Package 'MultiAssayExperiment'

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

Version 1.12.6

Description MultiAssayExperiment harmonizes data management of multiple 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.

Depends R (>= 3.6.0), SummarizedExperiment (>= 1.3.81)

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

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R topics documented:

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

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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

Author(s)

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- MultiAssay SIG <biocmultiassay@googlegroups.com> [contributor]

See Also

Useful links:

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

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`ExperimentList` *Construct an* `ExperimentList` *object for the* `MultiAssayExperiment` *object slot.*

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` *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.

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

## S4 method for signature 'ANY,missing'
```

```
assay(x, i, ...)

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

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

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

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

Arguments

object, x	An ExperimentList object
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

Details

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)

Methods (by generic)

- show: Show method for ExperimentList class
- isEmpty: check for zero length across all experiments
- dimnames: Get the dimension names for an ExperimentList using CharacterList
- mergeReplicates: Apply the mergeReplicates method on the ExperimentList elements
- assay: Obtain the specified assay with a numberic or character reference
- assays: 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:

```
\code{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)
```

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)

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

Arguments

listmap	A named list object containing DataFrames with "primary" and "colname" columns
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` *An integrative and matched-samples class for experiment data*

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 inputs.

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

```
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

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

##
## The following is the code used to create this mini dataset from the full ACC dataset.
## The full ACC MultiAssayExperiment was created by the pipeline at
## https://github.com/waldronlab/multiassayexperiment-tcga.
## Not run:
    ## See www.tinyurl.com/MAEOurls for more pre-built TCGA MultiAssayExperiment objects
    download.file("http://s3.amazonaws.com/multiassayexperiments/accMAEO.rds",
                  destfile = "accMAEO.rds")
    library(MultiAssayExperiment)
    library(RaggedExperiment) #needed for RaggedExperiment objects by updateObject()
    library(Biobase)

    acc <- readRDS("accMAEO.rds")
    acc <- updateObject(acc)
    protmap <- read.csv(paste0("http://genomeportal.stanford.edu/",
                        "pan-tcga/target_selection_send_data",
                        "?filename=Allprotein.txt"), as.is = TRUE
        )

    RPPAgenes <- Filter(function(x) x != "", protmap$Genes)
    RPPAgenes <- unlist(strsplit(RPPAgenes, ","))
    RPPAgenes <- unique(RPPAgenes)

    miniACC <-
        acc[RPPAgenes, , c("RNASeq2GeneNorm", "gistict", "RPPAArray", "Mutations")]
    mut <- assay(miniACC[["Mutations"]], i = "Variant_Classification")
    mut <- ifelse(is.na(mut) | mut == "Silent", 0, 1)

    miniACC[["Mutations"]] <- mut
    colData(miniACC) <- colData(miniACC)[, c(1:17, 810:822)]

    rpparowData <-
        protmap[match(rownames(miniACC[["RPPAArray"]]), protmap$Genes),]
    rpparowData <- AnnotatedDataFrame(rpparowData)
    featureData(miniACC[["RPPAArray"]]) <- rpparowData

    md <-
        list(
         title = "Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma",
            PMID = "27165744",
            sourceURL = "http://s3.amazonaws.com/multiassayexperiments/accMAEO.rds",
            RPPAfeatureDataURL = paste0("http://genomeportal.stanford.edu/",
                                        "pan-tcga/show_target_selection_file",
                                        "?filename=Allprotein.txt"),
        colDataExtrasURL = "http://www.cell.com/cms/attachment/2062093088/2063584534/mmc3.xlsx"
        )
    metadata(miniACC) <- md
```

```
    mirna <- acc[["miRNASeqGene"]]
    mirna <- mirna[rowSums(assay(mirna) >= 5) >= 5, ]
    experimentData(mirna)@abstract <-
        "Note: Rows not having at least 5 counts in at least 5 samples were removed."
    miniACC <- c(miniACC,
                 list(miRNASeqGene = mirna),
                 sampleMap = sampleMap(acc)[sampleMap(acc)$assay == "miRNASeqGene",])

     miniACC[["RNASeq2GeneNorm"]] <-
         as(miniACC[["RNASeq2GeneNorm"]], "SummarizedExperiment")
     miniACC[["RPPAArray"]] <-
         as(miniACC[["RPPAArray"]], "SummarizedExperiment")
     miniACC[["miRNASeqGene"]] <-
         as(miniACC[["miRNASeqGene"]], "SummarizedExperiment")

    save(miniACC, file = "data/miniACC.RData", compress = "bzip2")

## End(Not run)
```

`MultiAssayExperiment` *Construct a* `MultiAssayExperiment` *object*

Description

The constructor function for the MultiAssayExperiment-class 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

