

# Package ‘RFLOMICS’

April 14, 2025

**Title** Interactive web application for Omics-data analysis

**Version** 0.99.10

**Description** R-package with shiny interface, provides a framework for the analysis of transcriptomics, proteomics and/or metabolomics data. The interface offers a guided experience for the user, from the definition of the experimental design to the integration of several omics table together. A report can be generated with all settings and analysis results.

**URL** <https://github.com/RFLOMICS/RFLOMICS>

**BugReports** <https://github.com/RFLOMICS/RFLOMICS/issues>

**Depends** R (>= 4.4.0), SummarizedExperiment, MultiAssayExperiment, shinyBS, dplyr, ggplot2, htmltools, knitr, coseq

**biocViews** ShinyApps, DifferentialExpression, Metabolomics, Proteomics, Transcriptomics

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**Imports** vroom, org.At.tair.db, AnnotationDbi, circlize, clusterProfiler, ComplexHeatmap, data.table, DT, edgeR, EnhancedVolcano, enrichplot, FactoMineR, ggpubr, ggrepel, grDevices, grid, httr, limma, magrittr, methods, mixOmics, MOFA2, purrr, RColorBrewer, reshape2, reticulate, rmarkdown, S4Vectors, shiny, shinydashboard, shinyWidgets, stats, stringr, tidy, tibble, tidyselect, UpSetR,

**SystemRequirements** Python (>=3), numpy, pandas, h5py, scipy, argparse, sklearn, mofapy2 (>=0.7.1)

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createRflomicsMAE      *RflomicsMAE class constructor*

---

## Description

This function is a constructor for the class [RflomicsMAE-class](#). It initializes an object of class [RflomicsMAE-class](#) from a list of omics datasets, a vector of dataset names, a vector of omics types, and an experimental design.

**Usage**

```
createRfomicsMAE(
  projectName = NULL,
  omicsData = NULL,
  omicsNames = NULL,
  omicsTypes = NULL,
  ExpDesign = NULL,
  factorInfo = NULL
)
```

**Arguments**

projectName	Project name
omicsData	list of omics dataset: named list of data.frame, matrix or <a href="#">SummarizedExperiment</a> objects, or <a href="#">MultiAssayExperiment</a> object.
omicsNames	Vector of dataset names that we want to analyze.
omicsTypes	vector of dataset types: "RNAseq", "metabolomics", "proteomics"
ExpDesign	a data.frame which describes the experimental design.
factorInfo	a data.frame describing the experimental factors. <ul style="list-style-type: none"> <li>• factorName: factor names</li> <li>• factorRef: factor references</li> <li>• factorType: factor type : "Bio", "batch", "Meta"</li> <li>• factorLevels: levels of each factor with "," separation.</li> </ul>

**Value**

An object of class [RfomicsMAE-class](#)

**See Also**

[RfomicsMAE-class](#)

**Examples**

```
# load ecoseed data
data(ecoseed.mae)

factorInfo <- data.frame(
  "factorName" = c("Repeat", "temperature", "imbibition"),
  "factorType" = c("batch", "Bio", "Bio")
)

# create rfomicsMAE object with ecoseed data
MAE <- RFLOMICS::createRfomicsMAE(
  projectName = "Tests",
  omicsData = ecoseed.mae,
  omicsTypes = c("RNAseq", "proteomics", "metabolomics"),
  factorInfo = factorInfo)
```

```
names(MAE) <- c("RNAtest", "protetest", "metatest")

# generate upset plot
# MultiAssayExperiment::upsetSamples(MAE)

# generate data overview plot
# plotDataOverview(MAE)

# generate plot of coverage of condition by data
# plotConditionsOverview(MAE)
```

---

ecoseed.df

*EcoSeed project data*

---

## Description

This dataset is provided by the EcoSeed project (FP7-KBBE; Impacts of Environmental Conditions on Seed Quality). that investigates the effect of seed production temperature on the germination potential of *Arabidopsis thaliana*.

This dataset is a multi-omics dataset composed of three data matrices: transcriptomics (raw RNAseq read count data matrix), metabolomics and proteomics (relative abundance matrix as XIC).

These data are provided in 2 object: ecoseed.df and ecoseed.mae

## Usage

```
data("ecoseed.df")
```

## Format

A list of data.frame containing

- design: a data.frame with experiment design,
- RNAtest: a data.frame with RNAseq data,
- protetest: a data.frame with proteomics data,
- metatest: a data.frame with metabolomics data

## References

FP7-KBBE; Impacts of Environmental Conditions on Seed Quality

## Examples

```
data("ecoseed.df")

# list of data.frames
names(ecoseed.df)
head(ecoseed.df$design)
```

---

ecoseed.mae	<i>Ecoseed project data</i>
-------------	-----------------------------

---

## Description

This dataset is provided by the EcoSeed project (FP7-KBBE; Impacts of Environmental Conditions on Seed Quality). that investigates the effect of seed production temperature on the germination potential of *Arabidopsis thaliana*.

This dataset is a multi-omics dataset composed of three data matrices: transcriptomics (raw RNAseq read count data matrix), metabolomics and proteomics (relative abundance matrix as XIC).

These data are provided in 2 object: `ecoseed.df` and `ecoseed.mae`

## Usage

```
data("ecoseed.mae")
```

## Format

`ecoseed.mae`: a [MultiAssayExperiment](#) object, of RNAtest, protetest and metatest data in [SummarizedExperiment](#)

- ExperimentList class object of length 3:
  - RNAtest: a [SummarizedExperiment](#) object with RNAseq data,
  - protetest: a [SummarizedExperiment](#) object with proteomics data,
  - metatest: a [SummarizedExperiment](#) object with metabolomics data
- DataFrame with experiment design
- ...

## References

FP7-KBBE; Impacts of Environmental Conditions on Seed Quality

## Examples

```
data("ecoseed.mae")
```

---

```
generateExpressionContrast
```

*Contrast expressions*

---

## Description

Generate expression of contrasts based on choosed model formula.

- generateExpressionContrast: This function allows, from a model formulae, to give the expression contrast data frames. Three types of contrasts are expressed:
  - pairwise comparison
  - averaged expression
  - interaction expression
- setSelectedContrasts: Set the selected contrasts stored in metadata slot
- getSelectedContrasts: List the selected contrasts

## Usage

```
## S4 method for signature 'RflomicsSE'
generateExpressionContrast(object, contrastType = NULL)
```

```
## S4 method for signature 'RflomicsMAE'
generateExpressionContrast(object, contrastType = NULL)
```

```
## S4 method for signature 'RflomicsMAE'
setSelectedContrasts(object, contrastList = NULL)
```

```
## S4 method for signature 'RflomicsSE'
setSelectedContrasts(object, contrastList = NULL)
```

```
## S4 method for signature 'RflomicsMAE'
getSelectedContrasts(object)
```

```
## S4 method for signature 'RflomicsSE'
getSelectedContrasts(object)
```

## Arguments

object	an object of class <a href="#">RflomicsSE</a> or class <a href="#">RflomicsMAE-class</a>
contrastType	type of contrasts from which the possible contrasts are extracted ("average", "simple", "interaction"). Default is all contrasts types.
contrastList	a data.frame of contrasts generated by <a href="#">generateExpressionContrast</a>

**Value**

list of 1 or 3 data.frames of contrast expression

an object of [RflomicsSE](#) class or [RflomicsMAE-class](#) class

**Author(s)**

Christine Paysant-Le Roux, adapted by Nadia Bessoltane

**Examples**

```
library(RFLOMICS)

# load ecoseed data
data(ecoseed.mae)

factorInfo <- data.frame(
  "factorName" = c("Repeat", "temperature", "imbibition"),
  "factorType" = c("batch", "Bio", "Bio")
)

# create rflomicsMAE object with ecoseed data
MAE <- RFLOMICS::createRflomicsMAE(
  projectName = "Tests",
  omicsData = ecoseed.mae,
  omicsTypes = c("RNAseq", "proteomics", "metabolomics"),
  factorInfo = factorInfo)

# generate all statistical model formulae
formulae <- generateModelFormulae(MAE)

# chose and set model formula to rflomicsMAE object
MAE <- setModelFormula(MAE, formulae[[1]])

# Generate expression of contrasts from chosen model
contrastList <- generateExpressionContrast(MAE, "averaged")

# Set the contrasts List and choose the first 3 contrasts of type averaged
MAE <- setSelectedContrasts(MAE, contrastList = contrastList[c(1,2,3),])
```

---

generateModelFormulae *Statistical model formulae*

---

**Description**

These methods allow the user to select and set the formula of the statistical method.

