Package 'MultiDataSet'

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Description Implementation of the BRGE's (Bioinformatic Research Group in Epidemiology from Center for Research in Environmental Epidemiology) MultiDataSet and ResultSet. MultiDataSet is designed for integrating multi omics data sets and ResultSet is a container for omics results. This package contains base classes for MEAL and rexposome packages.

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`add_eset` *Method to add an* `eSet` *to* `MultiDataSet`.

Description

This method adds or overwrites a slot of a `MultiDataSet` with the content of the given `eSet`.

Usage

```
add_eset(
  object,
  set,
  dataset.type,
  dataset.name = NULL,
  sample.tables = NULL,
  feature.tables = NULL,
  warnings = TRUE,
  overwrite = FALSE,
  GRanges
)
```

Arguments

object	MultiDataSet that will be filled.
set	Object derived from eSet to be used to fill the slot.
dataset.type	Character with the type of data of the omic set (e.g. expression, methylation...)
dataset.name	Character with the specific name for this set (NULL by default). It is useful when there are several sets of the same type (e.g. multiple expression assays)
sample.tables	Character with the names of the slots with sample data besides phenoData.
feature.tables	Character with the names of the slots with feature data besides featureData.
warnings	Logical to indicate if warnings will be displayed.
overwrite	Logical to indicate if the set stored in the slot will be overwritten.
GRanges	GenomicRanges to be included in rowRanges slot.

Value

A new MultiDataSet with a slot filled.

See Also

add_methy, add_genexp, add_rnaseq, add_snps

Examples

```
multi <- createMultiDataSet()
eset <- new("ExpressionSet", exprs = matrix(runif(10), 5))
multi <- add_eset(multi, eset, "exampledata", GRanges = NA)
```

---

add_genexp *Method to add an expression microarray dataset to* MultiDataSet.

Description

This method adds or overwrites the slot "expression" of an MultiDataSet with the content of the given ExpressionSet. The fData of the ExpressionSet must contain the columns chromosome, start and end.

Usage

```
add_genexp(object, gexpSet, ...)
```

Arguments

object	MultiDataSet that will be filled.
gexpSet	ExpressionSet to be used to fill the slot.
...	Arguments to be passed to add_eset.

Value

A new MultiDataSet with the slot "expression" filled.

Examples

```
multi <- createMultiDataSet()
eset <- new("ExpressionSet", exprs = matrix(runif(4), 2))
fData(eset) <- data.frame(chromosome = c("chr1", "chr2"), start = c(12414, 1234321),
 end = c(121241, 124124114), stringsAsFactors = FALSE)
multi <- add_genexp(multi, eset)
```

---

add_methy *Method to add a slot of methylation to* MultiDataSet.

Description

This method adds or overwrites the slot "methylation" of an MultiDataSet with the content of the given MethylationSet or RatioSet. The fData of the input object must contain the columns chromosome and position.

Usage

```
add_methy(object, methySet, ...)
```

Arguments

object	MultiDataSet that will be filled.
methySet	MethylationSet or RatioSet to be used to fill the slot.
...	Further arguments to be passed to add_eset.

Value

A new MultiDataSet with the slot "methylation" filled.

Examples

```
if (require(brgedata)){
 multi <- createMultiDataSet()
 multi <- add_methy(multi, brge_methy[1:100, ])
}
```

---

add_rnaseq *Method to add an expression RNA seq dataset to* MultiDataSet.

Description

This method adds or overwrites the slot "rnaseq" of an MultiDataSet with the content of the given ExpressionSet. The fData of the ExpressionSet must contain the columns chromosome, start and end.

Usage

```
add_rnaseq(object, rnaSet, ...)
```

Arguments

object	MultiDataSet that will be filled.
rnaSet	ExpressionSet to be used to fill the slot.
...	Arguments to be passed to add_eset.

Value

A new MultiDataSet with the slot "rnaseq" filled.

Examples

```
multi <- createMultiDataSet()
eset <- new("ExpressionSet", exprs = matrix(runif(4), 2))
fData(eset) <- data.frame(chromosome = c("chr1", "chr2"), start = c(12414, 1234321),
 end = c(121241, 12122414), stringsAsFactors = FALSE)
multi <- add_genexp(multi, eset)
```

---

add_rse *Method to add a* RangedSummarizedExperiment *to* MultiDataSet.

