
    primary = c("Jack", "Jack", "Jill", "Barbara", "Bob"),
    colname = c("methyl1", "methyl2", "methyl3", "methyl4", "methyl5"),
    stringsAsFactors = FALSE)

rnamap <- data.frame(
    primary = c("Jack", "Jill", "Bob", "Barbara"),
    colname = c("samparray1", "samparray2", "samparray3", "samparray4"),
    stringsAsFactors = FALSE)

gistmap <- data.frame(
    primary = c("Jack", "Bob", "Jill"),
    colname = c("samp0", "samp1", "samp2"),
    stringsAsFactors = FALSE)

## Combine as a named list and convert to a DataFrame
maplist <- list(Affy = exprmap, Methyl450k = methylmap,
    RNASeqGene = rnamap, GISTIC = gistmap)

## Create a sampleMap
sampMap <- listToMap(maplist)
## Create an example phenotype data
colDat <- data.frame(sex = c("M", "F", "M", "F"), age = 38:41,
    row.names = c("Jack", "Jill", "Bob", "Barbara"))

## Create a MultiAssayExperiment instance
mae <- MultiAssayExperiment(experiments = ExpList, colData = colDat,
    sampleMap = sampMap)
```

`MultiAssayExperiment-class`

MultiAssayExperiment - An integrative multi-assay class for experiment data

---

Description

The MultiAssayExperiment class can be used to manage results of diverse assays on a collection of specimen. Currently, the class can handle assays that are organized instances of SummarizedExperiment, ExpressionSet, matrix, RaggedExperiment (inherits from GRangesList), and RangedVcfStack. Create new MultiAssayExperiment instances with the homonymous constructor, minimally with the argument ExperimentList, potentially also with the arguments colData (see section below) and sampleMap.

Usage

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

## S4 method for signature 'MultiAssayExperiment'
length(x)

## S4 method for signature 'MultiAssayExperiment'
names(x)

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

## S4 method for signature 'MultiAssayExperiment'
dimnames(x)

## S4 method for signature 'MultiAssayExperiment'
c(x, ..., sampleMap = NULL, mapFrom = NULL)

## S4 method for signature 'MultiAssayExperiment'
exportClass(
  object,
  dir = tempdir(),
  fmt,
  ext,
  match = FALSE,
  verbose = TRUE,
  ...
)

## S4 method for signature 'MultiAssayExperiment'
assays(x, withDimnames = TRUE, ...)

## S4 method for signature 'MultiAssayExperiment,missing'
assay(x, i, withDimnames = TRUE, ...)

## S4 method for signature 'MultiAssayExperiment,numeric'
assay(x, i, withDimnames = TRUE, ...)
```

```
## S4 method for signature 'MultiAssayExperiment,character'
assay(x, i, withDimnames = TRUE, ...)
```

Arguments

object, x	A MultiAssayExperiment object
...	Additional arguments for supporting functions. See details.
verbose	logical(1) Whether to print additional information (default TRUE)
sampleMap	c method: a sampleMap list or DataFrame to guide merge
mapFrom	Either a logical, character, or integer vector indicating the experiment(s) that have an identical colname order as the experiment input(s). If using a character input, the name must match exactly.
dir	character(1) A directory for saving exported data (default: tempdir())
fmt	character(1) or function() Either a format character atomic as supported by write.table either ('csv', or 'tsv') or a function whose first two arguments are 'object to save' and 'file location'
ext	character(1) A file extension supported by the format argument
match	logical(1) Whether to coerce the current object to a 'MatchedAssayExperiment' object (default: FALSE)
withDimnames	logical (default TRUE) whether to return dimension names included in the object
i	An integer or character scalar indicating the assay to return

Details

The dots (...) argument allows the user to specify additional arguments in several instances.

- subsetting [: additional arguments sent to findOverlaps.
- mergeReplicates: used to specify arguments for the simplify functional argument
- assay: may contain withDimnames, which is forwarded to assays
- combining **c**: compatible MultiAssayExperiment classes passed on to the ExperimentList constructor, can be a list, List, or a series of named arguments. See the examples below.

Value

A MultiAssayExperiment object

Methods (by generic)

- show(MultiAssayExperiment): Show method for a MultiAssayExperiment
- length(MultiAssayExperiment): Get the length of ExperimentList
- names(MultiAssayExperiment): Get the names of the ExperimentList
- updateObject(MultiAssayExperiment): Update old serialized MultiAssayExperiment objects to new API

- dimnames(MultiAssayExperiment): Get the dimension names for a MultiAssayExperiment object
- c(MultiAssayExperiment): Add a supported data class to the ExperimentList
- exportClass(MultiAssayExperiment): Export data from class to a series of text files
- assays(MultiAssayExperiment): Obtain a SimpleList of assay data for all available experiments in the object
- assay(x = MultiAssayExperiment, i = missing): Convenience function for extracting the assay of the first element (default) in the ExperimentList. A numeric or character index can also be provided

Slots

ExperimentList A ExperimentList class object for each assay dataset

colData A DataFrame of all clinical/specimen data available across experiments

sampleMap A DataFrame of translatable identifiers of samples and participants

metadata Additional data describing the MultiAssayExperiment object

drops A metadata list of dropped information

colData

The colData slot is a collection of primary specimen data valid across all experiments. This slot is strictly of class DataFrame but arguments for the constructor function allow arguments to be of class data.frame and subsequently coerced.