- generateModelFormulae(): From a vector of character giving the name of the factors of an omics experiment, and their type of effect: biological or batch, it returns all models formulae that can be formulated in association with this factors. Batch effect factors do not appear in interaction terms with biological factor. Model formulae stop in second order interaction.
- setModelFormula(): Set the model formula stored in metadata slot
- getModelFormula: Access to the model formula of the statistical analysis

### Usage

```
## S4 method for signature 'RflomicsMAE'
generateModelFormulae(object)

## S4 method for signature 'RflomicsMAE'
setModelFormula(object, modelFormula = NULL)

## S4 method for signature 'RflomicsSE'
setModelFormula(object, modelFormula = NULL)

## S4 method for signature 'RflomicsMAE'
getModelFormula(object)

## S4 method for signature 'RflomicsSE'
getModelFormula(object)
```

### Arguments

object            an object of class [RflomicsSE](#) or class [RflomicsMAE-class](#)  
modelFormula    a string of model formula generated by [generateModelFormulae](#)

### Value

a named list of object of class formula  
an object of [RflomicsSE](#) class or [RflomicsMAE-class](#) class

### Examples

```
library(RFLOMICS)

# load ecoseed data
data(ecoseed.mae)

factorInfo <- data.frame(
  "factorName" = c("Repeat", "temperature", "imbibition"),
  "factorType" = c("batch", "Bio", "Bio")
)

# create rflomicsMAE object with ecoseed data
MAE <- RFLOMICS::createRflomicsMAE(
```



```

projectName = "Tests",
omicsData   = ecoseed.mae,
omicsTypes  = c("RNAseq","proteomics","metabolomics"),
factorInfo  = factorInfo)

# generate all statistical model formulae
formulae <- generateModelFormulae(MAE)

# chose and set model formula to rflomicsMAE object
MAE <- setModelFormula(MAE, formulae[[1]])

# Generate expression of contrasts from chosen model
contrastList <- generateExpressionContrast(MAE, "averaged")

# Set the contrasts List and choose the first 3 contrasts of type averaged
MAE <- setSelectedContrasts(MAE, contrastList = contrastList[c(1,2,3),])

```

---

generateReport

*Generate RFLOMICS html report or archive*


---

## Description

This function is used to generate a html report from a [RflomicsMAE-class](#) object or archive with results.

## Usage

```

## S4 method for signature 'RflomicsMAE'
generateReport(
  object,
  reportName = NULL,
  archiveName = NULL,
  tmpDir = NULL,
  ...
)

```

## Arguments

object	a object of <a href="#">RflomicsSE</a> class or <a href="#">RflomicsMAE-class</a> class.
reportName	Name of the html report.
archiveName	Name of archive with all analysis results
tmpDir	temporary directory (default: working directory)
...	other arguments to pass into the render function.

## Value

An html report or archive (tar.gz)

## Examples

```
library(RFLOMICS)
# load ecoseed data
data(ecoseed.mae)

factorInfo <- data.frame(
  "factorName" = c("Repeat", "temperature", "imbibition"),
  "factorType" = c("batch", "Bio", "Bio")
)

# create rflomicsMAE object with ecoseed data
MAE <- createRflomicsMAE(
  projectName = "Tests",
  omicsData = ecoseed.mae,
  omicsTypes = c("RNAseq", "proteomics", "metabolomics"),
  factorInfo = factorInfo)

formulae <- generateModelFormulae(MAE)
MAE <- setModelFormula(MAE, modelFormula = formulae[[1]])

selectedContrasts <-
  generateExpressionContrast(MAE, contrastType="simple")

MAE <- setSelectedContrasts(MAE, contrastList = selectedContrasts)

## data processing
MAE <- runDataProcessing(
  object = MAE,
  SE.name = "protetest",
  samples=NULL,
  normMethod="none",
  transformMethod="none")

## diff analysis
MAE <- runDiffAnalysis(
  object = MAE,
  SE.name = "protetest",
  contrastList =
    selectedContrasts,
  p.adj.method="BH",
  method = "limlmFit",
  p.adj.cutoff = 0.05,
  logFC.cutoff = 0)

## Enrichment
# MAE <- runAnnotationEnrichment(
#   object = MAE,
#   SE.name = "protetest",
#   database = "GO",
#   domain = c("MF"),
#   list_args = list(OrgDb = "org.At.tair.db",
#                   keyType = "TAIR",
```

```
#           pvalueCutoff = 0.05))

# get name of performed analysis
getAnalyzedDatasetNames(MAE)

# generate report
#generateReport(object = MAE, reportName = "ecoseed_report.html")
```

---

getAnalysis

*Get results from RFLOMICS object*

---

## Description

Get a specific analysis results from a RflomicsMAE or a SE.

- getAnalyzedDatasetNames: return a list of performed analysis names.

## Usage

```
## S4 method for signature 'RflomicsMAE'
getAnalysis(object, name = NULL, subName = NULL)

## S4 method for signature 'RflomicsSE'
getAnalysis(object, name = NULL, subName = NULL)

## S4 method for signature 'RflomicsMAE'
getAnalyzedDatasetNames(object, analyses = NULL)
```

## Arguments

object	The RflomicsMAE or RflomicsSE object from which to extract the analysis.
name	the name of element to add to metadata slot.
subName	the name of sub element to add to metadata slot.
analyses	vector of list of analysis name

## Value

The analysis metadata slot (a list of results)

- getAnalysis: return list of results from a specific analysis.

## Examples

```
# See generateReport for an example that includes getAnalyzedDatasetNames
```

---

```
prepareForIntegration,RflomicsMAE-method
```

*Preparation step for integration*

---

## Description

This function transforms a `RflomicsMAE` produced by `rflomics` into an untrained MOFA object or a list to use for `mixOmics`. It checks for batch effects to correct them before integration. It also transforms RNASeq counts data into continuous data using `voom`. This is the second step into the integration.

## Usage

```
## S4 method for signature 'RflomicsMAE'
prepareForIntegration(
  object,
  omicsNames = NULL,
  rnaSeq_transfo = "limma (voom)",
  variableLists = NULL,
  group = NULL,
  method = "MOFA",
  transformData = TRUE,
  cmd = FALSE
)
```

## Arguments

<code>object</code>	An object of class <code>RflomicsMAE-class</code> . It is expected the MAE object is produced by RFLOMICS previous analyses, as it relies on their results.
<code>omicsNames</code>	vector of characters strings, referring to the names of the filtered table in <code>'object@ExperimentList'</code> .
<code>rnaSeq_transfo</code>	character string, only supports <code>'limma (voom)'</code> for now. Transformation of the rnaSeq data from counts to continuous data.
<code>variableLists</code>	list of variables to keep per dataset. Default is keeping all features.
<code>group</code>	Not implemented yet in the interface. Useful for MOFA2 run.
<code>method</code>	one of MOFA or <code>mixOmics</code> . Method for which the object is prepared.
<code>transformData</code>	boolean. Transform the data with the transform and normalization method? Default is TRUE.
<code>cmd</code>	used in the interface. Print cmd lines.

## Value

An untrained MOFA object or a list of dataset

**Examples**

```

library(RFLOMICS)

# load ecoseed data
data("ecoseed.mae")

factorInfo <- data.frame(
  "factorName" = c("Repeat", "temperature", "imbibition"),
  "factorType" = c("batch", "Bio", "Bio")
)

# create rflomicsMAE object with ecoseed data
MAE <- RFLOMICS::createRflomicsMAE(
  projectName = "Tests",
  omicsData = ecoseed.mae,
  omicsTypes = c("RNAseq", "proteomics", "metabolomics"),
  factorInfo = factorInfo)
names(MAE) <- c("RNAtest", "protetest", "metatest")

formulae <- generateModelFormulae( MAE)
MAE <- setModelFormula(MAE, formulae[[1]])
contrastList <- Reduce(rbind, generateExpressionContrast(MAE))

MAE <- MAE |>
  setSelectedContrasts(contrastList[c(3,6,25)]) |>
  runDataProcessing(SE.name = "metatest",
    transformMethod = "log2",
    normMethod = "median") |>
  runDataProcessing(SE.name = "protetest",
    transformMethod = "none",
    normMethod = "median") |>
  runDiffAnalysis(SE.name = "metatest", method = "limlmFit") |>
  runDiffAnalysis(SE.name = "protetest", method = "limlmFit")

# Integration using MOFA
# Prepare mofa object:
mofaObj <- prepareForIntegration(MAE,
  omicsNames = c("protetest", "metatest"),
  variableLists = rownames(MAE),
  method = "MOFA")

class(mofaObj)

# Integration using MixOmics
mixObj <- prepareForIntegration(MAE,
  omicsNames = c("protetest", "metatest"),
  variableLists = rownames(MAE),
  method = "mixOmics")

class(mixObj)

```

## Description

RflomicsMAE is a class that extends the [MultiAssayExperiment](#) class by imposing a structure to the metadata slot. This class is used by the Rflomics analysis workflow to store the experimental design, the settings and results of a multi-omics integration analysis.

## Usage

```
## S4 method for signature 'RflomicsMAE'
getProjectName(object)

## S4 method for signature 'RflomicsMAE'
getDesignMat(object)

## S4 method for signature 'RflomicsMAE'
getDatasetNames(object)

## S4 method for signature 'RflomicsMAE'
getOmicsTypes(object)

## S4 method for signature 'RflomicsMAE'
getFactorNames(object)

## S4 method for signature 'RflomicsMAE'
getFactorTypes(object)

## S4 method for signature 'RflomicsMAE'
getBioFactors(object)

## S4 method for signature 'RflomicsMAE'
getBatchFactors(object)

## S4 method for signature 'RflomicsMAE'
getMetaFactors(object)

## S4 method for signature 'RflomicsMAE'
getRflomicsSE(object, datasetName = NULL)

## S4 method for signature 'RflomicsMAE'
getFactorModalities(object, factorName)

## S4 method for signature 'RflomicsMAE'
subRflomicsMAE(object, omicNames = NULL)

## S4 method for signature 'RflomicsMAE'
plotDataOverview(object, omicNames = NULL, realSize = FALSE)

## S4 method for signature 'RflomicsMAE'
plotConditionsOverview(object, omicNames = NULL)
```

**Arguments**

object	An object of class <a href="#">RflomicsMAE-class</a>
datasetName	the name of the RflomicsSE to retrieve
factorName	factor name
omicNames	a vector with dataset names
realSize	booleen value

**Value**

A RflomicsMAE object.