Description

This method adds or overwrites a slot of a MultiDataSet with the content of the given RangedSummarizedExperiment.

Usage

```
add_rse(
  object,
  set,
  dataset.type,
  dataset.name = NULL,
  sample.tables = NULL,
  feature.tables = NULL,
  warnings = TRUE,
  overwrite = FALSE
)
```

Arguments

object	MultiDataSet that will be filled.
set	Object derived from RangedSummarizedExperiment to be used to fill the slot.
dataset.type	Character with the type of data of the omic set (e.g. expression, methylation...)
dataset.name	Character with the specific name for this set (NULL by default). It is useful when there are several sets of the same type (e.g. multiple expression assays)
sample.tables	Character with the names of the slots with sample data besides colData.
feature.tables	Character with the names of the slots with feature data besides rowData.
warnings	Logical to indicate if warnings will be displayed.
overwrite	Logical to indicate if the set stored in the slot will be overwritten.

Value

A new MultiDataSet with a slot filled.

Examples

```
if (require(GenomicRanges) & require(SummarizedExperiment)){
multi <- createMultiDataSet()
counts <- matrix(runif(200 * 6, 1, 1e4), 200)
rowRanges <- GRanges(rep(c("chr1", "chr2"), c(50, 150)),
                     IRanges(floor(runif(200, 1e5, 1e6)), width=100),
                     strand=sample(c("+", "-"), 200, TRUE),
                     feature_id=sprintf("ID%03d", 1:200))
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
                    row.names=LETTERS[1:6], id = LETTERS[1:6])
names(rowRanges) <- 1:200
rse <- SummarizedExperiment(assays=SimpleList(counts=counts),
                            rowRanges=rowRanges, colData=colData)
multi <- add_rse(multi, rse, "rseEx")
}
```

---

add_se *Method to add a* SummarizedExperiment *to* MultiDataSet.

Description

This method adds or overwrites a slot of a MultiDataSet with the content of the given SummarizedExperiment.

Usage

```
add_se(
  object,
  set,
  dataset.type,
  dataset.name = NULL,
  sample.tables = NULL,
  feature.tables = NULL,
  warnings = TRUE,
  overwrite = FALSE,
  GRanges
)
```

Arguments

object	MultiDataSet that will be filled.
set	Object derived from SummarizedExperiment to be used to fill the slot.
dataset.type	Character with the type of data of the omic set (e.g. expression, methylation...)
dataset.name	Character with the specific name for this set (NULL by default). It is useful when there are several sets of the same type (e.g. multiple expression assays)
sample.tables	Character with the names of the slots with sample data besides colData.
feature.tables	Character with the names of the slots with feature data besides rowData.

warnings	Logical to indicate if warnings will be displayed.
overwrite	Logical to indicate if the set stored in the slot will be overwritten.
GRanges	GenomicRanges to be included in rowRanges slot.

Value

A new MultiDataSet with a slot filled.

Examples

```
multi <- createMultiDataSet()
se <- SummarizedExperiment::SummarizedExperiment(matrix(runif(10), 5))
multi <- add_se(multi, se, "exampledata", GRanges = NA)
```

---

add_snps *Method to add a slot of SNPs to* MultiDataSet.

Description

This method adds or overwrites the slot "snps" of an MultiDataSet with the content of the given SnpSet. The fData of the SnpSet must contain the columns chromosome and position.

Usage

```
add_snps(object, snpSet, ...)
```

Arguments

object	MultiDataSet that will be filled.
snpSet	SnpSet to be used to fill the slot.
...	Arguments to be passed to add_eset.

Value

A new MultiDataSet with the slot "snps" filled.

Examples

```
multi <- createMultiDataSet()
geno <- matrix(c(3,1,2,1), ncol = 2)
colnames(geno) <- c("VAL0156", "VAL0372")
rownames(geno) <- c("rs3115860", "SNP1-1628854")
map <- AnnotatedDataFrame(data.frame(chromosome = c("chr1", "chr2"), position = c(12414, 1234321),
     stringsAsFactors = FALSE))
rownames(map) <- rownames(geno)
snpSet <- new("SnpSet", call = geno, featureData = map)
pheno <- data.frame(id = c("VAL0156", "VAL0372"))
rownames(pheno) <- c("VAL0156", "VAL0372")
pData(snpSet) <- pheno
multi <- add_snps(multi, snpSet)
```

add_table *Method to add a* matrix *to* MultiDataSet.