ExperimentList

The ExperimentList slot is designed to contain results from each experiment/assay. It contains a SimpleList.

sampleMap

The sampleMap contains a DataFrame of translatable identifiers of samples and participants or biological units. The standard column names of the sampleMap are "assay", "primary", and "colname". Note that the "assay" column is a factor corresponding to the names of each experiment in the ExperimentList. In the case where these names do not match between the sampleMap and the experiments, the documented experiments in the sampleMap take precedence and experiments are dropped by the harmonization procedure. The constructor function will generate a sampleMap in the case where it is not provided and this method may be a 'safer' alternative for creating the MultiAssayExperiment (so long as the rownames are identical in the colData, if provided). An empty sampleMap may produce empty experiments if the levels of the "assay" factor in the sampleMap do not match the names in the ExperimentList.

coercion

Convert a list or S4 List to a MultiAssayExperiment object using the methods::as function.

In the following example, x is either a list or List:

```
as(x, "MultiAssayExperiment")
```

Convert a MultiAssayExperiment to MAF class object using the methods::as function.

In the following example, x is a MultiAssayExperiment:

```
MultiAssayExperimentToMAF(x)
```

See Also

MultiAssayExperiment-methods for slot modifying methods, MultiAssayExperiment API

Examples

```
example("MultiAssayExperiment")

## Subsetting
# Rows (i) Rows/Features in each experiment
mae[1, , ]
mae[c(TRUE, FALSE), , ]

# Columns (j) Rows in colData
mae[, rownames(colData(mae))[3:2],  ]

# Assays (k)
mae[, , "Affy"]

## Complete cases (returns logical vector)
completes <- complete.cases(mae)
compMAE <- mae[, completes, ]
compMAE
colData(compMAE)

example("MultiAssayExperiment")

## Add an experiment
test1 <- mae[[1L]]
colnames(test1) <- rownames(colData(mae))

## Combine current MultiAssayExperiment with additional experiment
## (no sampleMap)
c(mae, newExperiment = test1)

test2 <- mae[[3L]]
c(mae, newExp = test2, mapFrom = 3L)

## Add experiment using experiment name in mapFrom
c(mae, RNASeqGeneV2 = test2, mapFrom = "RNASeqGene")
```

MultiAssayExperiment-helpers

A group of helper functions for manipulating and cleaning a MultiAssayExperiment

---

Description

A set of helper functions were created to help clean and manipulate a MultiAssayExperiment object. `intersectRows` also works for `ExperimentList` objects.

- complete.cases: Returns a logical vector corresponding to 'colData' rows that have data across all experiments
- isEmpty: Returns a logical `TRUE` value for zero length `MultiAssayExperiment` objects
- intersectRows: Takes all common rows across experiments, excludes experiments with empty rownames
- intersectColumns: A wrapper for `complete.cases` to return a `MultiAssayExperiment` with only those biological units that have measurements across all experiments
- replicated: Identifies, via logical vectors, `colnames` that originate from a single biological unit within each assay
- replicates: Provides the replicate `colnames` found with the `replicated` function by their name, empty list if none
- anyReplicated: Whether the assay has replicate measurements
- showReplicated: Displays the actual columns that are replicated per assay and biological unit, i.e., `primary` value (`colData` rowname) in the `sampleMap`
- mergeReplicates: A function that combines replicated / repeated measurements across all experiments and is guided by the replicated return value
- longForm: A `MultiAssayExperiment` method that returns a small and skinny `DataFrame`. The `colDataCols` arguments allows the user to append `colData` columns to the data.
- wideFormat: A function to reshape the data in a `MultiAssayExperiment` to a "wide" format `DataFrame`. Each row in the `DataFrame` represents an observation (corresponding to an entry in the `colData`). If replicates are present, their data will be appended at the end of the corresponding row and will generate additional `NA` data. It is recommended to remove or consolidate technical replicates with `mergeReplicates`. Optional `colDataCols` can be added when the original object is a `MultiAssayExperiment`.
- hasRowRanges: A function that identifies ExperimentList elements that have a `rowRanges` method
- hasRowData: A function that identifies ExperimentList elements that have a `rowData` method
- getWithColData: A convenience function for extracting an assay and associated colData
- renamePrimary: A convenience function to rename the primary biological units as represented in the `rownames(colData)`
- renameColname: A convenience function to rename the colnames of a particular assay

Usage

```
## S4 method for signature 'MultiAssayExperiment'
complete.cases(...)

## S4 method for signature 'MultiAssayExperiment'
isEmpty(x)
```

```
intersectRows(x)

intersectColumns(x)

replicated(x)

## S4 method for signature 'MultiAssayExperiment'
replicated(x)

anyReplicated(x)

## S4 method for signature 'MultiAssayExperiment'
anyReplicated(x)

showReplicated(x)

## S4 method for signature 'MultiAssayExperiment'
showReplicated(x)

replicates(x, ...)

## S4 method for signature 'MultiAssayExperiment'
replicates(x, ...)

mergeReplicates(x, replicates = list(), simplify = BiocGenerics::mean, ...)

## S4 method for signature 'MultiAssayExperiment'
mergeReplicates(
  x,
  replicates = replicated(x),
  simplify = BiocGenerics::mean,
  ...
)

## S4 method for signature 'ANY'
mergeReplicates(x, replicates = list(), simplify = BiocGenerics::mean, ...)

## S4 method for signature 'MultiAssayExperiment'
longForm(object, colDataCols = NULL, i = 1L, ...)

## S4 method for signature 'ExperimentList'
longForm(object, colDataCols, i = 1L, ...)

## S4 method for signature 'ANY'
longForm(object, colDataCols, i = 1L, ...)

wideFormat(
  object,
```

```
  colDataCols = NULL,
  check.names = TRUE,
  collapse = "_",
  i = 1L
)

hasRowRanges(x)

## S4 method for signature 'MultiAssayExperiment'
hasRowRanges(x)

## S4 method for signature 'ExperimentList'
hasRowRanges(x)

hasRowData(x)

## S4 method for signature 'MultiAssayExperiment'
hasRowData(x)

## S4 method for signature 'ExperimentList'
hasRowData(x)

getWithColData(x, i, mode = c("append", "replace"), verbose = FALSE)

renamePrimary(x, value)

renameColname(x, i, value)

splitAssays(x, hitList)

## S4 method for signature 'MultiAssayExperiment'
splitAssays(x, hitList)

makeHitList(x, patternList)
```