**Slots**

- ExperimentList:
  - A ExperimentList class object of [RflomicsSE](#) object for each assay dataset
- colData: see [MultiAssayExperiment](#)
- sampleMap: see [MultiAssayExperiment](#)
- metadata:
  - projectName: string. Project name.
  - omicList: list. Contains the list of omics datasets, with the type and name.
  - design: The experimental design.
  - IntegrationAnalysis: A list containing the multi-omics integration analysis settings and results.
  - design: The experimental design
  - sessionInfo:
  - IntegrationAnalysis: A list containing the multi-omics integration analysis settings and results.

**Constructor**

[createRflomicsMAE](#)

**Accessors**

- getProjectName: return a string with the name of the project
- getDesignMat: return a data.frame with experimental design.
- getDatasetNames: return a vector with dataset names.
- getOmicsTypes: return a named vector with omics type of each dataset ("RNAseq", "proteomics", "metabolomics")
- getFactorNames: return a vector with the experimental factor names.
- getFactorTypes: return a named vector with experimental factor types ("bio", "batch" or "meta").

- `getBioFactors`: return a vector with the biological factor names.
- `getBatchFactors`: return a vector with the batch factor names.
- `getMetaFactors`: return a vector with the metadata factor names.
- `getRflomicsSE`: return a [RflomicsSE](#) object with selected dataset
- `getFactorModalities`: return a vector with the modality names of selected factor.
- `subRflomicsMAE`: return a [RflomicsMAE-class](#) object with selected datasets.

### Plots

- `plotDataOverview`: This function plot an overview of the loaded datasets displaying per sample (n=number of entities (genes/metabolites/proteins); k=number of samples)
- `plotConditionsOverview`: A complete design and at least one biological and one batch factors are required for using RFLOMICS workflow.

### Methods

[generateModelFormulae](#) [generateExpressionContrast](#) [runDataProcessing](#) [runDataProcessing](#)  
[runDiffAnalysis](#) [runCoExpression](#) [runAnnotationEnrichment](#)

### See Also

[MultiAssayExperiment](#)

### Examples

```
# load ecoseed data
data(ecoseed.mae)

factorInfo <- data.frame(
  "factorName" = c("Repeat", "temperature", "imbibition"),
  "factorType" = c("batch", "Bio", "Bio")
)

# create rflomicsMAE object with ecoseed data
MAE <- RFLOMICS::createRflomicsMAE(
  projectName = "Tests",
  omicsData = ecoseed.mae,
  omicsTypes = c("RNAseq", "proteomics", "metabolomics"),
  factorInfo = factorInfo)
names(MAE) <- c("RNAtest", "protetest", "metatest")

# generate upset plot
# MultiAssayExperiment::upsetSamples(MAE)

# generate data overview plot
# plotDataOverview(MAE)
```



```
# generate plot of coverage of condition by data
# plotConditionsOverview(MAE)
# See createRflomicsMAE for an example that includes plotDataOverview
# See createRflomicsMAE for an example that includes plotConditionsOverview
```

---

rflomicsMAE2MAE	<i>convert a RflomicsMAE to a MultiAssayExperiment</i>
-----------------	--

---

### Description

Convert RflomicsMAE object to MultiAssayExperiment object.

### Usage

```
## S4 method for signature 'RflomicsMAE'
rflomicsMAE2MAE(object, raw = FALSE)
```

### Arguments

object	The RflomicsMAE object to convert.
raw	Boolean. If TRUE raw omics data values.

### Value

object of MultiAssayExperiment class.

---

RflomicsSE-class	<i>RflomicsSE Class</i>
------------------	-------------------------

---

### Description

RflomicsSE is a class that extends the [SummarizedExperiment](#) by imposing a structure on the meta-data slot. This class is used by the Rflomics analysis workflow to store the experimental design, the settings and results of a single omic analysis. The slot metadata is structured as follows:

### Usage

```
## S4 method for signature 'RflomicsSE'
getDesignMat(object)

## S4 method for signature 'RflomicsSE'
getDatasetNames(object)

## S4 method for signature 'RflomicsSE'
getOmicsTypes(object)
```

```
## S4 method for signature 'RflomicsSE'  
getFactorNames(object)  
  
## S4 method for signature 'RflomicsSE'  
getFactorTypes(object)  
  
## S4 method for signature 'RflomicsSE'  
getBioFactors(object)  
  
## S4 method for signature 'RflomicsSE'  
getBatchFactors(object)  
  
## S4 method for signature 'RflomicsSE'  
getMetaFactors(object)  
  
## S4 method for signature 'RflomicsSE'  
getFactorModalities(object, factorName)
```

### Arguments

object	An object of class <a href="#">RflomicsSE</a>
factorName	factor name

### Value

A RflomicsSE object.

### Slots

See [SummarizedExperiment](#)

The slot metadata is structured as follows:

- omicType: the type of omics dataset
- design: experimental design
- DataProcessing: a list containing the data processing settings and results
- PCAlist: a list containing the PCA settings and results
- DiffExpAnal: a list containing the Differential Analysis settings and results
- CoExpAnal: a list containing the Coexpression Analysis settings and results
- DiffExpEnrichAnal: a list containing the enrichment analysis of the list of DE features settings and results
- CoExpEnrichAnal: a list containing the enrichment analysis of the list of co-expressed features settings and results

### Accessors

- getDesignMat: return a data.frame with experimental design.
- getDatasetNames: return a string with dataset name.
- getOmicsTypes: return a named vector with omics type of dataset ("RNAseq", "proteomics", "metabolomics")
- getFactorNames: return a vector with the experimental factor names.
- getFactorTypes: return a named vector with experimental factor types ("bio", "batch" or "meta").
- getBioFactors: return a vector with the biological factor names.
- getBatchFactors: return a vector with the batch factor names.
- getMetaFactors: return a vector with the metadata factor names.
- getFactorModalities: return a vector with the modality names of selected factor.

### See Also

[SummarizedExperiment](#)

---

runAnnotationEnrichment

*Run Gene Enrichment Analysis and process results*

---

### Description

This function performs over representation analysis (ORA) using clusterprofiler functions. It can be used with custom annotation file (via enricher), GO (enrichGO) or KEGG (enrichKEGG) annotations.

### Usage

```
## S4 method for signature 'RflomicsSE'  
runAnnotationEnrichment(  
  object,  
  featureList = NULL,  
  from = "DiffExp",  
  universe = NULL,  
  database = "custom",  
  domain = "no-domain",  
  annotation = NULL,  
  OrgDb = NULL,  
  organism = NULL,
```

```
keyType = NULL,
pvalueCutoff = 0.05,
qvalueCutoff = 1,
minGSSize = 10,
maxGSSize = 500,
...
)

## S4 method for signature 'RflomicsMAE'
runAnnotationEnrichment(
  object,
  SE.name,
  featureList = NULL,
  from = "DiffExp",
  universe = NULL,
  database = "custom",
  domain = "no-domain",
  annotation = NULL,
  OrgDb = NULL,
  organism = NULL,
  keyType = NULL,
  pvalueCutoff = 0.05,
  qvalueCutoff = 1,
  minGSSize = 10,
  maxGSSize = 500,
  ...
)

## S4 method for signature 'RflomicsSE'
plotClusterProfiler(
  object,
  featureListName = NULL,
  database = NULL,
  domain = "no-domain",
  plotType = "dotplot",
  showCategory = 15,
  searchExpr = "",
  nodeLabel = "all",
  p.adj.cutoff = NULL,
  ...
)

## S4 method for signature 'RflomicsSE'
plotEnrichComp(
  object,
  from = "DiffExp",
  database = NULL,
  domain = "no-domain",
```

```

    matrixType = "FC",
    nClust = NULL,
    ...
)

## S4 method for signature 'RflomicsSE'
getEnrichRes(
  object,
  featureListName = NULL,
  from = "DiffExp",
  database = "GO",
  domain = NULL
)

## S4 method for signature 'RflomicsMAE'
getEnrichRes(
  object,
  experiment,
  featureListName = NULL,
  from = "DiffExp",
  database = "GO",
  domain = NULL
)

## S4 method for signature 'RflomicsSE'
sumORA(object, from = "DiffExp", database = NULL, featureListName = NULL)

## S4 method for signature 'RflomicsSE'
getEnrichSettings(object, from = "DiffExp", database = "GO")

## S4 method for signature 'RflomicsMAE'
getAnnotAnalysesSummary(object, from = "DiffExp", matrixType = "presence", ...)