Description

This method adds or overwrites a slot of a MultiDataSet with the content of the given matrix.

Usage

```
add_table(
  object,
  set,
  dataset.type,
  dataset.name = NULL,
  warnings = TRUE,
  overwrite = FALSE
)
```

Arguments

object	MultiDataSet that will be filled.
set	matrix used to fill the slot.
dataset.type	Character with the type of data
dataset.name	Character with the specific name for this set (NULL by default). It is useful when there are several sets of the same type.
warnings	Logical to indicate if warnings will be displayed.
overwrite	Logical to indicate if the set stored in the slot will be overwritten.

Value

A new MultiDataSet with a slot filled.

Examples

```
multi <- createMultiDataSet()
mat <- matrix(runif(12), nrow = 3)
colnames(mat) <- paste0("S", 1:4)
rownames(mat) <- paste0("F", 1:3)
multi <- add_table(multi, mat, "exampledata")
```

chrNumToChar *Convert chr numbers to chr strings*

Description

Given a vector of number representing the chromosomes, convert them to string (e.g 1 to chr1). 23 is consider chrX, 24 is chrY, 25 is chrXY (probes shared between chromosomes X and Y) and 26 is chrMT.

Usage

```
chrNumToChar(vector)
```

Arguments

vector	The vector with the chromosome numbers

Value

A vector with the chromosomes in string format.

Examples

```
chromosomes <- c(1, 3, 4, 23, 15)
stringChrs <- chrNumToChar(chromosomes)
stringChrs
```

commonIds *Get the name of the ids common to all datasets*

Description

Get the name of the ids common to all datasets

Usage

```
commonIds(object)
```

Arguments

object	MultiDataSet that will be filtered.

Value

Character vector with the common ids.

Examples

```
multi <- createMultiDataSet()
eset <- new("ExpressionSet", exprs = matrix(runif(9), ncol = 3))
fData(eset) <- data.frame(chromosome = c("chr1", "chr1", "chr1"),
                          start = c(1, 5, 10),end = c(4, 6, 14),
                          stringsAsFactors = FALSE)
sampleNames(eset) <- c("S1", "S2", "S3")
pData(eset) <- data.frame(id = c("S1", "S2", "S3"))
rownames(pData(eset)) <- c("S1", "S2", "S3")
multi <- add_genexp(multi, eset, dataset.name = "g1")
eset <- new("ExpressionSet", exprs = matrix(runif(8), ncol = 2))
fData(eset) <- data.frame(chromosome = c("chr1", "chr1", "chr1", "chr1"),
                          start = c(1, 14, 25, 104),end = c(11, 16, 28, 115),
                          stringsAsFactors = FALSE)
sampleNames(eset) <- c("S1", "G2")
pData(eset) <- data.frame(id = c("S1", "G2"))
rownames(pData(eset)) <- c("S1", "G2")

multi <- add_genexp(multi, eset, dataset.name="g2")
commonIds(multi)
```

---

commonSamples *Method to select samples that are present in all datasets.*

Description

This method subsets the datasets to only contain the samples that are in all datasets. All sets will have the samples in the same order, taking into account that there can be duplicates.

Usage

```
commonSamples(object, unify.names = FALSE)
```

Arguments

object	MultiDataSet that will be filtered.
unify.names	Logical indicating if sample names of the sets should be unified.

Details

If unify.names is TRUE, the sample names of the sets will be unified using the id column of phenodata. This option is only possible when there are no duplicated ids.

Value

A new MultiDataSet with only the common samples.