Arguments

`...`	Additional arguments. See details for more information.
`x`	A MultiAssayExperiment or ExperimentList
`replicates`	A list of `LogicalList`s indicating multiple / duplicate entries for each biological unit per assay, see `replicated` (default `replicated(x)`).
`simplify`	A function for merging repeat measurements in experiments as indicated by the `replicated` method for `MultiAssayExperiment`
`object`	Any supported class object
`colDataCols`	A `character`, `logical`, or `numeric` index for `colData` columns to be included
`i`	longForm: The i-th assay in `SummarizedExperiment`-like objects. A vector input is supported in the case that the `SummarizedExperiment` object(s) has more

	than one assay (default 1L), renameColname: Either a `numeric` or `character` index indicating the assay whose colnames are to be renamed
`check.names`	`logical(1)` Column names of the output `DataFrame` will be run through `make.names` to ensure syntactic validity (default `TRUE`).
`collapse`	`character(1)` A single string delimiter (default "_") for output column names. In `wideFormat`, experiments and `rownames` (and when replicate samples are present, `colnames`) are separated by this delimiter
`mode`	String indicating how `MultiAssayExperiment` column-level metadata should be added to the `SummarizedExperiment` `colData`.
`verbose`	`logical(1)` Whether to `suppressMessages` on subsetting operations in `getWithColData` (default FALSE)
`value`	renamePrimary: A `character` vector of the same length as the existing `rownames(colData)` to use for replacement, renameColname: A `CharacterList` or `list` with matching `lengths` to replace `colnames(x)`
`hitList`	a named `list` or `List` of logical vectors that indicate groupings in the assays
`patternList`	a named `list` or `List` of atomic character vectors that are the input to `grepl` for identifying groupings in the assays

Details

The `replicated` function finds replicate measurements in each assay and returns a list of `LogicalList`s. Each element in a single `LogicalList` corresponds to a biological or *primary* unit as in the `sampleMap`. Below is a small graphic for one particular biological unit in one assay, where the logical vector corresponds to the number of measurements/samples in the assay:

```
>      replicated(MultiAssayExperiment)
(list str)       '-- $ AssayName
(LogicalList str)      '-- [[ "Biological Unit" ]]
Replicated if sum(...) > 1          '-- TRUE TRUE FALSE FALSE
```

`anyReplicated` determines if any of the assays have at least one replicate. *Note*. These methods are not available for the `ExperimentList` class due to a missing `sampleMap` structure (by design). `showReplicated` returns a list of `CharacterList`s where each element corresponds to the the biological or *primary* units that are replicated in that assay element. The values in the inner list are the `colnames` in the assay that are technical replicates.

The `replicates` function (noun) returns the `colnames` from the `sampleMap` that were identified as replicates. It returns a list of `CharacterList`s for each assay present in the `MultiAssayExperiment` and an inner entry for each biological unit that has replicate observations in that assay.

The `mergeReplicates` function is a house-keeping method for a `MultiAssayExperiment` where only `complete.cases` are returned. This by-assay operation averages replicate measurements (by default) and columns are aligned by the row order in `colData`. Users can provide their own function for merging replicates with the `simplify` functional argument. Additional inputs `...` are sent to the 'simplify' function.

The `mergeReplicates` "ANY" method consolidates duplicate measurements for rectangular data structures, returns object of the same class (endomorphic). The ellipsis or `...` argument allows the user to provide additional arguments to the `simplify` functional argument.

The longForm "ANY" class method, works with classes such as ExpressionSet and SummarizedExperiment as well as matrix to provide a consistent long and skinny DataFrame.

The hasRowRanges method identifies assays that support a rowRanges method *and* return a GRanges object.

The hasRowData method identifies assays that support a rowData method *and* return a DataFrame object.

Value

See the itemized list in the description section for details.

Functions

- hasRowData(MultiAssayExperiment): The hasRowData method identifies experiments that have a rowData method via direct testing
- hasRowData(ExperimentList): The hasRowData method identifies experiments that have a rowData method via direct testing

mergeReplicates

The mergeReplicates function makes use of the output from replicated which will point out the duplicate measurements by biological unit in the MultiAssayExperiment. This function will return a MultiAssayExperiment with merged replicates. Additional arguments can be provided to the simplify argument via the ellipsis (...). For example, when replicates "TCGA-B" and "TCGA-A" are found in the assay, the name of the first appearing replicate is taken (i.e., "B"). Note that a typical use case of merging replicates occurs when there are multiple measurements on the **same** sample (within the same assay) and can therefore be averaged.

longForm

The 'longForm' method takes data from the ExperimentList in a MultiAssayExperiment and returns a uniform DataFrame. The resulting DataFrame has columns indicating primary, rowname, colname and value. This method can optionally include columns of the MultiAssayExperiment colData named by colDataCols character vector argument. (MultiAssayExperiment method only). The i argument allows the user to specify the assay value for the SummarizedExperiment assay function's i argument.

wideFormat

The wideFormat function returns standardized wide DataFrame where each row represents a biological unit as in the colData. Depending on the data and setup, biological units can be patients, tumors, specimens, etc. Metadata columns are generated based on the names produced in the wide format DataFrame. These can be accessed via the mcols() function. See the wideFormat section for description of the colDataCols and i arguments.

hasRowRanges

The hasRowRanges method identifies assays with associated ranged row data by directly testing the method on the object. The result from the test must be a GRanges class object to satisfy the test.

getWithColData

The `getWithColData` function allows the user to conveniently extract a particular assay as indicated by the `i` index argument. It will also attempt to provide the `colData` along with the extracted object using the `colData<-` replacement method when possible. Typically, this method is available for `SummarizedExperiment` and `RaggedExperiment` classes.