```

### Arguments

object	An object of class <a href="#">RflomicsSE</a> or class <a href="#">RflomicsMAE-class</a>
featureList	name of contrasts (tags or names) from which to extract DE genes if from is DiffExpAnal.
from	indicates if the enrichment results are taken from differential analysis results (DiffExp) or from the co-expression analysis results (CoExp)
universe	description
database	which database (GO, KEGG, custom...)
domain	the subontology or subdomain for the database (eg CC, MF or BP for GO.)
annotation	for custom annotation, a data frame of the annotation. The data frame must contains at least two columns: gene and term, with the omics name and the associated term id respectively. A column name can be added with the full name of the term (if term is not the full name already). The column domain can be

	used to indicate either different databases (grouped analyses of kegg and go for example) or different domains for a single database (CC, MF and BP) for GO.
OrgDb	OrgDb (with enrichGO)
organism	supported organism listed in 'https://www.genome.jp/kegg/catalog/org_list.html' (with enrichKEGG)
keyType	keytype of input gene with enrichGO (one of "kegg", 'ncbi-geneid', 'ncbi-proteinid' and 'uniprot' with enrichKEGG)
pvalueCutoff	adjusted pvalue cutoff on enrichment tests to report
qvalueCutoff	qvalue cutoff on enrichment tests to report as significant. Tests must pass i) pvalueCutoff on unadjusted pvalues, ii) pvalueCutoff on adjusted pvalues and iii) qvalueCutoff on qvalues to be reported.
minGSSize	minimal size of genes annotated by Ontology term for testing.
maxGSSize	maximal size of genes annotated for testing
...	more arguments for ComplexHeatmap::Heatmap.
SE.name	SE.name the name of the dataset if the input object is a <a href="#">RflomicsMAE-class</a>
featureListName	the contrastName or clusterName to retrieve the results from. If NULL, all results are returned.
plotType	type of plot. Define the function used inside. One of dotplot, heatplot or cnetplot.
showCategory	max number of terms to show.
searchExpr	expression to search in the showCategory terms.
nodeLabel	same as in enrichplot::cnetplot function, defines
p.adj.cutoff	pvalueCutoff to define the enrichment threshold.
matrixType	Heatmap matrix to plot, one of GeneRatio, p.adjust or presence.
nClust	number of separate cluster to plot on the heatmap, based on the clustering.
experiment	if the object is a RflomicsMAE, then experiment is the name of the RflomicsSE to look for.

### Value

A RflomicsMAE or a RflomicsSE, depending on the class of object parameter. The enrichment results are added to the metadata slot, either in DiffExpEnrichAnal or CoExpEnrichAnal.

a list of tables or a table

a list with all settings

### Accessors

A set of getters and setters generic functions to access and modify objects of the slot metadata of a [RflomicsMAE-class](#) object or a [RflomicsMAE-class](#) object.

- getEnrichRes: get a particular enrichment result. return enrichment results given in the form of lists of clusterProfiler results.

- `sumORA`: Get summary tables from ORA analyses - once an enrichment has been conducted.
- `getEnrichSettings`: get the settings of an enrichment analysis.
- `getAnnotAnalysesSummary`: return A list of heatmaps, one for each ontology/domain.

## Plots

A collection of functions for plotting results from omics analysis steps.

- `plotClusterProfiler`: Plot a dotplot, a cnetplot or an heatmap, using `enrichplot` package. It is a wrapper method destined for the `RflomicsSE` class..
- `plotEnrichComp`: plot an heatmap of all the enriched term found for a given database and a given source (differential analysis or coexpression clusters). Allow for the comparison of several enrichment results.

## Examples

```
# load ecoseed data
library(RFLOMICS)
data(ecoseed.mae)

factorInfo <- data.frame(
  "factorName" = c("Repeat", "temperature", "imbibition"),
  "factorType" = c("batch", "Bio", "Bio")
)

# create rflomicsMAE object with ecoseed data
MAE <- createRflomicsMAE(
  projectName = "Tests",
  omicsData = ecoseed.mae,
  omicsTypes = c("RNAseq", "proteomics", "metabolomics"),
  factorInfo = factorInfo
)
#names(MAE) <- c("RNAtest", "protetest", "metatest")

# Set the statistical model and contrasts to test
formulae <- generateModelFormulae(MAE)
MAE <- setModelFormula(MAE, formulae[[1]])

# Get the contrasts List and choose the first 3 contrasts of type averaged
contrastList <- generateExpressionContrast(MAE, "averaged")

MAE <- setSelectedContrasts(MAE, contrastList = contrastList[c(1, 2, 3),])

# Run the data preprocessing and perform the differential analysis
MAE <- runDataProcessing(MAE, SE.name = "protetest",
  transformMethod = "log2",
  normMethod = "median")

MAE <- runDiffAnalysis(MAE,
  SE.name = "protetest",
  method = "limlmFit")
```

```

# Run GO annotation (enrichGO)
# Not run: need org.At.tair.db package
# MAE <- runAnnotationEnrichment(MAE, SE.name = "protetest",
#                               list_args = list(OrgDb = "org.At.tair.db",
#                                                keyType = "TAIR",
#                                                pvalueCutoff = 0.05),
#                               from = "DiffExp", database = "GO",
#                               domain = "CC")

# Run KEGG annotation (enrichKEGG)
# need internet connection
# MAE <- runAnnotationEnrichment(MAE, SE.name = "protetest",
#                               list_args = list(organism = "ath",
#                                                keyType = "kegg",
#                                                pvalueCutoff = 0.05),
#                               from = "DiffExp", database = "KEGG")

# Search for the pvalue cutoff:
# sumORA(MAE[["protetest"]], from = "DiffExp", database = "KEGG")

# need internet connection
# pathview package
# plotKEGG(MAE[["protetest"]], pathway_id = "ath00710", species = "ath",
#          contrastName = "cluster.4", from = "Coexp")

# From differential analysis proteins lists:
# plotClusterProfiler(MAE[["protetest"]],
#                     contrastName = "(temperatureElevated - temperatureMedium) in mean",
#                     database = "KEGG", from = "DiffExp",
#                     plotType = "heatplot", p.adj.cutoff = 0.05,
#                     domain = "no-domain")
# plotEnrichComp(MAE[["protetest"]], from = "DiffExp",
#                database = "KEGG", matrixType = "FC")

# Get all results from KEGG on differential expression lists:
# results <- getEnrichRes(MAE[["protetest"]],
#                         from = "diffexp", database = "KEGG")

# Search for the pvalue cutoff:
# usedPvalue <-
#   getEnrichPvalue(MAE[["protetest"]], from = "diffexp", database = "KEGG")
# settings <-
#   getEnrichSettings(MAE[["protetest"]], from = "diffexp", database = "KEGG")

```



**Description**

This method performs a co-expression/co-abundance analysis of omic-data.

**Usage**

```
## S4 method for signature 'RflomicsSE'
runCoExpression(
  object,
  K = 2:20,
  replicates = 5,
  contrastNames = NULL,
  merge = "union",
  model = "Normal",
  GaussianModel = NULL,
  transformation = NULL,
  normFactors = NULL,
  meanFilterCutoff = NULL,
  scale = NULL,
  min.data.size = 100,
  ...
)

## S4 method for signature 'RflomicsMAE'
runCoExpression(
  object,
  SE.name,
  K = 2:20,
  replicates = 5,
  contrastNames = NULL,
  merge = "union",
  model = "Normal",
  GaussianModel = NULL,
  transformation = NULL,
  normFactors = NULL,
  meanFilterCutoff = NULL,
  scale = NULL,
  min.data.size = 100,
  ...
)

## S4 method for signature 'RflomicsMAE'
getCoExpAnalysesSummary(object, omicNames = NULL)

## S4 method for signature 'RflomicsSE'
plotCoExpression(object)

## S4 method for signature 'RflomicsMAE'
plotCoExpression(object, SE.name)
```

```

## S4 method for signature 'RflomicsSE'
plotCoExpressionProfile(
  object,
  cluster = 1,
  condition = "groups",
  features = NULL
)

## S4 method for signature 'RflomicsMAE'
plotCoExpressionProfile(
  object,
  SE.name,
  cluster = 1,
  condition = "groups",
  features = NULL
)

## S4 method for signature 'RflomicsSE'
plotCoseqContrasts(object)

## S4 method for signature 'RflomicsMAE'
plotCoseqContrasts(object, SE.name)

## S4 method for signature 'RflomicsSE'
getCoexpSettings(object)

## S4 method for signature 'RflomicsMAE'
getCoexpSettings(object, SE.name)

## S4 method for signature 'RflomicsSE'
getCoexpClusters(object, clusterName = NULL)

## S4 method for signature 'RflomicsMAE'
getCoexpClusters(object, SE.name, clusterName = NULL)

```

### Arguments

object	An object of class <a href="#">RflomicsSE</a> or class <a href="#">RflomicsMAE-class</a>
K	Number of clusters (a single value or a vector of values)
replicates	The number of iteration for each K.
contrastNames	names of the contrasts from which the DE entities have to be taken. Can be NULL, in that case every contrasts from the differential analysis are taken into consideration.
merge	"union" or "intersection"
model	Type of mixture model to use "Poisson" or "normal". By default, it is the normal.

GaussianModel	Type of GaussianModel to be used for the Normal mixture model only. This parameters is set to "Gaussian_pk_Lk_Ck" by default and doesn't have to be changed except if an error message proposed to try another model like "Gaussian_pk_Lk_Bk".
transformation	The transformation type to be used. By default, it is the "arcsin" one.
normFactors	The type of estimator to be used to normalize for differences in library size. By default, it is the "TMM" one.
meanFilterCutoff	a cutoff to filter a gene with a mean expression lower than this value. (only for RNAseq data, set to NULL for others).
scale	Boolean. If TRUE scale all variables to unit variance.
min.data.size	The minimum allowed number of variables (default: 100)
...	Additional arguments.
SE.name	SE.name the name of the dataset if the input object is a <a href="#">RflomicsMAE-class</a>
omicNames	the name of the experiment to summarize.
cluster	cluster number
condition	Default is group.
features	Default is NULL.
clusterName	name of the cluster

## Details

For now, only the coseq function of the coseq package is used. For RNAseq data, parameters used are those recommended in DiCoExpress workflow (see the reference). This parameters are: model="normal", transformation="arcsin", GaussianModel="Gaussian\_pk\_Lk\_Ck", normFactors="TMM", meanFilterCutoff = 50 For proteomics or metabolomics, data are scaled by protein or metabolite to group them by expression profiles rather than by expression intensity. After data scaling, recommended parameters (from coseq developers) for co-expression analysis are: model="normal", transformation="none", GaussianModel="Gaussian\_pk\_Lk\_Ck", normFactors="none", meanFilterCutoff = NULL.