Examples

```
multi <- createMultiDataSet()
eset <- new("ExpressionSet", exprs = matrix(runif(9), ncol = 3))
fData(eset) <- data.frame(chromosome = c("chr1", "chr1", "chr1"),
                          start = c(1, 5, 10),end = c(4, 6, 14),
                          stringsAsFactors = FALSE)
sampleNames(eset) <- c("S1", "S2", "S3")
pData(eset) <- data.frame(id = c("S1", "S2", "S3"))
rownames(pData(eset)) <- c("S1", "S2", "S3")
multi <- add_genexp(multi, eset, dataset.name = "g1")
eset <- new("ExpressionSet", exprs = matrix(runif(8), ncol = 2))
fData(eset) <- data.frame(chromosome = c("chr1", "chr1", "chr1", "chr1"),
                          start = c(1, 14, 25, 104),end = c(11, 16, 28, 115),
                          stringsAsFactors = FALSE)
sampleNames(eset) <- c("S1", "G2")
pData(eset) <- data.frame(id = c("S1", "G2"))
rownames(pData(eset)) <- c("S1", "G2")

multi <- add_genexp(multi, eset, dataset.name="g2")
commonSamples(multi)
```

---

getAssociation *Method to extrat feature result from a ResultSet*

Description

Homologous methods from limma, getAssociation resturns a data.frame with the logFC and PValue per featrue for the selcted coef and for given result (rid).

Usage

```
getAssociation(object, rid = 1, coef = 2, contrast = NULL, fNames = NULL, ...)
```

Arguments

object	A ResultSet object.
rid	The name or index of the result to be extracted.
coef	(default 2) Index of the coefficient to be extracted.
contrast	(default 1) When code corresponds to a multicategorical variable, contasr selects the comparison.
fNames	(default c("chromosome", "start", "end", "genesymbol")) Corresponds to the columns selected from fData that will be incorporated into the resulting data.frame.
...	Further arguments passed to topTable

Value

A data.frame with the result of the association study, including P-Value and Fold Change.

Examples

```
data(rset)
getAssociation(rset, rid=1, fNames = c("chromosome", "position"))
```

lambdaClayton *Lambda Calculation for a vector of P-Values*

Description

Implementation of Clayton's lambda score for a vector of P-Values

Usage

```
lambdaClayton(x, trim = 0.5)
```

Arguments

x	Vector of P-Value
trim	(default 0.5)

Value

A lambda value, indicating the inflation/deflation of the analysis.

Author(s)

Juan R. Gonzalez

Examples

```
lambdaClayton(runif(30))
```

mae2mds *Convert a* MultiAssayExperiment *to a* MultiDataSet

Description

This function creates a MultiDataSet using the data of a MultiAssayExperiment.

Usage

```
mae2mds(MAE, warnings = TRUE)
```

Arguments

MAE	a MultiAssayExperiment
warnings	Logical to indicate if warnings will be displayed.

Value

MultiDataSet with the of the incoming MultiAssayExperiment.

mds2mae *Convert a* MultiDataSet *to a* MultiAssayExperiment

Description

This function creates a MultiAssayExperiment using the data of a MultiDataSet.

Usage

```
mds2mae(MDS)
```

Arguments

MDS	a MultiDataSet

Value

MultiAssayExperiment with the of the incoming MultiDataSet.

MultiDataSet *MultiDataSet: Implementation of the BRGE's basic classes*

Description

Implementation of the BRGE's (Bioinformatic Research Group in Epidemiology from Center for Research in Environmental Epidemiology) MultiDataSet and MethylationSet. MultiDataSet is designed for integrating multi omics data sets and MethylationSet to contain normalized methylation data. MultiDataSet for integrating multi omics data sets

See Also

MultiDataSet

MultiDataSet-class *MultiDataSet instances*

Description

The class MultiDataSet is a superior class to store multiple datasets in form of triplets (assayData-phenoData-featureData). The datasets can be eSet or SummarizedExperiment derived or matrices.

