Package 'gINTomics'

November 12, 2026

Title Multi-Omics data integration

Version 1.8.0

Description gINTomics is an R package for Multi-Omics data integration and visualization.
gINTomics is designed to detect the association between the expression of a target and of its regulators, taking into account also their genomics modifications such as Copy Number Variations (CNV) and methylation.
What is more, gINTomics allows integration results visualization via a Shiny-based interactive app.

License AGPL-3

biocViews GeneExpression, RNASeq, Microarray, Visualization, CopyNumberVariation, GeneTarget

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Imports BiocParallel, biomaRt, OmnipathR, edgeR, ggplot2, ggridges, gtools, MultiAssayExperiment, plyr, stringi, stringr, SummarizedExperiment, methods, stats, reshape2, randomForest, limma, org.Hs.eg.db, org.Mm.eg.db, BiocGenerics, GenomicFeatures, ReactomePA, clusterProfiler, dplyr, AnnotationDbi, TxDb.Hsapiens.UCSC.hg38.knownGene, TxDb.Mmusculus.UCSC.mm10.knownGene, shiny, GenomicRanges, ggtree, shinydashboard, plotly, DT, MASS, InteractiveComplexHeatmap, ComplexHeatmap, visNetwork, shiny.gosling, ggvenn, RColorBrewer, utils, grDevices, callr, circlize, MethylMix, shinyjs

Depends R (>= 4.4.0)

LazyData false

Suggests BiocStyle, knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

BugReports https://github.com/angelovelle96/gINTomics/issues

URL https://github.com/angelovelle96/gINTomics

git_url https://git.bioconductor.org/packages/gINTomics

git_branch RELEASE_3_23

git_last_commit a84669e

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-11

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gINTomics-package *gINTomics: Multi-Omics data integration*

Description

gINTomics is an R package for Multi-Omics data integration and visualization. gINTomics is designed to detect the association between the expression of a target and of its regulators, taking into account also their genomics modifications such as Copy Number Variations (CNV) and methylation. What is more, gINTomics allows integration results visualization via a Shiny-based interactive app.

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See Also

Useful links:

- https://github.com/angelovelle96/gINTomics
- Report bugs at https://github.com/angelovelle96/gINTomics/issues

create_multiassay *MultiAssayExperiment generation*

Description

This function will generate a proper MultiAssayExperiment suitable for the **run_multiomics** function.

Usage

```
create_multiassay(
  methylation = NULL,
  cnv_data = NULL,
  gene_exp = NULL,
  miRNA_exp = NULL,
  miRNA_cnv_data = NULL,
  ...
)
```

Arguments

methylation	Matrix or SummarizedExperiment for Methylation data
cnv_data	Matrix or SummarizedExperiment for genes' Copy Number Variation data
gene_exp	Matrix or SummarizedExperiment for Gene expression data
miRNA_exp	Matrix or SummarizedExperiment for miRNA expression data
miRNA_cnv_data	Matrix or SummarizedExperiment for miRNA's Copy Number Variations data
...	Additional arguments to be passed to the function

Value

A MultiAssayExperiment object containing the provided assays.

Examples

```
# Example usage:
library(MultiAssayExperiment)
data('mmultiassay_ov')
gene_exp_matrix <- as.matrix(assay(mmultiassay_ov[['gene_exp']]))
miRNA_exp_matrix <- as.matrix(assay(mmultiassay_ov[['miRNA_exp']]))
meth_matrix <- as.matrix(assay(mmultiassay_ov[['methylation']]))
gene_cnv_matrix <- as.matrix(assay(mmultiassay_ov[['cnv_data']]))
miRNA_cnv_matrix <- as.matrix(assay(mmultiassay_ov[['miRNA_cnv_data']]))
create_multiassay(methylation=meth_matrix, cnv_data=gene_cnv_matrix,
 gene_exp=gene_exp_matrix, miRNA_exp=miRNA_exp_matrix,
 miRNA_cnv_data=miRNA_cnv_matrix)
```

---

dot_plotly *plotting enrichment*

Description

plotting enrichment

Usage

```
dot_plotly(
  enrich_result,
  title = NULL,
  showCategory = 10,
  width = 800,
  height = 700
)
```

Arguments

enrich_result	Enrichment analysis results.
title	Title of the plot.
showCategory	Number of categories to display.
width	Width of the plot.
height	Height of the plot.

Value

A plotly object containing the dot plot.