## Value

An S4 object of class [RflomicsSE](#) All the results are stored as a named list CoExpAnal in the metadata slot of a given RflomicsSE object. Objects are: The runCoExpression method return several results, for [coseq](#) method, objects are:

- settings: co-expression analysis settings. See `getCoexpSetting`
- results: boolean indicating if the co-expression analysis succeed
  - coseqResults: the raw results of coseq
  - clusters: a List of clusters
  - cluster.nb: The number of cluster
  - plots: The plots of coseq results
  - stats: A tibble summarizing failed jobs: reason, proportion, if any
- errors: error list.

## Accessors

A set of getters and setters generic functions to access and modify objects of the slot metadata of a [RflomicsMAE-class](#) object or a [RflomicsMAE-class](#) object.

- `getCoexpSettings`: Access to the co-expression analysis settings of a given omics dataset
- `getCoexpClusters`: get members of a cluster. return The list of entities inside this cluster.

## Plots

A collection of functions for plotting results from omics analysis steps.

- `getCoExpAnalysesSummary`: ...
- `plotCoExpression`: list plot of ICL, logLikelihood and coseq object with min ICL
- `plotCoExpressionProfile`: ...
- `plotCoseqContrasts`: This function describes the composition of clusters according to the contrast to which the gene belongs

## References

Lambert, I., Paysant-Le Roux, C., Colella, S. et al. DiCoExpress: a tool to process multifactorial RNAseq experiments from quality controls to co-expression analysis through differential analysis based on contrasts inside GLM models. *Plant Methods* 16, 68 (2020).

## See Also

[coseq](#)  
[createRflomicsMAE](#)  
[generateModelFormulae](#)  
[generateExpressionContrast](#)  
[runDataProcessing](#)  
[runDiffAnalysis](#)

## Examples

```
# load ecoseed data
data(ecoseed.mae)

factorInfo <- data.frame(
  "factorName" = c("Repeat", "temperature", "imbibition"),
  "factorType" = c("batch", "Bio", "Bio")
)

# create rflomicsMAE object with ecoseed data
MAE <- RFLOMICS::createRflomicsMAE(
  projectName = "Tests",
```

```
omicsData = ecoseed.mae,
omicsTypes = c("RNAseq","proteomics","metabolomics"),
factorInfo = factorInfo)

# Set the statistical model and contrasts to test
formulae <- generateModelFormulae(MAE)
MAE <- setModelFormula(MAE, formulae[[1]])

# Get the contrasts List and choose the first 3 contrasts of type averaged
contrastList <- generateExpressionContrast(MAE, "averaged")

MAE <- setSelectedContrasts(MAE, contrastList = contrastList[c(1, 2, 3),])

# Run the data preprocessing and perform the differential analysis
MAE <- runDataProcessing(MAE, SE.name = "protetest",
                        transformMethod = "log2",
                        normMethod = "median")
MAE <- runDiffAnalysis(MAE, SE.name = "protetest")

# Run co-expression analysis
MAE <- runCoExpression(MAE, SE.name = "protetest",
                      K = 2:5, replicates = 5,
                      merge = "union")

# get parametres used to run co-expression analysis
coExp.set.list <- getCoexpSettings(MAE[["protetest"]])
coExp.set.list$method

# get results
clusters <- getCoexpClusters(MAE[["protetest"]], clusterName = "cluster_1")

# plots
#plotCoExpression(MAE[["protetest"]])

#plotCoExpressionProfile(MAE[["protetest"]], cluster = 2)

#plotCoseqContrasts(MAE[["protetest"]])
```

---

runDataProcessing      *Data Exploratory and processing*

---

## Description

These functions applied a data processing (filtering, normalization and/or transformation, PCA) on RNAseq, proteomics, or metabolomics data.

runDataProcessing() calls the following functions:

- runSampleFiltering: This function applied sample filtering on an dataset.

- `runFeatureFiltering`: This function allows filtering variables in omics data. In the case of RNA-seq data, it involves filtering out transcripts with low counts, while in the case of proteomics and metabolomics data, it applies the imputation procedure.
- `runTransformData`: This function applied a transformation to the dataset. The transformation method is chosen according to the dataset omicstype (RNAseq: none, metabolomics/proteomics: log2)
- `runNormalization`: This function applied a normalization on a dataset. The normalization method is chosen according to the dataset omics type (RNAseq: TMM, metabolomics/proteomics: median)
- `runOmicsPCA`: This function performs a principal component analysis on omic data stored in an object of class `RflomicsSE-class` Results are stored in the metadata slot of the same object. If a "Normalization" slot is present in the metadata slot, then data are normalized before running the PCA according to the indicated transform method.

This function performs a principal component analysis on omic data stored in an object of class `RflomicsSE-class` Results are stored in the metadata slot of the same object. If a "Normalization" slot is present in the metadata slot, then data are normalized before running the PCA according to the indicated transform method.

- `checkExpDesignCompleteness`: return a string with message. This method checks some experimental design characteristics. A complete design (all combinations of factor modalities with at least 2 replicates for each have to be present) with at least one biological and one batch factors are required to use the RFLOMICS workflow.
- `plotDataDistribution`: return boxplot or density plot of expression or abundance distribution.

## Usage

```
## S4 method for signature 'RflomicsSE'
runDataProcessing(
  object,
  samples = NULL,
  filterStrategy = NULL,
  cpmCutoff = NULL,
  transformMethod = NULL,
  normMethod = NULL,
  imputMethod = NULL,
  userTransMethod = "unknown",
  userNormMethod = "unknown"
)

## S4 method for signature 'RflomicsMAE'
runDataProcessing(
  object,
  SE.name,
  samples = NULL,
  filterStrategy = NULL,
```

```
    cpmCutoff = NULL,  
    transformMethod = NULL,  
    normMethod = NULL,  
    userTransMethod = "unknown",  
    userNormMethod = "unknown"  
  )  
  
  ## S4 method for signature 'RflomicsSE'  
  runSampleFiltering(object, samples = NULL)  
  
  ## S4 method for signature 'RflomicsMAE'  
  runSampleFiltering(object, SE.name, samples = NULL)  
  
  ## S4 method for signature 'RflomicsSE'  
  runFeatureFiltering(  
    object,  
    filterMethod = NULL,  
    filterStrategy = NULL,  
    cpmCutoff = NULL,  
    imputMethod = NULL  
  )  
  
  ## S4 method for signature 'RflomicsMAE'  
  runFeatureFiltering(  
    object,  
    SE.name,  
    filterMethod = NULL,  
    filterStrategy = NULL,  
    cpmCutoff = NULL,  
    imputMethod = NULL  
  )  
  
  ## S4 method for signature 'RflomicsSE'  
  runTransformData(object, transformMethod = NULL, userTransMethod = "unknown")  
  
  ## S4 method for signature 'RflomicsMAE'  
  runTransformData(  
    object,  
    SE.name,  
    transformMethod = NULL,  
    userTransMethod = "unknown"  
  )  
  
  ## S4 method for signature 'RflomicsSE'  
  runNormalization(object, normMethod = NULL, userNormMethod = "unknown")  
  
  ## S4 method for signature 'RflomicsMAE'  
  runNormalization(  