Usage

```
## S4 method for signature 'MultiDataSet,eSet'
add_eset(
  object,
  set,
  dataset.type,
  dataset.name = NULL,
  sample.tables = "protocolData",
  feature.tables = NULL,
  warnings = TRUE,
  overwrite = FALSE,
  GRanges
)

## S4 method for signature 'MultiDataSet,ExpressionSet'
add_genexp(object, gexpSet, ...)

## S4 method for signature 'MultiDataSet,ExpressionSet'
add_rnaseq(object, rnaSet, ...)

## S4 method for signature 'MultiDataSet,GenomicRatioSet'
add_methy(object, methySet, ...)

## S4 method for signature 'MultiDataSet,RangedSummarizedExperiment'
add_rse(
  object,
  set,
  dataset.type,
  dataset.name = NULL,
  sample.tables = NULL,
  feature.tables = "elementMetadata",
  warnings = TRUE,
  overwrite = FALSE
)

## S4 method for signature 'MultiDataSet,SummarizedExperiment'
add_se(
  object,
  set,
  dataset.type,
  dataset.name = NULL,
  sample.tables = NULL,
  feature.tables = "elementMetadata",
  warnings = TRUE,
  overwrite = FALSE,
  GRanges
)

## S4 method for signature 'MultiDataSet,SnpSet'
add_snps(object, snpSet, ...)

## S4 method for signature 'MultiDataSet,matrix'
```

```
add_table(
  object,
  set,
  dataset.type,
  dataset.name = NULL,
  warnings = TRUE,
  overwrite = FALSE
)

## S4 method for signature 'MultiDataSet'
as.list(x)

## S4 method for signature 'MultiDataSet'
commonIds(object)

## S4 method for signature 'MultiDataSet'
commonSamples(object, unify.names = FALSE)

createMultiDataSet()

## S4 method for signature 'MultiDataSet'
dims(x)

## S4 method for signature 'MultiDataSet'
w_iclusterplus(object, commonSamples = TRUE, ...)

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

## S4 method for signature 'MultiDataSet'
w_mcia(object, ...)

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

## S4 method for signature 'MultiDataSet'
ncol(x)

## S4 method for signature 'MultiDataSet'
nrow(x)

## S4 method for signature 'MultiDataSet'
rowRangesElements(object)

## S4 method for signature 'MultiDataSet'
sampleNames(object)

## S4 method for signature 'MultiDataSet'
assayData(object)

## S4 method for signature 'MultiDataSet'
fData(object)
```

```
## S4 method for signature 'MultiDataSet'
featureData(object)

## S4 method for signature 'MultiDataSet'
pData(object)

## S4 method for signature 'MultiDataSet'
phenoData(object)

## S4 method for signature 'MultiDataSet'
rowRanges(x)

## S4 method for signature 'MultiDataSet,ANY,ANY'
x[[i]]

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

## S4 method for signature 'MultiDataSet'
subset(x, feat, phe, warnings = TRUE, keep = TRUE)
```

Arguments

object	MultiDataSet
set	Object derived from eSet to be used to fill the slot.
dataset.type	Character with the type of data of the omic set (e.g. expression, methylation...)
dataset.name	Character with the specific name for this set (NULL by default). It is useful when there
sample.tables	Character with the names of the slots with sample data besides phenoData.
feature.tables	Character with the names of the slots with feature data besides featureData.
warnings	Logical to indicate if warnings will be displayed.
overwrite	Logical to indicate if the set stored in the slot will be overwritten.
GRanges	GenomicRanges to be included in rowRanges slot.
gexpSet	ExpressionSet to be used to fill the slot.
...	Further arguments passed to add_rse or add_se
rnaSet	ExpressionSet to be used to fill the slot.
methySet	GenomicRatioSet to be used to fill the slot.
snpSet	SnpSet to be used to fill the slot.
x	MultiDataSet
unify.names	Logical indicating if sample names of the sets should be unified.
commonSamples	Logical to indicate if common samples are selected
i	Character corresponding to selected sample names. They should match the id column of phenoData.
j	Character with the name of the selected tables.
k	GenomicRange used to filter the features.
drop	If TRUE, sets with no samples or features will be discarded

feat	Logical expression indicating features to keep
phe	Logical expression indicating the phenotype of the samples to keep
keep	If FALSE, sets where the expression cannot be evaluated will be discarded.

Details

The names of the three lists (assayData, phenoData and featureData) must be the same.

