

# Package ‘MultiDataSet’

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**Type** Package

**Title** Implementation of MultiDataSet and ResultSet

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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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**LazyData** TRUE

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limma

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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	<i>Method to add a RangedSummarizedExperiment to MultiDataSet.</i>
---------	--

---

**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	<i>Method to add a slot of SNPs to MultiDataSet.</i>
----------	--

---

**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	<i>Method to add a matrix to MultiDataSet.</i>
-----------	--

---

### 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	<i>Convert chr numbers to chr strings</i>
--------------	---

---

**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	<i>Get the name of the ids common to all datasets</i>
-----------	---

---

**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	<i>Method to extract feature result from a ResultSet</i>
----------------	--

---

**Description**

Homologous methods from limma, getAssociation returns a data.frame with the logFC and PValue per feature for the selected coef and for given result (rid).

**Usage**

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

**Arguments**

object	A <a href="#">ResultSet</a> 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, contrast 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 <a href="#">topTable</a>

**Value**

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

**Examples**

```

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

```

---

lambdaClayton	<i>Lambda Calculation for a vector of P-Values</i>
---------------	--

---

**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	<i>Convert a MultiAssayExperiment to a MultiDataSet</i>
---------	---

---

**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	<i>Convert a MultiDataSet to a MultiAssayExperiment</i>
---------	---

---

### Description

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

### Usage

```
mds2mae(MDS)
```

### Arguments

MDS	a <code>MultiDataSet</code>
-----	-----------------------------

### Value

`MultiAssayExperiment` with the of the incoming `MultiDataSet`.

---

<code>MultiDataSet</code>	<i>MultiDataSet: Implementation of the BRGE's basic classes</i>
---------------------------	---

---

### 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](#)

---

<code>MultiDataSet-class</code>	<i>MultiDataSet instances</i>
---------------------------------	-------------------------------

---

### 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	SnpsSet 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, fName = 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, fName = 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,
  fName = 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 returned, 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 <a href="#">topTable</a>
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	Character 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 amount 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())
```

---

<code>rowRangesElements</code>	<i>Get the name of the datasets that have rowRanges</i>
--------------------------------	---

---

**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	<i>Example ResultSet</i>
------	--------------------------

---

**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	<i>Function to draw a Volcano Plot</i>
--------------	--

---

**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) Size 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 $-\log_{10}(0.001)$ ) 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 $2^{\log_{2}FC}$ instead to the default $\log_{2}FC$ .

**Value**

A ggplot object

**Examples**

```
data(rset)
w1 <- getAssociation(rset, rid = 1, fName = 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 <a href="#">iClusterPlus</a>

**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**

<code>object</code>	<code>MultiDataSet</code>
<code>...</code>	Arguments passed to function <code>mcia</code>

**Value**

A list of results from `mcia`

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