The setting of `mode` determines how the `colData` is added. If `mode="append"`, the `MultiAssayExperiment` metadata is appended onto that of the `SummarizedExperiment`. If any fields are duplicated by name, the values in the `SummarizedExperiment` are retained, with a warning emitted if the values are different. For `mode="replace"`, the `MultiAssayExperiment` metadata replaces that of the `SummarizedExperiment`, while for `mode="none"`, no replacement or appending is performed.

rename*

The `renamePrimary` function allows the user to conveniently change the actual names of the primary biological units as seen in `rownames(colData)`. `renameColname` allows the user to change the names of a particular assay based on index `i`. `i` can either be a single numeric or character value. See `colnames<-` method for renaming multiple colnames in a `MultiAssayExperiment`.

splitAssays

The `splitAssays` method separates columns in each of the assays based on the `hitList` input. The `hitList` can be generated using the `makeHitList` helper function. To use the `makeHitList` helper, the user should input a list of patterns that will match on the column names of each assay. These matches should be mutually exclusive as to avoid repetition of columns across assays. See the examples section.

Examples

```
example(MultiAssayExperiment)

complete.cases(mae)

isEmpty(MultiAssayExperiment())


## renaming biological units (primary)

mae2 <- renamePrimary(mae, paste0("pt", 1:4))
colData(mae2)
sampleMap(mae2)


## renaming observational units (colname)

mae2 <- renameColname(mae, i = "Affy", paste0("ARRAY", 1:4))
colnames(mae2)
sampleMap(mae2)


patts <- list(
```

```
    normals = "TCGA-[A-Z0-9]{2}-[A-Z0-9]{4}-11",
    tumors = "TCGA-[A-Z0-9]{2}-[A-Z0-9]{4}-01"
)

data("miniACC")

hits <- makeHitList(miniACC, patts)

## only turmors present
splitAssays(miniACC, hits)
```

MultiAssayExperiment-methods

Accessing and modifying information in MultiAssayExperiment

Description

A set of accessor and setter generic functions to extract either the sampleMap, the ExperimentList, colData, or metadata slots of a MultiAssayExperiment object

Usage

```
## S4 method for signature 'MultiAssayExperiment'
sampleMap(x)

## S4 method for signature 'MultiAssayExperiment'
experiments(x)

## S4 method for signature 'MultiAssayExperiment'
colData(x, ...)

## S4 method for signature 'MultiAssayExperiment'
drops(x)

## S4 replacement method for signature 'MultiAssayExperiment,DataFrame'
sampleMap(object) <- value

## S4 replacement method for signature 'MultiAssayExperiment,ANY'
sampleMap(object) <- value

drops(x, ...) <- value

## S4 replacement method for signature 'MultiAssayExperiment,ExperimentList'
experiments(object) <- value

## S4 replacement method for signature 'MultiAssayExperiment,List'
experiments(object) <- value
```

```
## S4 replacement method for signature 'MultiAssayExperiment,DataFrame'
colData(x, ...) <- value

## S4 replacement method for signature 'MultiAssayExperiment,ANY'
colData(x, ...) <- value

## S4 replacement method for signature 'MultiAssayExperiment'
drops(x, ...) <- value

## S4 replacement method for signature 'MultiAssayExperiment'
x$name <- value

## S4 replacement method for signature 'MultiAssayExperiment'
names(x) <- value

## S4 replacement method for signature 'MultiAssayExperiment,List'
colnames(x) <- value

## S4 replacement method for signature 'MultiAssayExperiment,list'
colnames(x) <- value

## S4 method for signature 'MultiAssayExperiment'
x$name

## S4 method for signature 'MultiAssayExperiment'
metadata(x, ...)

## S4 replacement method for signature 'MultiAssayExperiment'
metadata(x, ...) <- value
```

Arguments

...	Argument not in use
object, x	A MultiAssayExperiment object
value	See details.
name	A column in colData

Value

Accessors: Either a sampleMap, ExperimentList, or DataFrame object

Setters: A MultiAssayExperiment object

Accessors

Eponymous names for accessing MultiAssayExperiment slots with the exception of the ExperimentList accessor named experiments.

- colData: Access the `colData` slot
- sampleMap: Access the `sampleMap` slot
- experiments: Access the `ExperimentList` slot
- `[[`: Access the `ExperimentList` slot
- `$`: Access a column in `colData`
- `drops`: Get a vector of dropped `ExperimentList` names

Setters

Setter method values (i.e., '`function(x) <- value`'):

- experiments<-: An `ExperimentList` object containing experiment data of supported classes
- sampleMap<-: A `DataFrame` object relating samples to biological units and assays
- colData<-: A `DataFrame` object describing the biological units
- metadata<-: A `list` object of metadata
- `[[<-`: Equivalent to the `experiments<-` setter method for convenience
- `$<-`: A vector to replace the indicated column in `colData`
- `drops<-`: Trace `ExperimentList` names that have been removed

Examples

```
## Load example MultiAssayExperiment
example(MultiAssayExperiment)

## Access the sampleMap
sampleMap(mae)

## Replacement method for a MultiAssayExperiment sampleMap
sampleMap(mae) <- S4Vectors::DataFrame()

## Access the ExperimentList
experiments(mae)

## Replace with an empty ExperimentList
experiments(mae) <- ExperimentList()

## Access the metadata
metadata(mae)

## Replace metadata with a list
metadata(mae) <- list(runDate =
    format(Sys.time(), "%B %d, %Y"))

## Access the colData
colData(mae)

## Access a column in colData
mae$age
```

```
## Replace a column in colData
mae$age <- mae$age + 1
```

MultiAssayExperimentToMAF *Convert MultiAssayExperiment to MAF class*

Description

Take a MultiAssayExperiment object with specific mutation assays and convert these into a maftools representation. The names provided via synAssay and nonSynAssay must match exactly those assays in the MultiAssayExperiment.