Value

MultiDataSet

MultiDataSet

Methods (by generic)

- add_eset: Method to add an eSet to MultiDataSet.
- add_genexp: Method to add a slot of expression to MultiDataSet.
- add_rnaseq: Method to add a slot of (RNASeq) expression to MultiDataSet.
- add_methy: Method to add a slot of methylation to MultiDataSet from a GenomicRatioSet.
- add_rse: Method to add a RangedSummarizedExperiment to MultiDataSet.
- add_se: Method to add a SummarizedExperiment to MultiDataSet.
- add_snps: Method to add a slot of SNPs to MultiDataSet.
- add_table: Method to add a matrix to MultiDataSet.
- as.list: Returns a list with the first matrix of each dataset.
- commonIds: Get the name of the ids common to all datasets
- commonSamples: Get a MultiDataSet only with the samples present in all the tables
- dims: Returns the dimensions of the sets
- w_iclusterplus: Apply iClusterPlus clustering method to a MultiDataSet object
- length: Returns the number of sets into the object.
- w_mcia: Apply mcia integration method to a MultiDataSet object
- names: Get the names of the slots.
- ncol: Get number of samples of each set
- nrow: Get number of features of each set
- rowRangesElements: Get the name of the datasets that have rowRanges
- sampleNames: Get sample names
- assayData: Retrieve all assay data blocks.
- fData: Retrieve information on features.
- featureData: Retrieve information on features.
- pData: Retrieve information on experimental phenotypes
- phenoData: Retrieve information on experimental phenotypes
- rowRanges: Retrieve information on feature ranges.
- [[: Get a set from a slot
- [: Subset a MultiDataSet
- subset: Filter a subset using feature ids or phenotypes

Slots

`assayData` List of `assayData` elements.

`phenoData` List of `AnnotatedDataFrame` containing the phenoData of each `assayData`.

`featureData` List of `AnnotatedDataFrame` containing the featureData of each `assayData`.

`rowRanges` List of `GenomicRanges` containing the rowRanges of each `assayData`.

`extraData` List of other slots of the original object.

`return_method` List of functions used to create the original object.

See Also

`add_eset`, `add_rse`

Examples

```
createMultiDataSet()
```

---

opt *Method to get the options sued to create the ResultSet*

Description

Method that returns a list with the options used to create the `ResultSet`.

Usage

```
opt(object)
```

Arguments

`object`	A `ResultSet` object.

Value

A list with the options used to create the `ResultSet`.

Examples

```
data(rset)
opt(rset)
```

qq_plot *Function to draw a QQ Plot from a vector of numbers*

Description

Function to draw a QQ Plot from a vector of numbers

Usage

```
qq_plot(values, show.lambda = TRUE)
```

Arguments

values	Numeric vector of P.Values
show.lambda	(default: TRUE) If TRUE shows lambda score for the given model.

Value

An object obtained from ggplot.

Examples

```
data(rset)
rst <- getAssociation(rset, rid = 1, fNames = NULL)
qq_plot(rst$P.Value)
```

ResultSet *Class ResultSet*

Description

Class ResultSet used to encapsulate results from MEAL and omicrexposome.

Usage

```
## S4 method for signature 'ResultSet'
fData(object)

## S4 method for signature 'ResultSet'
getAssociation(object, rid = 1, coef = 2, contrast = NULL, fNames = NULL, ...)

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

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

## S4 method for signature 'ResultSet'
opt(object)
```

```
## S4 method for signature 'ResultSet,ANY'
plot(
  x,
  y,
  rid = 1,
  coef = 2,
  contrast = NULL,
  type,
  tFC = 2,
  tPV = -log10(0.001),
  show.labels = TRUE,
  show.effect = FALSE,
  show.lambda = TRUE,
  fNames = c("chromosome", "start"),
  subset,
  highlight,
  ...
)

## S4 method for signature 'ResultSet'
varLabels(object)

create_resultset(fOrigin, lResults, fData, lOptions = list())
```

Arguments

object	A ResultSet object.
rid	Name or index of the internal result to be used
coef	Coefficient to be returne, usually 2
contrast	Numeric matrix with the contrasts used to perform the analyses
fNames	Character vector with the names of the fData columns that will be added to the results data.frame.
...	Further arguments passed to topTable
x	A ResultSet object.
y	-
type	Type of plot to be drawn
tFC	Threshold for log FC of effect
tPV	Threshold for P-Value
show.labels	(default TRUE) If set to TRUE, features are labelled.
show.effect	(default: TRUE). Used in volcano plot. If TRUE, effect is shown as FC instead of logFC.
show.lambda	(default: TRUE) If TRUE shows lambda score for the given model.
subset	GenomicRanges used to zoom a region in Manhattan plot
highlight	GenomicRanges used to highlight a region in Manhattan plot
fOrigin	Chracter with the function used to run the analysis.
lResults	List with the results
fData	List with the feature data.
lOptions	List with additional options