```

```
    object,
    SE.name,
    normMethod = NULL,
    userNormMethod = "unknown"
)

## S4 method for signature 'RflomicsSE'
runOmicsPCA(object, ncomp = 5, raw = FALSE)

## S4 method for signature 'RflomicsMAE'
runOmicsPCA(object, SE.name, ncomp = 5, raw = FALSE)

## S4 method for signature 'RflomicsSE'
checkExpDesignCompleteness(object, sampleList = NULL)

## S4 method for signature 'RflomicsMAE'
checkExpDesignCompleteness(object, omicName, sampleList = NULL)

## S4 method for signature 'RflomicsSE'
getProcessedData(
  object,
  filter = FALSE,
  trans = FALSE,
  norm = FALSE,
  log = FALSE
)

## S4 method for signature 'RflomicsMAE'
getProcessedData(
  object,
  SE.name,
  filter = FALSE,
  trans = FALSE,
  norm = FALSE,
  log = FALSE
)

## S4 method for signature 'RflomicsSE'
getTransSettings(object)

## S4 method for signature 'RflomicsMAE'
getTransSettings(object, SE.name)

## S4 method for signature 'RflomicsSE'
getFilterSettings(object)

## S4 method for signature 'RflomicsMAE'
getFilterSettings(object, SE.name)
```



```
## S4 method for signature 'RflomicsSE'
getFilteredFeatures(object)

## S4 method for signature 'RflomicsMAE'
getFilteredFeatures(object, SE.name)

## S4 method for signature 'RflomicsSE'
getSelectedSamples(object)

## S4 method for signature 'RflomicsMAE'
getSelectedSamples(object, SE.name)

## S4 method for signature 'RflomicsSE'
getCoeffNorm(object)

## S4 method for signature 'RflomicsMAE'
getCoeffNorm(object, SE.name)

## S4 method for signature 'RflomicsSE'
getNormSettings(object)

## S4 method for signature 'RflomicsMAE'
getNormSettings(object, SE.name)

## S4 method for signature 'RflomicsSE'
plotLibrarySize(object, raw = FALSE)

## S4 method for signature 'RflomicsMAE'
plotLibrarySize(object, SE.name, raw = FALSE)

## S4 method for signature 'RflomicsSE'
plotDataDistribution(object, plot = "boxplot", raw = FALSE)

## S4 method for signature 'RflomicsMAE'
plotDataDistribution(object, SE.name, plot = "boxplot", raw = FALSE)

## S4 method for signature 'RflomicsSE'
plotOmicsPCA(object, raw = TRUE, axes = c(1, 2), groupColor = "groups")

## S4 method for signature 'RflomicsMAE'
plotOmicsPCA(
  object,
  SE.name,
  raw = FALSE,
  axes = c(1, 2),
  groupColor = "groups"
)
```

```

## S4 method for signature 'RflomicsSE'
plotExpDesignCompleteness(object, sampleList = NULL)

## S4 method for signature 'RflomicsMAE'
plotExpDesignCompleteness(object, omicName, sampleList = NULL)

## S4 method for signature 'RflomicsSE'
isProcessedData(
  object,
  filter = FALSE,
  trans = FALSE,
  norm = FALSE,
  log = FALSE
)

## S4 method for signature 'RflomicsMAE'
isProcessedData(
  object,
  SE.name,
  filter = TRUE,
  trans = TRUE,
  norm = TRUE,
  log = FALSE
)

```

### Arguments

object	An object of class <a href="#">RflomicsSE-class</a> .
samples	samples to keep.
filterStrategy	The filtering strategy ("NbConditions" or "NbReplicates") for RNAseq data.
cpmCutoff	The CPM cutoff for RNAseq data.
transformMethod	The transformation method to store in the metadata
normMethod	Normalization method. Accepted values: TMM for RNAseq, and median, total-Sum, or none for proteomics and metabolomics data. Default values: TMM for RNAseq data and median for proteomics and metabolomics data
imputMethod	The imputation method ("MVI") for proteomics and metabolomics data.
userTransMethod	method used by user to transform data.
userNormMethod	method used by user to normalize data.
SE.name	the name of the data the normalization have to be applied to.
filterMethod	The filtering model ("CPM") for RNAseq data.
ncomp	Number of components to compute. Default is 5.
raw	boolean. Does the pca have to be ran on raw data or transformed

sampleList	list of samples to check.
omicName	a character string with the name of the dataset
filter	boolean. If TRUE, check if data is filtered (low counts/RNAseq)
trans	boolean. If TRUE, check if data is transformed
norm	boolean. If TRUE, check if data is normalized
log	boolean. If TRUE, check if the data has been log-transformed (RNAseq).
plot	plot type ("boxplot" or "density")
axes	A vector giving the two axis that have to be drawn for the factorial map
groupColor	All combination of level's factor

### Details

Low count filtering procedure: By default, transcript with 0 count are removed from the data. The function then computes the count per million or read (CPM) for each gene in each sample and gives by genes the number of sample(s) which are over the cpmCutoff (NbOfsample\_over\_cpm). Then Two filtering strategies are proposed:

- NbConditions: keep gene if the NbOfsample\_over\_cpm  $\geq$  NbConditions
- NbReplicates: keep gene if the NbOfsample\_over\_cpm  $\geq$  min(NbReplicates)
- filterByExpr: the default filtering method implemented in the edgeR filterByExpr() function.

Missing value imputation: This approach, applied to proteomics and metabolomics data, replaces missing values (0 or NA) with the minimum value among all non-zero values. Additionally, variables with at least one condition group without any missing values are retained without further filtering.

### Value

An object of class [RflomicsSE](#) or class [RflomicsSE](#)

An object of class [RflomicsSE](#) The applied normalization method and computed scaling factors (by samples) are stored as a named list ("normalization") of two elements (respectively "method" and "coefNorm") in the metadata slot of a given data set, stored itself in the ExperimentList slot of a [RflomicsSE](#) object.

An object of class [RflomicsSE](#)

### Accessors

- getProcessedData: return RflomicsSE object with a processed data (filtering, normalization and/or transformation)
- getTransSettings: return a list of transformation settings of a given omics dataset
- getFilterSettings: return a list the filtering settings of a given omics dataset
- getFilteredFeatures: return a vector of filtered features of a given omics dataset
- getSelectedSamples: return a vector of selected samples of a given omics dataset

- `getCoeffNorm`: return a named vector with normalization coefficients of a given omics dataset
- `getNormSettings`: return a list of normalization settings of a given omics dataset
- `isProcessedData`: return

### Plots

- `plotLibrarySize`: return barplot of library size by sample.
- `plotOmicsPCA`: This function plot the factorial map from a PCA object stored in a [RflomicsSE-class](#) object. By default, samples are colored by groups (all combinations of level's factor)
- `plotExpDesignCompleteness`: This method checks that experimental design constraints are satisfied and plot a summary of the design. A complete design (all combinations of factor modalities with at least 2 replicates for each have to be present) with at least one biological and one batch factors are required to use the RFLOMICS workflow.

### References

Lambert, I., Paysant-Le Roux, C., Colella, S. et al. DiCoExpress: a tool to process multifactorial RNAseq experiments from quality controls to co-expression analysis through differential analysis based on contrasts inside GLM models. *Plant Methods* 16, 68 (2020).

### See Also

[RflomicsMAE-class](#) [RflomicsSE-class](#) [getProcessedData](#) [getTransSettings](#) [getFilterSettings](#) [getFilteredFeatures](#) [getCoeffNorm](#) [getNormSettings](#) [plotLibrarySize](#) [plotDataDistribution](#) [plotOmicsPCA](#)

### Examples

```
# load ecoseed data
data(ecoseed.mae)

factorInfo <- data.frame(
  "factorName" = c("Repeat", "temperature", "imbibition"),
  "factorType" = c("batch", "Bio", "Bio")
)

# create rflomicsMAE object with ecoseed data
MAE <- RFLOMICS::createRflomicsMAE(
  projectName = "Tests",
  omicsData = ecoseed.mae,
  omicsTypes = c("RNAseq", "proteomics", "metabolomics"),
  factorInfo = factorInfo)

# Set the statistical model
formulae <- generateModelFormulae(MAE)
MAE <- setModelFormula(MAE, formulae[[1]])

# set the contrast list
```

```

contrastList <- generateExpressionContrast(MAE, "averaged")
MAE <- setSelectedContrasts(MAE, contrastList = contrastList[c(1, 2, 3),])

# Data processing of RNAseq dataset : RNAtest
## using data processing functions for RNAseq data
### filter low RNAseq count
# MAE <- filterLowAbundance(MAE, SE.name = "RNAtest",
#                             filterStrategy = "NbReplicates",
#                             cpmCutoff = 1)
# ### filter outlier samples
# MAE <- runSampleFiltering(MAE, SE.name = "RNAtest",
#                             samples = colnames(MAE[["RNAtest"]])[-1])
# ### data normalisation outlier samples
# MAE <- runNormalization(MAE, SE.name = "RNAtest",
#                             normMethod = "TMM")

## use runDataProcessing function that combines the previous three functions
MAE <- runDataProcessing(MAE, SE.name = "RNAtest",
                          samples = colnames(MAE[["RNAtest"]])[-1],
                          filterStrategy = "NbReplicates",
                          cpmCutoff = 1,
                          normMethod = "TMM")

## check completeness of RNAtest data
checkExpDesignCompleteness(MAE, omicName = "RNAtest")$messages

# Data processing of proteomics dataset : protetest
# ## transform data
# MAE <- runTransformData(MAE, SE.name = "protetest", transformMethod = "log2")
# ## normalise data
# MAE <- runNormalization(MAE, SE.name = "protetest", normMethod = "median")

## use runDataProcessing function
MAE <- runDataProcessing(MAE, SE.name = "protetest",
                          normMethod = "median",
                          transformMethod = "log2")

# plotExpDesignCompleteness(MAE[["RNAtest"]])

# plot Library Size
# plotDataDistribution(MAE[["RNAtest"]], raw=TRUE)
# plotDataDistribution(MAE[["RNAtest"]], raw=FALSE)

# plot gene expression distribution
# plotDataDistribution(MAE[["RNAtest"]], raw=TRUE, plot = "boxplot")
# plotDataDistribution(MAE[["RNAtest"]], raw=FALSE, plot = "boxplot")

# plot PCA
# plotOmicsPCA(MAE[["RNAtest"]], raw="raw", groupColor = "imbibition")
# plotOmicsPCA(MAE[["RNAtest"]], raw="norm", groupColor = "imbibition")

# See runDataProcessing for an example that includes getTransSettings
# See runDataProcessing for an example that includes getFilterSettings

```

```

# See runDataProcessing for an example that includes getFilteredFeatures
# See runDataProcessing for an example that includes getSelectedSamples
# See runDataProcessing for an example that includes getCoeffNorm
# See runDataProcessing for an example that includes getNormSettings
# See runDataProcessing for an example that includes plotLibrarySize
# See runDataProcessing for an example that includes plotDataDistribution
# See runDataProcessing for an example that includes plotOmicsPCA
# See runDataProcessing for an example that includes plotExpDesignCompleteness

```

---

runDiffAnalysis

*Run Differential Expression Analysis and process results*


---

## Description

This is an interface method which run a differential analysis on omics datasets stored in an object of class [RflomicsSE](#) or [RflomicsMAE-class](#). According to the type of omics and to a list of contrasts, a differential analysis is performed for each contrasts. Two methods are available according to the type of object:

- For RNAseq data: the `glmFit` function/model of the `edgeR` package is applied.
- For proteomics and metabolomics data: the `lmFit` function/model of the `limma` package is applied.
- `filterDiffAnalysis`: The `filterDiffAnalysis` method allows filtering the results of the differential analysis based on a new cutoff for p-value and fold change.
- `setValidContrasts`: Set the valid contrasts stored in metadata slot.