Examples

```
# Example usage:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
#multiomics_integration <- run_multiomics(data = mmultiassay_ov)
#gen_enr <- run_genomic_enrich(multiomics_integration,
#                              qvalueCutoff = 1,
#                              pvalueCutoff = 0.05,
#                              pAdjustMethod = "none")
#dot_plotly(gen_enr, title = "Enrichment Analysis",showCategory = 10)
```

---

extract_model_res *Setting method for extracting results*

Description

Setting method for extracting results

Usage

```
extract_model_res(model_results, ...)

## S4 method for signature 'list'
extract_model_res(
  model_results,
  outliers = TRUE,
  species = "hsa",
  filters = c("hgnc_symbol", "ensembl_gene_id", "entrezgene_id"),
  genes_info = NULL,
  ...
)
```

```
## S4 method for signature 'MultiClass'
extract_model_res(
  model_results,
  outliers = TRUE,
  species = "hsa",
  filters = c("hgnc_symbol", "ensembl_gene_id", "entrezgene_id"),
  genes_info = NULL,
  ...
)

## S4 method for signature 'MultiOmics'
extract_model_res(
  model_results,
  outliers = TRUE,
  species = "hsa",
  filters = c("hgnc_symbol", "ensembl_gene_id", "entrezgene_id"),
  genes_info = NULL,
  ...
)
```

Arguments

model_results	The model results object from which to extract results.
...	Additional arguments to be passed to specific methods.
outliers	if TRUE (by default), it removes outliers
species	species for the analysis
filters	Specific filters to apply
genes_info	genes info

Value

A dataframe containing the results of all the integration models provided

Examples

```
# example code
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
gene_cnv_matrix <- t(as.matrix(assay(mmultiassay_ov[["cnv_data"]])))
gene_exp_matrix <- t(as.matrix(assay(mmultiassay_ov[["gene_exp"]])))
cnv_integration <- run_cnv_integration(
    expression = gene_exp_matrix,
    cnv_data = gene_cnv_matrix
)
data_table <- extract_model_res(cnv_integration)
head(data_table)
```

`mirna_hsa` *miRNA IDs. Dataset containing lastly definition of miRNAs (Names, Accessions, Sequences, Families and others) from different miRBase versions (From miRBase version 6 to version 22).*

Description

miRNA IDs. Dataset containing lastly definition of miRNAs (Names, Accessions, Sequences, Families and others) from different miRBase versions (From miRBase version 6 to version 22).

Usage

```
data(mirna_hsa)
"mirna_hsa"
```

Format

data.frame

Value

An object of class data.frame.

Examples

```
# example code
data(mirna_hsa)
head(mirna_hsa)
```

`mmultiassay_ov` *Example data for a standard workflow. This is an example dataset containing a MultiAssayExperiment of 20 ovarian cancer (OVC) patients extracted from the Cancer Genome Atlas (TCGA) database. The object contains all the available input data types: Gene expression data, miRNA expression data, gene methylation data, gene Copy Number Variations and miRNA Copy Number Variations.*

Description

Example data for a standard workflow. This is an example dataset containing a MultiAssayExperiment of 20 ovarian cancer (OVC) patients extracted from the Cancer Genome Atlas (TCGA) database. The object contains all the available input data types: Gene expression data, miRNA expression data, gene methylation data, gene Copy Number Variations and miRNA Copy Number Variations.

Usage

```
data(mmultiassay_ov)
"mmultiomics_ov"
```

Format

MultiAssayExperiment

Value

An object of class MultiAssayExperiment.

Examples

```
# example code
data(mmultiassay_ov)
mmultiassay_ov
```

MultiClass-class *MultiClass Class*

Description

S4 class containing the output of a single integration integration, for which classes has been provided. It's a list in which each element represents the result of the integration for a given class. The length will be equal to the number of classes defined.

Value

MultiOmics Class

MultiOmics-class *MultiOmics Class*

Description

S4 class containing the output of a multiomics integration. It's a list in which each element represents the result of an integration. If all the available omics are provided, it will be a list of integrations: **gene_genomic_res**, **mirna_cnv_res**, **tf_res**, **tf_mirna_res** and **mirna_target_res**

Value

MultiOmics Class

plot_chr_distribution *plotting chr distribution*

Description

plotting chr distribution

Usage

```
plot_chr_distribution(data_table, omics = NULL, cnv_met = NULL, pval = 0.05)
```

Arguments

data_table	The data table containing information for plotting chromosome distribution.
omics	Optional. The type of omics data for the plot.
cnv_met	Optional. The type of copy number variation or methylation data.
pval	Optional. The p-value threshold for significance. Default is 0.05.

Value

A histogram plot showing chromosome distribution.

Examples

```
# Example usage:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
# multiomics_integration <- run_multiomics(data = mmultiassay_ov)
# data_table <- extract_model_res(multiomics_integration)
# plot_chr_distribution(data_table, omics = "gene_genomic_res")
```

plot_heatmap *plotting heatmap*

Description

plotting heatmap

Usage

```
plot_heatmap(
  multiomics_integration,
  data_table,
  omics,
  scale = "none",
  genes_number = 50,
  samples_number = 50,
  pval = 0.05
)
```

Arguments

multiomics_integration	The multiomics integration object.
data_table	The data table containing information for the heatmap.
omics	The type of omics data for the heatmap.
scale	Optional. The scale type for the heatmap. Default is "none".
genes_number	Optional. The number of genes to include in the heatmap. Default is 50.
samples_number	Number of samples to include in the heatmap. If this number is inferior to the total number of samples, the n most variable samples will be selected
pval	Optional. The p-value threshold for significance in the heatmap. Default is 0.05.

Value

A heatmap plot.