Usage

```
MultiAssayExperimentToMAF(x, synAssay = "maf_syn", nonSynAssay = "maf_nonSyn")
```

Arguments

x	A MultiAssayExperiment object
synAssay	character(1) The name of the ExperimentList element in the MultiAssayExperiment that identifies synonymous variant classifications (default "maf_syn").
nonSynAssay	character(1) The name of the ExperimentList element in the MultiAssayExperiment that identifies non-synonymous variant classifications (default "maf_nonSyn").

Value

A MAF class object

See Also

?maftools::MAF

---

prepMultiAssay *Prepare a* MultiAssayExperiment *instance*

Description

The purpose of this helper function is to faciltate the creation of a MultiAssayExperiment object by detecting any inconsistencies with all types of names in either the ExperimentList, the colData, or sampleMap.

Usage

```
prepMultiAssay(ExperimentList, colData, sampleMap, ...)
```

Arguments

ExperimentList	A list of all combined experiments
colData	A DataFrame of the phenotype data for all participants
sampleMap	A DataFrame of sample identifiers, assay samples, and assay names
...	Optional arguments for the MultiAssayExperiment constructor function such as metadata and drops.

Value

A list containing all the essential components of a MultiAssayExperiment as well as a "drops" metadata element that indicates non-matched names. The names of the resulting list correspond to the arguments of the MultiAssayExperiment constructor function.

Checks

The prepMultiAssay function checks that all columns in the sampleMap are character.

It checks that all names and lengths match in both the ExperimentList and in the unique assay names of the sampleMap.

If ExperimentList names and assay names only differ by case and are not duplicated, the function will standardize all names to lowercase.

If names cannot be matched between the colname column of the sampleMap and the colnames of the ExperimentList, those unmatched will be dropped and found in the "drops" element of the resulting list.

Names in the "primary" column of the sampleMap, will be matched to those in the colData. Unmatched "primary" column rows will be dropped from the sampleMap. Suggestions for name fixes in either the ExperimentList or colnames will be made when necessary.

Examples

```
## Run example
example("MultiAssayExperiment")

## Check if there are any inconsistencies within the different names
preparedMAE <- prepMultiAssay(ExpList, colDat, sampMap)

## Results in a list of components for the MultiAssayExperiment constructor
## function
MultiAssayExperiment(preparedMAE$experiments, preparedMAE$colData,
preparedMAE$sampleMap)

## Alternatively, use the do.call function
do.call(MultiAssayExperiment, preparedMAE)
```

reexports *Objects exported from other packages*

Description

These objects are imported from other packages. Click on the function name to see their documentation.