## Usage

```

## S4 method for signature 'RflomicsSE'
runDiffAnalysis(
  object,
  contrastList = NULL,
  method = NULL,
  p.adj.method = "BH",
  p.adj.cutoff = 0.05,
  logFC.cutoff = 0,
  cmd = FALSE,
  ...
)

## S4 method for signature 'RflomicsMAE'
runDiffAnalysis(
  object,
  SE.name,
  contrastList = NULL,
  method = NULL,

```

```
p.adj.method = "BH",
p.adj.cutoff = 0.05,
logFC.cutoff = 0,
cmd = FALSE,
...
)

## S4 method for signature 'RflomicsSE'
filterDiffAnalysis(object, p.adj.cutoff = 0.05, logFC.cutoff = 0)

## S4 method for signature 'RflomicsMAE'
filterDiffAnalysis(object, SE.name, p.adj.cutoff = 0.05, logFC.cutoff = 0)

## S4 method for signature 'RflomicsSE'
setValidContrasts(object, contrastList = NULL)

## S4 method for signature 'RflomicsMAE'
setValidContrasts(object, omicName = NULL, contrastList = NULL)

## S4 method for signature 'RflomicsSE'
plotDiffAnalysis(
  object,
  contrastName,
  typeofplots = c("MA.plot", "volcano", "histogram")
)

## S4 method for signature 'RflomicsMAE'
plotDiffAnalysis(
  object,
  SE.name,
  contrastName,
  typeofplots = c("MA.plot", "volcano", "histogram")
)

## S4 method for signature 'RflomicsSE'
plotHeatmapDesign(
  object,
  contrastName,
  splitFactor = "none",
  title = "",
  annotNames = NULL,
  modalities = NULL,
  drawArgs = list(),
  heatmapArgs = list()
)

## S4 method for signature 'RflomicsMAE'
plotHeatmapDesign(
```

```
    object,
    SE.name,
    contrastName,
    splitFactor = "none",
    title = "",
    annotNames = NULL,
    modalities = NULL,
    drawArgs = list(),
    heatmapArgs = list()
)

## S4 method for signature 'RflomicsSE'
plotBoxplotDE(object, featureName = NULL, groupColor = "groups", raw = FALSE)

## S4 method for signature 'RflomicsMAE'
plotBoxplotDE(
  object,
  SE.name,
  featureName = NULL,
  groupColor = "groups",
  raw = FALSE
)

## S4 method for signature 'RflomicsSE'
getDEMatrix(object)

## S4 method for signature 'RflomicsMAE'
getDEMatrix(object, SE.name)

## S4 method for signature 'RflomicsSE'
getDEList(object, contrasts = NULL, operation = "union")

## S4 method for signature 'RflomicsMAE'
getDEList(object, SE.name, contrasts = NULL, operation = "union")

## S4 method for signature 'RflomicsSE'
getDiffSettings(object)

## S4 method for signature 'RflomicsMAE'
getDiffSettings(object, SE.name)

## S4 method for signature 'RflomicsSE'
getValidContrasts(object)

## S4 method for signature 'RflomicsMAE'
getValidContrasts(object, omicName)

## S4 method for signature 'RflomicsSE'
```



```

getDiffStat(object)

## S4 method for signature 'RflomicsMAE'
getDiffStat(object, SE.name = NULL)

## S4 method for signature 'RflomicsMAE'
getDiffAnalysesSummary(
  object,
  plot = FALSE,
  ylabelLength = 30,
  nbMaxLabel = 20,
  interface = FALSE
)

```

### Arguments

object	An object of class <a href="#">RflomicsSE</a> or class <a href="#">RflomicsMAE-class</a>
contrastList	A data.frame of contrast
method	A character vector giving the name of the differential analysis method to run. Either "edgeRglmfit" or "limmalmFit".
p.adj.method	The method chosen to adjust pvalue. Takes the same values as the ones of adj.p.adjust method.
p.adj.cutoff	adjusted pvalue cutoff. Default is the parameter from the differential analysis.
logFC.cutoff	cutoff for absolute value of log2FC. Default is the parameter from the differential analysis.
cmd	Boolean. Used in the interface. If TRUE, print cmd for the user.
...	Additional arguments.
SE.name	SE.name the name of the dataset if the input object is a <a href="#">RflomicsMAE-class</a>
omicName	a dataset name
contrastName	The contrastName for which the MAplot has to be drawn
typeofplots	The plots you want to return. Default is all possible plots: MA plot, Volcano plot and non adjusted pvalues histogram.
splitFactor	characters. Default to none. Name of a feature in the design matrix, splits the samples on the heatmap according to its modalities.
title	characters. Title of the heatmap.
annotNames	vector. Names of the annotations to keep in the Heatmap. Default takes all available information.
modalities	named list of vectors of modalities to subset and print on the heatmap.
drawArgs, heatmapArgs	named lists. Any additional parameter passed to <code>ComplexHeatmap::Heatmap</code> or <code>ComplexHeatmap::draw</code>
featureName	variable name (gene/protein/metabolite name)
groupColor	default to groups, indicate a variable in the design to color the boxplots accordingly.

raw	Boolean. Plot the raw data or the transformed ones (TRUE)
contrasts	Vector of characters, expect to be contrast names. Default is null, the operation (union) is performed on every contrasts found.
operation	character. Either union or intersection. Defines the operation to perform on the DE lists from the contrasts.
plot	FALSE or TRUE
ylabLength	max length of the labels (characters)
nbMaxLabel	number of labels to print
interface	Boolean. Is this plot for the interface or commandline?

### Details

Functions and parameters used for RNAseq are those recommended in DiCoExpress workflow (see the paper in reference). Functions and parameters used for proteomics and metabolomics data are those recommended in the (Efstathiou \*et al.\*, 2017)

### Value

A [RflomicsSE](#) or a [RflomicsMAE-class](#) object. All the results are stored as a named list `DiffExpAnal` in the metadata slot of a given [RflomicsSE](#) object. Objects are:

- stats: data.frame giving a summary of the differential statistical analysis results by contrast: number of DE features, number of up and down regulated features
- setting: Parameters used for the differential analysis
- method: The method used for the differential analysis
- p.adj.method: The applied p-value correction method
- p.adj.cutoff: The cut-off applied for the adjusted p-value
- logFC.cutoff: The absolute log FC cut-off
- RawDEFres: a list giving for each contrast the raw results of the differential analysis method
- DEF: a list giving for each contrast a data.frame of non filtered differential expressed features with their statistics
- TopDEF: a list giving for each contrast a data.frame of differential expressed features ordered and filtered by p.adj.cutoff with their statistics
- mergeDEF: a data frame of 0 and 1 indicating for each features in row, if it is DE in a given contrasts in column
- contrasts: a data.table of the contrasts used for the differential analysis

a data.frame with differential analyses summary

### Accessors

- getDEMatrix: return a matrix of experimental design.
- getDEList: return a vector of union or intersection of differential expressed features from list of contrasts.

- `getDiffSettings`: return a list of differential expression analysis settings of a given omics dataset
- `getValidContrasts`: return a `data.frame` of validated contrasts
- `getDiffStat`: Get summary table from `diffExpAnalysis` analysis
- `getDiffAnalysesSummary`: ...

## Plots

- `plotDiffAnalysis` method draws a `MPlot`, a volcano plot and the p-values distribution from the results of a differential analysis.
- `plotHeatmapDesign` method draws a heatmap from the results of a differential analysis.
- `plotBoxplotDE` method draws a boxplot showing the expression of given differentially expressed feature.

## References

Lambert, I., Paysant-Le Roux, C., Colella, S. et al. DiCoExpress: a tool to process multifactorial RNAseq experiments from quality controls to co-expression analysis through differential analysis based on contrasts inside GLM models. *Plant Methods* 16, 68 (2020).

Efstathiou G, Antonakis AN, Pavlopoulos GA, et al. ProteoSign: an end-user online differential proteomics statistical analysis platform. *Nucleic Acids Res.* 2017;45(W1):W300-W306.