See Also

MultiAssayExperiment-class

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`
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'
exportClass(
  object,
  dir = tempdir(),
  fmt,
  ext,
  match = FALSE,
  verbose = TRUE,
  ...
)

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

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

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

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

## S4 method for signature 'MultiAssayExperiment,numeric'
assay(x, i, ...)

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

Arguments

object	A MultiAssayExperiment object
x	A MultiAssayExperiment object
...	Additional arguments for supporting functions. See details.
verbose	logical (default FALSE) whether to print extra messages
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)
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)
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: Show method for a MultiAssayExperiment
- length: Get the length of ExperimentList
- names: Get the names of the ExperimentList
- updateObject: Update old serialized MultiAssayExperiment objects to new API
- exportClass: Export data from class to a series of text files
- dimnames: Get the dimension names for a MultiAssayExperiment object
- c: Add a supported data class to the ExperimentList
- assays: Obtain a SimpleList of assay data for all available experiments in the object
- assay: 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. Standard column names of the sampleMap are "assay", "primary", and "colname".

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)
```

`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: A function that identifies multiple samples that originate from a single biological unit within each assay
- anyReplicated: Displays which assays have replicate measurements
- mergeReplicates: A function that combines replicated / repeated measurements across all experiments and is guided by the replicated return value
- longFormat: 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 return a wide DataFrame where each row represents an observation. Optional `colDataCols` can be added when using a `MultiAssayExperiment`.
- hasRowRanges: A function that identifies ExperimentList elements that have a rowRanges method
- getWithColData: A convenience function for extracting an assay and associated colData

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)

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, ...)

longFormat(object, colDataCols = NULL, 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)

getWithColData(x, i)
```

Arguments

`...`	Additional arguments. See details for more information.
`x`	A MultiAssayExperiment or ExperimentList
`replicates`	A list of LogicalLists 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	The assay indicator for SummarizedExperiment objects (default 1L)
check.names	(logical default TRUE) Column names of the output DataFrame will be checked for syntactic validity and made unique, if necessary
collapse	(character default "_") A single string delimiter for output column names. In wideFormat, experiments and rownames (and when replicate samples are present, colnames) are seperated by this delimiter

Details

The replicated function finds replicate measurements in each assay and returns a list of LogicalLists. 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).

The mergeReplicates function is a house-keeping method for a MultiAssayExperiment where only complete.cases are returned, replicate measurements are averaged (by default), and columns are aligned by the row order in colData. Additional arguments can be passed on 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 longFormat "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.

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 (...).

longFormat

The longFormat 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 colData columns with the colDataCols argument (MultiAssayExperiment method only). The i argument allows the user to specify the assay value in a SummarizedExperiment. It directly relates to the i argument in the assay method.

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. Optionally, `colData` columns can be added to the wide data output (see the `colDataCols` argument). Metadata columns are generated based on the names produced in the wide format DataFrame. These can be accessed via the mcols function. See the `Arguments` and `longFormat` sections for argument descriptions.

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.

`MultiAssayExperiment-methods`

Accessing/modifying slot information

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'
metadata(x)

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

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

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

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

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

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

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

Arguments

x	A MultiAssayExperiment object
...	Argument not in use
object	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

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

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
```

---

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

Examples

```
DataFrame()
```

subsetBy *Subsetting a MultiAssayExperiment object*

Description

A set of functions for extracting and dividing a `MultiAssayExperiment`

Usage

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

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, ...)

## S4 method for signature 'MultiAssayExperiment,ANY'
```

```
subsetByColumn(x, y)

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

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

## 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	Any argument used for subsetting, can be a character, logical, integer, list or List vector
...	Additional arguments passed on to lower level functions.
i	Either a character, integer, logical or GRanges object for subsetting by rows
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 TRUE) whether to drop 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

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")
```

`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 = length(MultiAssayExperiment),
  nintersects = 24,
  order.by = "freq",
  nameFilter = force,
  check.names = FALSE,
  ...
)
```

Arguments

MultiAssayExperiment	A MultiAssayExperiment instance
nsets	integer number of sets to analyze
nintersects	Number of intersections to plot. If set to NA, 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.
nameFilter	function, defaulting to force, to manipulate colnames of incidence matrix
check.names	logical(1) used when incidence matrix is coerced to data.frame for use in UpSetR::upset
...	parameters passed to 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 upset function requires data.frame input and has many parameters to tune appearance of the result. Assay name handling is important for interpretability, and the nameFilter parameter may be useful to simplify resulting outputs.

Author(s)

Vincent J Carey

Examples

```
data(miniACC)
upsetSamples(miniACC)
upsetSamples(miniACC, nameFilter = function(x) substr(x, 1, 5))
```

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