Value

An object of class ResultSet

Methods (by generic)

- fData: Returns data.frame with feature's data.
- getAssociation: Getter to obtain the raw data.frame from association and integration analysis.
- length: Returns the amoung of analyses stored in the ResultSet.
- names: Returns the names of the omics data used to create the ResultSet.
- opt: Returns a list with the options used to create the ResultSet
- plot: Allows to plot a series of plots (QQ plot, Manhattan plot and Volcano plot) depending on the results stored in the ResultSet.
- varLabels: Returns the names of the variables of the models used in a ResultSet.

Slots

fun_origin Character containing the function that creates the object.

results List containing the results of the association/integration.

fData List containing the feature-data of the original objects.

options list of options used to create the ResultSet.

Examples

```
create_resultset("hello", list(), list(), list())
```

---

rowRangesElements *Get the name of the datasets that have rowRanges*

Description

Get the name of the datasets that have rowRanges

Usage

```
rowRangesElements(object)
```

Arguments

object	MultiDataSet

Value

Character vector with the slots that have rowRanges.

Examples

```
multi <- createMultiDataSet()
eset <- new("ExpressionSet", exprs = matrix(runif(10), 5))
eset2 <- new("ExpressionSet", exprs = matrix(runif(8), ncol = 2))
fData(eset2) <- data.frame(chromosome = c("chr1", "chr1", "chr1", "chr1"),
                           start = c(1, 14, 25, 104),end = c(11, 16, 28, 115),
                           stringsAsFactors = FALSE)
multi <- add_eset(multi, eset, "exampledata", GRanges = NA)
multi <- add_genexp(multi, eset2)
rowRangesElements(multi)
```

---

rset *Example* ResultSet

Description

Example ResultSet used in the functions examples and in the tests. The script used to generate it can be found in inst/scripts.

Usage

```
rset
```

Format

```
ResultSet
```

---

volcano_plot *Function to draw a Volcano Plot*

Description

Function that takes two numeric vectors (P-Value and fold change) and draws a volcano plot using ggplot2

Usage

```
volcano_plot(
  pval,
  fc,
  names,
  size = 2,
  tFC = 2,
  tPV = -log10(0.001),
  show.labels = TRUE,
  show.effect = FALSE
)
```

Arguments

pval	numeric vector of P.Values
fc	numeric vector of fold change
names	character vector with the feature's names.
size	(default 2) Sice of the labels in case they are placed.
tFC	(default 2) fold change threshold. It can be set to NULL to not filter.
tPV	(default -log10(0.001)) P-Value threshold. It can be set to NULL to not filter.
show.labels	(default TRUE) If set to TRUE, features are labelled.
show.effect	(default FALSE) If set to TRUE, the X-axis will should 2^logFC instead to the default logFC.

Value

A ggplot object

Examples

```
data(rset)
w1 <- getAssociation(rset, rid = 1, fNames = NULL)
volcano_plot(w1$P.Value, w1$logFC, rownames(w1))
```

---

w_iclusterplus *Apply iClusterPlus clustering method to a MultiDataSet object*

Description

Method iClusterPlus is applied on a MultiDataSet object after getting the common samples along all the contained datasets.

Usage

```
w_iclusterplus(object, commonSamples = TRUE, ...)
```

Arguments

object	MultiDataSet
commonSamples	Logical to indicate if common samples are selected
...	Arguments passed to function iClusterPlus

Value

A list of results from iClusterPlus

Note

Argument type for iClusterPlus is filled within the method.

`w_mcia` *Apply mcia integration method to a MultiDataSet object*

Description

Method mcia is applied on a MultiDataSet object after getting the common samples along all the contained datasets.

Usage

```
w_mcia(object, ...)
```

Arguments

`object`	`MultiDataSet`
`...`	Arguments passed to function mcia

Value

A list of results from mcia

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