## See Also

[getDiffSettings](#), [getDEList](#), [getDEMatrix](#)  
[plotDiffAnalysis](#), [plotHeatmapDesign](#), [plotBoxplotDE](#)

## Examples

```
# load ecoseed data
library(RFLOMICS)
data(ecoseed.mae)

factorInfo <- data.frame(
  "factorName" = c("Repeat", "temperature", "imbibition"),
  "factorType" = c("batch", "Bio", "Bio")
)

# create rflomicsMAE object with ecoseed data
MAE <- RFLOMICS::createRflomicsMAE(
  projectName = "Tests",
  omicsData = ecoseed.mae,
  omicsTypes = c("RNAseq", "proteomics", "metabolomics"),
  factorInfo = factorInfo)

# Set the statistical model and contrasts to test
```

```

formulae <- generateModelFormulae(MAE)
MAE <- setModelFormula(MAE, formulae[[1]])

# Get the contrasts List and choose the first 3 contrasts of type averaged
contrastList <- generateExpressionContrast(MAE, "averaged")

MAE <- setSelectedContrasts(MAE, contrastList = contrastList[c(1, 2, 3),])

# Run the data preprocessing and perform the differential analysis
MAE <- runDataProcessing(MAE, SE.name = "protetest",
                        transformMethod = "log2",
                        normMethod = "median")

MAE <- runDiffAnalysis(MAE, SE.name = "protetest",
                      method = "limlmFit")

# or
# MAE[["protetest"]] <- runDiffAnalysis(MAE[["protetest"]],
#                                     method = "limlmFit",
#                                     contrastList = contrastList)

# Filter the results of the differential analysis with new cut-off values
# for p-value and fold change.
MAE <- filterDiffAnalysis(MAE, SE.name = "protetest",
                         p.adj.cutoff = 0.01,
                         logFC.cutoff = 0)

# or
# MAE[["protetest"]] <- filterDiffAnalysis(MAE[["protetest"]],
#                                     p.adj.cutoff = 0.01,
#                                     logFC.cutoff = 0)

# Access to the diff analysis settings
## Get DE matrix from DiffExpAnalysis
head(getDEMatrix(MAE[["protetest"]]))

## Get union or intersection from list of contrasts
getDEList(MAE[["protetest"]], contrasts = "(temperatureMedium - temperatureLow) in mean")

## Get diff setting
getDiffSettings(MAE[["protetest"]])

# generate plot results of a differential analysis
thiscontrast <- "(temperatureMedium - temperatureLow) in mean"

## generate MAplot from diff analysis
# plotDiffAnalysis(MAE[["protetest"]],
#                 contrastName = thiscontrast,
#                 typeofplots = "MA.plot")

## plot the heatmap
# plotHeatmapDesign(MAE[["protetest"]],
#                  contrastName = thiscontrast)

## plot boxplot with feature expression

```

```

# plotBoxplotDE(MAE[["protetest"]],
#               features = "AT1G47128",
#               groupColor = "temperature")
# plotBoxplotDE(MAE[["protetest"]],
#               features = "AT1G79550",
#               groupColor = "imbibition")

# See runDiffAnalysis for an example that includes plotDiffAnalysis
# See runDiffAnalysis for an example that includes plotHeatmapDesign
# See runDiffAnalysis for an example that includes plotBoxplotDE
# See runDiffAnalysis for an example that includes getDEMatrix
# See runDiffAnalysis for an example that includes getDEList
# See runDiffAnalysis for an example that includes getDiffSettings

```

---

```

runOmicsIntegration,RflomicsMAE-method
      runOmicsIntegration

```

---

## Description

Runs the integration according to the selected method (MOFA or mixOmics) and the settings given by the user. Requires to have the correct entry format in preparedObject before running.

These methods are used to directly access the results of multi-omics analyses or their settings, usually stored in the metadata of the [RflomicsMAE-class](#) object. Setters are also available.

## Usage

```

## S4 method for signature 'RflomicsMAE'
runOmicsIntegration(
  object,
  preparedObject = NULL,
  method = "MOFA",
  scale_views = FALSE,
  maxiter = 1000,
  num_factors = 10,
  selectedResponse = NULL,
  ncomp = 2,
  link_datasets = 1,
  link_response = 1,
  sparsity = FALSE,
  cases_to_try = 5,
  cmd = FALSE,
  ...
)

## S4 method for signature 'RflomicsMAE'
getMixOmics(object, response = NULL, onlyResults = TRUE)

```

```

## S4 method for signature 'RflomicsMAE'
getMOFA(object, onlyResults = TRUE)

## S4 method for signature 'RflomicsMAE'
getMOFASettings(object)

## S4 method for signature 'RflomicsMAE'
getMixOmicsSettings(object)

## S4 method for signature 'RflomicsMAE'
setMOFA(object, results = NULL)

## S4 method for signature 'RflomicsMAE'
setMixOmics(object, results = NULL)

## S4 method for signature 'RflomicsMAE'
sumMixOmics(object, selectedResponse = NULL)

```

### Arguments

<code>object</code>	a <code>RflomicsMAE</code> object.
<code>preparedObject</code>	An untrained MOFA object or a list of dataset. Usually a result of <code>prepareForIntegration</code> .
<code>method</code>	one of MOFA or <code>mixOmics</code> . Method for which the object is prepared.
<code>scale_views</code>	boolean. If TRUE, scale each dataset to unit variance.
<code>maxiter</code>	MOFA2 parameter. Number of max iteration (otherwise stop when converged).
<code>num_factors</code>	MOFA2 parameter. The number of factor to compute.
<code>selectedResponse</code>	a character. Useful if <code>MixOmics</code> was run on several response variable. If NULL, all variables are taken into account.
<code>ncomp</code>	<code>mixOmics</code> parameter. Number of components to compute.
<code>link_datasets</code>	<code>mixOmics</code> parameter. Link between datasets in the computation.
<code>link_response</code>	<code>mixOmics</code> parameter. Link between dataset and response.
<code>sparsity</code>	boolean. Used to determine which <code>mixOmics</code> function to apply (either <code>block.plsda</code> if FALSE or <code>block.splsda</code> if TRUE).
<code>cases_to_try</code>	integer. If <code>sparsity</code> is set to TRUE, then <code>cases_to_try</code> is used to determine the number of sets of variables to test for tuning.
<code>cmd</code>	boolean. Used in the interface. If TRUE, print <code>cmd</code> in the console.
<code>...</code>	not in use at the moment
<code>response</code>	a character giving the response variable to access specifically.
<code>onlyResults</code>	default return only the <code>MixOmics</code> or MOFA2 results. If you want to access all information of the integration, set <code>onlyResults</code> to FALSE. In <code>MixOmics</code> case, works only when <code>response</code> is specified.
<code>results</code>	The MOFA or <code>mixOmics</code> results to set in the object. If null, set to NULL.

**Value**

a RflomicsMAE object with the correct metadata slot filled with the results and the settings.

For getters: in getMixOmics, if response is NULL, then all the mixOmics results are returned. Otherwise, it gives the particular mixOmics result. For MOFA, returns the untrained object and the trained object as a list.

For setters: always returns a RflomicsMAE-class object.

sumMixOmics: A data frame or a list of dataframe (if selectedResponse is NULL) presenting the summary of mixOmics analyses.

**Examples**

```
# load ecoseed data
library(RFLOMICS)
data(ecoseed.mae)

factorInfo <- data.frame(
  "factorName" = c("Repeat", "temperature", "imbibition"),
  "factorType" = c("batch", "Bio", "Bio")
)

# create rflomicsMAE object with ecoseed data
MAE <- RFLOMICS::createRflomicsMAE(
  projectName = "Tests",
  omicsData = ecoseed.mae,
  omicsTypes = c("RNAseq", "proteomics", "metabolomics"),
  factorInfo = factorInfo)

formulae <- generateModelFormulae( MAE)
MAE <- setModelFormula(MAE, formulae[[1]])
contrastList <- Reduce(rbind, generateExpressionContrast(MAE))

MAE <- MAE |>
  setSelectedContrasts(contrastList[c(3,6,25)]) |>
  runDataProcessing(SE.name = "metatest",
    transformMethod = "log2",
    normMethod = "median") |>
  runDataProcessing(SE.name = "protetest",
    transformMethod = "none",
    normMethod = "median") |>
  runDiffAnalysis(SE.name = "metatest", method = "limmaFit") |>
  runDiffAnalysis(SE.name = "protetest", method = "limmaFit")

# Integration using MOFA
# Prepare mofa object:
mofaObj <- prepareForIntegration(MAE,
  omicsNames = c("protetest", "metatest"),
  variableLists = rownames(MAE),
  method = "MOFA")

# Perform integration:
# Not run: MAEtest <- runOmicsIntegration(MAE,
```

```
#                                     preparedObject = mofaObj,
#                                     method = "MOFA", num_factors = 5)

# Integration using MixOmics
mixObj <- prepareForIntegration(MAE,
                              omicsNames = c("protetest", "metatest"),
                              variableLists = rownames(MAE),
                              method = "mixOmics")
MAEtest <- runOmicsIntegration(MAE, preparedObject = mixObj,
                              method = "mixOmics")

# Access mixOmics results:
# getMixOmics(MAEtest, response = "temperature")
getMixOmicsSettings(MAEtest)
# mixOmics::plotIndiv(getMixOmics(MAEtest, response = "imbibition"))

# Access MOFA2 results:
# getMOFA(MAEtest)
# getMOFASettings(MAEtest)
# MOFA2::plot_variance_explained(getMOFA(MAEtest))
```

---

runRFLOMICS

*Run RFLOMICS interface*

---

## Description

running this function will open the shiny application. Run the shiny application

## Usage

```
runRFLOMICS(...)
```

## Arguments

... More arguments to pass to shinyApp.

## Value

shinyApp

## Examples

```
library(RFLOMICS)
## Not run: runRFLOMICS()
```



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