- S4Vectors::DataFrame

Value

- S4Vectors::DataFrame: A DataFrame class object

Examples

```
DataFrame()
```

subsetBy *Subsetting a MultiAssayExperiment object*

Description

A set of functions for extracting and dividing a MultiAssayExperiment

Usage

```
subsetByRow(x, y, ...)

subsetByRowData(x, y, rowDataCol, ...)

subsetByColData(x, y)

subsetByColumn(x, y)

subsetByAssay(x, y)

## S4 method for signature 'ExperimentList,ANY'
subsetByRow(x, y, ...)

## S4 method for signature 'ExperimentList,list'
subsetByRow(x, y, ...)

## S4 method for signature 'ExperimentList,List'
subsetByRow(x, y, ...)
```

```
## S4 method for signature 'ExperimentList,logical'
subsetByRow(x, y, ...)

## S4 method for signature 'ExperimentList,list'
subsetByColumn(x, y)

## S4 method for signature 'ExperimentList,List'
subsetByColumn(x, y)

## S4 method for signature 'ExperimentList,logical'
subsetByColumn(x, y)

## S4 method for signature 'ExperimentList'
subsetByAssay(x, y)

## S4 method for signature 'MultiAssayExperiment,ANY'
subsetByColData(x, y)

## S4 method for signature 'MultiAssayExperiment,character'
subsetByColData(x, y)

## S4 method for signature 'MultiAssayExperiment,ANY'
subsetByRow(x, y, i = TRUE, ...)

## S4 method for signature 'MultiAssayExperiment,list'
subsetByRow(x, y, ...)

## S4 method for signature 'MultiAssayExperiment,List'
subsetByRow(x, y, ...)

## S4 method for signature 'MultiAssayExperiment,ANY'
subsetByColumn(x, y)

## S4 method for signature 'MultiAssayExperiment'
subsetByAssay(x, y)

## S4 method for signature 'MultiAssayExperiment,character,character'
subsetByRowData(x, y, rowDataCol, i = TRUE, ...)

intersectByRowData(x, y, rowDataCol, i, ...)

## S4 method for signature 'MultiAssayExperiment,character,character'
intersectByRowData(x, y, rowDataCol, i = TRUE, ...)

## S4 method for signature 'MultiAssayExperiment,ANY,ANY,ANY'
x[i, j, k, ..., drop = FALSE]
```

```
## S4 method for signature 'MultiAssayExperiment,ANY,ANY'
x[[i, j, ...]]

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

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

Arguments

x	A MultiAssayExperiment or ExperimentList
y	Either a character, integer, logical, list, List, or GRanges object for subsetting by rows *within the experiments*
...	Additional arguments passed on to lower level functions.
rowDataCol	character(1) The name of the column in the rowData. If the column is not present, the experiment will be skipped. When rowDataCol is "rownames" or "row.names", the values of y will be matched with the row names in the rowData of the experiment.
i	For the subsetByRow and subsetByRowData MultiAssayExperiment methods, either a character, logical, or numeric vector to selectively subset experiments with y (default is TRUE). For **bracket** ([) methods, see y input.
j	Either a character, logical, or numeric vector for subsetting by colData rows. See details for more information.
k	Either a character, logical, or numeric vector for subsetting by assays
drop	logical (default FALSE) whether to drop all empty assay elements in the ExperimentList
value	An assay compatible with the MultiAssayExperiment API

Details

Subsetting a MultiAssayExperiment by the **j** index can yield a call to either subsetByColData or subsetByColumn. For vector inputs, the subset will be applied to the colData rows. For List-type inputs, the List will be applied to each of the elements in the ExperimentList. The order of the subsetting elements in the List must match that of the ExperimentList in the MultiAssayExperiment.

- subsetBycolData: Select biological units by vector input types
- subsetByColumn: Select observations by assay or for each assay
- subsetByRow: Select rows by assay or for each assay
- subsetByAssay: Select experiments
- subsetByRowData: Select rows by values in the rowData
- intersectByRowData: Intersect with values in the rowData

Value

subsetBy*: operations are endomorphic and return either MultiAssayExperiment or ExperimentList depending on the input.

rowData

Some assays may have additional metadata associated with the rows. This metadata is stored in the `rowData` slot of the object, typically a `SummarizedExperiment` or `RangedSummarizedExperiment`.

`subsetByRowData` allows the user to subset the rows of the assays based on the values in the `rowData`.

`intersectByRowData` is a special case of `subsetByRowData` where the `rowData` values are intersected with the `y` values. Naturally, the `y` values are expected to be of type `character`.

Note that `rowDataCol` allows the user to specify a particular column from which to extract the values for subsetting. This column name must be consistent across assays. If the column is not present in an assay, the assay will be skipped and considered a no-op. Assays are also skipped when there are no values in the `rowData` that match the `y` values.

Note that the use of `rownames` or `row.names` as the `rowDataCol` requires that the assay class have a `rownames()` method.

Examples

```
## Load the example MultiAssayExperiment
example("MultiAssayExperiment")

## Using experiment names
subsetByAssay(mae, "Affy")

## Using numeric indices
subsetByAssay(mae, 1:2)

## Using a logical vector
subsetByAssay(mae, c(TRUE, FALSE, TRUE))

## Subset by character vector (Jack)
subsetByColData(mae, "Jack")

## Subset by numeric index of colData rows (Jack and Bob)
subsetByColData(mae, c(1, 3))

## Subset by logical indicator of colData rows (Jack and Jill)
subsetByColData(mae, c(TRUE, TRUE, FALSE, FALSE))

subsetByColumn(mae, list(Affy = 1:2,
    Methyl450k = c(3,5,2), RNASeqGene = 2:4, GISTIC = 1))

subsetWith <- S4Vectors::mendoapply(`[`, colnames(mae),
    MoreArgs = list(1:2))
subsetByColumn(mae, subsetWith)

## Use a GRanges object to subset rows where ranged data present
egr <- GenomicRanges::GRanges(seqnames = "chr2",
    IRanges::IRanges(start = 11, end = 13), strand = "-")
subsetByRow(mae, egr)

## Use a logical vector (recycling used)
```

```
subsetByRow(mae, c(TRUE, FALSE))

## Use a character vector
subsetByRow(mae, "ENST00000355076")

## Use i index to selectively subsetByRow
subsetByRow(mae, "ENST00000355076", i = c(TRUE, TRUE, FALSE, FALSE))

## only subset assays with rowRanges with GRanges input
subsetByRow(mae, egr, i = hasRowRanges(mae))

## Use i index to selectively subsetByRowData
subsetByRowData(
    mae, "ENST00000355076", "rownames", i = "Affy"
)

## use miniACC as example MAE
data("miniACC")

## intersect values of y with rownames in rowData
intersectByRowData(
    x = miniACC,
    y = c("G6PD", "PETN"),
    rowDataCol = "rownames",
    i = c("RNASeq2GeneNorm", "gistict")
)

## no-op when rowDataCol is not present or there is no data
intersectByRowData(
    x = miniACC, y = c("G6PD", "PETN"), rowDataCol = "Genes",
    i = c("RNASeq2GeneNorm", "gistict")
)
```

`upsetSamples` *Create a generalized Venn Diagram analog for sample membership in multiple assays, using the upset algorithm in* `UpSetR`

Description

Create a generalized Venn Diagram analog for sample membership in multiple assays, using the upset algorithm in `UpSetR`

Usage

```
upsetSamples(
  MultiAssayExperiment,
  nsets = NULL,
  sets = names(MultiAssayExperiment),
  nintersects = NA_integer_,
  order.by = "freq",
```

```
  check.names = FALSE,
  ...
)
```

Arguments

MultiAssayExperiment	A MultiAssayExperiment object
nsets	numeric(1) The number of sets to analyze. If specified, sets will be ignored.
sets	character() A character vector of names in MultiAssayExperiment to use. If specified, nsets will be ignored.
nintersects	numeric(1) The number of intersections to plot. By default, all intersections will be plotted.
order.by	How the intersections in the matrix should be ordered by. Options include frequency (entered as "freq"), degree, or both in any order.
check.names	logical(1) Whether to munge names as in the data.frame() constructor (default FALSE).
...	parameters passed to UpSetR::upset

Value

Produces a visualization of set intersections using the UpSet matrix design

Note

This function is intended to provide convenient visualization of assay availability configurations in MultiAssayExperiment instances. The UpSetR::upset function requires data.frame input and has many parameters to tune appearance of the result. Assay name handling is important for interpretability.

Author(s)

Vincent J Carey

Examples

```
data(miniACC)
upsetSamples(miniACC)
upsetSamples(miniACC, nsets = 3, nintersects = 3)
```

Index

∗ **data**
miniACC, 11
[,MultiAssayExperiment,ANY,ANY,ANY-method (subsetBy), 30
[,MultiAssayExperiment,ANY-method (subsetBy), 30
[<-,MultiAssayExperiment,ANY,ANY,ANY-method (subsetBy), 30
[[,MultiAssayExperiment,ANY,ANY-method (subsetBy), 30
[[<-,MultiAssayExperiment,ANY,ANY-method (subsetBy), 30
$,MultiAssayExperiment-method (MultiAssayExperiment-methods), 25
$<-,MultiAssayExperiment-method (MultiAssayExperiment-methods), 25

anyReplicated (MultiAssayExperiment-helpers), 18
anyReplicated,MultiAssayExperiment-method (MultiAssayExperiment-helpers), 18
assay,ANY,missing-method (ExperimentList-class), 5
assay,ExperimentList,character-method (ExperimentList-class), 5
assay,ExperimentList,missing-method (ExperimentList-class), 5
assay,ExperimentList,numeric-method (ExperimentList-class), 5
assay,MultiAssayExperiment,character-method (MultiAssayExperiment-class), 14
assay,MultiAssayExperiment,missing-method (MultiAssayExperiment-class), 14
assay,MultiAssayExperiment,numeric-method (MultiAssayExperiment-class), 14
assays,ExperimentList-method (ExperimentList-class), 5
assays,MultiAssayExperiment-method (MultiAssayExperiment-class), 14

c,MultiAssayExperiment-method (MultiAssayExperiment-class), 14
CharacterList, *6*, *22*
coerce,List,ExperimentList-method (ExperimentList-class), 5
coerce,list,ExperimentList-method (ExperimentList-class), 5
coerce,List,MultiAssayExperiment-method (MultiAssayExperiment-class), 14
coerce,list,MultiAssayExperiment-method (MultiAssayExperiment-class), 14
coerce,MultiAssayExperiment,MatchedAssayExperiment-method (MatchedAssayExperiment-class), 10
coerce-ExperimentList (ExperimentList-class), 5
coerce-MultiAssayExperiment (MultiAssayExperiment-class), 14
colData, *24*
colData,MultiAssayExperiment-method (MultiAssayExperiment-methods), 25
colData<-,MultiAssayExperiment,ANY-method (MultiAssayExperiment-methods), 25
colData<-,MultiAssayExperiment,DataFrame-method (MultiAssayExperiment-methods), 25

colnames,ExperimentList-method
(ExperimentList-class), 5
colnames<-,MultiAssayExperiment,List-method
(MultiAssayExperiment-methods), 25
colnames<-,MultiAssayExperiment,list-method
(MultiAssayExperiment-methods), 25
complete.cases,MultiAssayExperiment-method
(MultiAssayExperiment-helpers), 18

DataFrame, *10*, *13*, *17*, *19*, *23*, *27*, *29*
DataFrame (reexports), 30
dimnames,ExperimentList-method
(ExperimentList-class), 5
dimnames,MultiAssayExperiment-method
(MultiAssayExperiment-class), 14
drops (MultiAssayExperiment-methods), 25
drops,MultiAssayExperiment-method
(MultiAssayExperiment-methods), 25
drops<- (MultiAssayExperiment-methods), 25
drops<-,MultiAssayExperiment-method
(MultiAssayExperiment-methods), 25

ExperimentList, 4, *6–8*, *13*, *15–17*, *23*, *25–29*
ExperimentList-class, 5
experiments
(MultiAssayExperiment-methods), 25
experiments,MultiAssayExperiment-method
(MultiAssayExperiment-methods), 25
experiments<-
(MultiAssayExperiment-methods), 25
experiments<-,MultiAssayExperiment,ExperimentList-method
(MultiAssayExperiment-methods), 25
experiments<-,MultiAssayExperiment,List-method
(MultiAssayExperiment-methods), 25
exportClass
(MultiAssayExperiment-class), 14
exportClass,MultiAssayExperiment-method
(MultiAssayExperiment-class), 14
ExpressionSet, *15*, *23*

findOverlaps, *16*

getWithColData
(MultiAssayExperiment-helpers), 18
GRanges, *23*
GRangesList, *15*

hasAssay, 7
hasRowData
(MultiAssayExperiment-helpers), 18
hasRowData,ExperimentList-method
(MultiAssayExperiment-helpers), 18
hasRowData,MultiAssayExperiment-method
(MultiAssayExperiment-helpers), 18
hasRowRanges
(MultiAssayExperiment-helpers), 18
hasRowRanges,ExperimentList-method
(MultiAssayExperiment-helpers), 18
hasRowRanges,MultiAssayExperiment-method
(MultiAssayExperiment-helpers), 18
HDF5MultiAssayExperiment, 8

intersectByRowData (subsetBy), 30
intersectByRowData,MultiAssayExperiment,character,characte
(subsetBy), 30
intersectColumns
(MultiAssayExperiment-helpers), 18
intersectRows
(MultiAssayExperiment-helpers), 18
isEmpty,ExperimentList-method
(ExperimentList-class), 5
isEmpty,MultiAssayExperiment-method
(MultiAssayExperiment-helpers), 18

length,MultiAssayExperiment-method
(MultiAssayExperiment-class), 14
List, 7, 16, 17
listToMap, 9
loadHDF5MultiAssayExperiment
(HDF5MultiAssayExperiment), 8
LogicalList, 6, 21, 22
longForm,ANY-method
(MultiAssayExperiment-helpers), 18
longForm,ExperimentList-method
(MultiAssayExperiment-helpers), 18
longForm,MultiAssayExperiment-method
(MultiAssayExperiment-helpers), 18

makeHitList
(MultiAssayExperiment-helpers), 18
makeMatchList
(MultiAssayExperiment-helpers), 18
mapToList (listToMap), 9
MatchedAssayExperiment
(MatchedAssayExperiment-class), 10
MatchedAssayExperiment-class, 10
mcols(), 23
mergeReplicates
(MultiAssayExperiment-helpers), 18
mergeReplicates,ANY-method
(MultiAssayExperiment-helpers), 18
mergeReplicates,ExperimentList-method
(ExperimentList-class), 5
mergeReplicates,MultiAssayExperiment-method
(MultiAssayExperiment-helpers), 18
metadata,MultiAssayExperiment-method
(MultiAssayExperiment-methods), 25
metadata<-,MultiAssayExperiment-method
(MultiAssayExperiment-methods), 25
methods::as, 17, 18
miniACC, 11
MultiAssayExperiment, 8, 11, 12, 12, 14, 25, 28, 29
MultiAssayExperiment-class, 14
MultiAssayExperiment-helpers, 18
MultiAssayExperiment-methods, 18, 25
MultiAssayExperiment-package, 3
MultiAssayExperimentToMAF, 28

names,MultiAssayExperiment-method
(MultiAssayExperiment-class), 14
names<-,MultiAssayExperiment-method
(MultiAssayExperiment-methods), 25

prepMultiAssay, 28

reexports, 30
renameColname
(MultiAssayExperiment-helpers), 18
renamePrimary
(MultiAssayExperiment-helpers), 18
replicated
(MultiAssayExperiment-helpers), 18
replicated,MultiAssayExperiment-method
(MultiAssayExperiment-helpers), 18
replicates
(MultiAssayExperiment-helpers), 18
replicates,MultiAssayExperiment-method
(MultiAssayExperiment-helpers), 18
rowData, 19, 23
rownames, 6
rownames,ExperimentList-method
(ExperimentList-class), 5
rowRanges, 19, 23

S4Vectors::DataFrame, 30
sampleMap, 13, 15, 17, 28, 29
sampleMap
(MultiAssayExperiment-methods), 25
sampleMap,MultiAssayExperiment-method
(MultiAssayExperiment-methods), 25

sampleMap<-
(MultiAssayExperiment-methods), 25
sampleMap<-,MultiAssayExperiment,ANY-method
(MultiAssayExperiment-methods), 25
sampleMap<-,MultiAssayExperiment,DataFrame-method
(MultiAssayExperiment-methods), 25
saveHDF5MultiAssayExperiment
(HDF5MultiAssayExperiment), 8
show,ExperimentList-method
(ExperimentList-class), 5
show,MultiAssayExperiment-method
(MultiAssayExperiment-class), 14
showReplicated
(MultiAssayExperiment-helpers), 18
showReplicated,MultiAssayExperiment-method
(MultiAssayExperiment-helpers), 18
SimpleList, *13*, *17*
splitAssays
(MultiAssayExperiment-helpers), 18
splitAssays,MultiAssayExperiment-method
(MultiAssayExperiment-helpers), 18
subset (subsetBy), 30
subsetBy, 30
subsetByAssay (subsetBy), 30
subsetByAssay,ExperimentList-method
(subsetBy), 30
subsetByAssay,MultiAssayExperiment-method
(subsetBy), 30
subsetByColData (subsetBy), 30
subsetByColData,MultiAssayExperiment,ANY-method
(subsetBy), 30
subsetByColData,MultiAssayExperiment,character-method
(subsetBy), 30
subsetByColumn (subsetBy), 30
subsetByColumn,ExperimentList,List-method
(subsetBy), 30
subsetByColumn,ExperimentList,list-method
(subsetBy), 30
subsetByColumn,ExperimentList,logical-method
(subsetBy), 30
subsetByColumn,MultiAssayExperiment,ANY-method
(subsetBy), 30
subsetByRow (subsetBy), 30
subsetByRow,ExperimentList,ANY-method
(subsetBy), 30
subsetByRow,ExperimentList,List-method
(subsetBy), 30
subsetByRow,ExperimentList,list-method
(subsetBy), 30
subsetByRow,ExperimentList,logical-method
(subsetBy), 30
subsetByRow,MultiAssayExperiment,ANY-method
(subsetBy), 30
subsetByRow,MultiAssayExperiment,List-method
(subsetBy), 30
subsetByRow,MultiAssayExperiment,list-method
(subsetBy), 30
subsetByRowData (subsetBy), 30
subsetByRowData,MultiAssayExperiment,character,character-m
(subsetBy), 30
SummarizedExperiment, *15*, *23*, *24*

updateObject,MultiAssayExperiment-method
(MultiAssayExperiment-class), 14
UpSetR::upset, *35*
upsetSamples, 34

wideFormat
(MultiAssayExperiment-helpers), 18
writeHDF5Array, *9*