Examples

```
# Example usage:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
# multiomics_integration <- run_multiomics(data = mmultiassay_ov)
# data_table <- extract_model_res(multiomics_integration)
# data_table <- data_table[!is.na(data_table$cnv_met),]
# plot_heatmap(multiomics_integration, data_table, omics = "gene_genomic_res")
```

---

plot_network *Plotting network*

Description

Plotting network

Usage

```
plot_network(data_table, num_interactions = 300, pval = 0.05)
```

Arguments

data_table	The data table containing network information.
num_interactions	The number of interactions to display in the network (default: 300).
pval	The p-value threshold for selecting interactions (default: 0.05).

Value

A network plot.

Examples

```
# Example usage:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
# multiomics_integration <- run_multiomics(data = mmultiassay_ov)
# data_table <- extract_model_res(multiomics_integration)
# plot_network(data_table)
```

---

plot_ridge *plotting ridge*

Description

plotting ridge

Usage

```
plot_ridge(data_table, omics = NULL, cnv_met = NULL)
```

Arguments

data_table	The data table containing information for the ridge plot.
omics	Optional. The omics type for the ridge plot.
cnv_met	Optional. Indicates whether the ridge plot is for CNV or MET omics (only applicable if omics is specified).

Value

A ridge plot.

Examples

```
# Example usage:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
gene_cnv_matrix <- t(as.matrix(assay(mmultiassay_ov[["cnv_data"]])))
gene_exp_matrix <- t(as.matrix(assay(mmultiassay_ov[["gene_exp"]])))
cnv_integration <- run_cnv_integration(
    expression = gene_exp_matrix,
    cnv_data = gene_cnv_matrix
)
data_table <- extract_model_res(cnv_integration)
data_table <- data_table[data_table$cov!="(Intercept)",]
plot_ridge(data_table)
```

---

plot_tf_distribution *plotting TF distribution*

Description

plotting TF distribution

Usage

```
plot_tf_distribution(data_table, pval = 0.05)
```

Arguments

data_table	The data table containing TF information.
pval	Optional. The p-value threshold for significance in the distribution plot. Default is 0.05.

Value

A TF distribution plot.

Examples

```
# Example usage:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
# multiomics_integration <- run_multiomics(data = mmultiassay_ov)
# data_table <- extract_model_res(multiomics_integration)
# plot_tf_distribution(data_table, pval=0.5)
```

plot_venn *plotting venn*

Description

plotting venn

Usage

```
plot_venn(data_table)
```

Arguments

data_table	The data table containing information for the Venn diagram.

Value

A Venn diagram plot.

Examples

```
# Example usage:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
# multiomics_integration <- run_multiomics(data = mmultiassay_ov)
# data_table <- extract_model_res(multiomics_integration)
# plot_venn(data_table)
```

plot_volcano *plotting volcano*

Description

plotting volcano

Usage

```
plot_volcano(data_table, omics = NULL, cnv_met = NULL)
```

Arguments

data_table	The data table containing information for the volcano plot.
omics	Optional. The omics type for the volcano plot.
cnv_met	Optional. Indicates whether the volcano plot is for CNV or MET omics (only applicable if omics is specified).

Value

A volcano plot.

Examples

```
# Example usage:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
multiomics_integration <- run_multiomics(data = mmultiassay_ov)
data_table <- extract_model_res(multiomics_integration)
plot_volcano(data_table, omics = "gene_genomic_res", cnv_met = "cnv")
```

---

run_cnv_integration *Integration of expression and Copy Number Variations*

Description

This function will perform an integration of expression data and Copy Number Variations data

Usage

```
run_cnv_integration(
  expression,
  cnv_data,
  sequencing_data = TRUE,
  normalize = TRUE,
  norm_method = "TMM",
  class = NULL,
  run_deg = TRUE,
  BPPARAM = SerialParam(),
  ...
)
```

Arguments

expression	Matrix or data.frame containing the expression values for each model. Rows represent samples, while each column represents the different response variables of the models.
cnv_data	Matrix or data.frame containing the Copy Number variation status for the models. Rows represent samples, while columns represent the different covariates. If **interactions** are not provided, they will be automatically generated and for each gene contained in **expression** the model will look for the same gene in **cnv_data**
sequencing_data	logical. Are expression data obtained from RNA sequencing ? Default is set to TRUE

normalize	logical.Should expression data be normalized ? Default is set to TRUE
norm_method	Normalization method to be used for expression data. One of "TMM" (default), "TMMwsp", "RLE", "upperquartile", "none".
class	Character vector specifying the classes for differential expression analysis.
run_deg	Logical. Should differential expression analysis be performed? Default is set to TRUE.
BPPARAM	A BiocParallelParam object specifying the parallel backend to be used.
...	Additional arguments to be passed to internal functions.

Value

A list or a MultiClass object if **class** is provided containing the results of the CNV integration

Examples

```
# Example usage_multi:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
gene_cnv_matrix <- t(as.matrix(assay(mmultiassay_ov[["cnv_data"]])))
gene_exp_matrix <- t(as.matrix(assay(mmultiassay_ov[["gene_exp"]])))
cnv_integration <- run_cnv_integration(
    expression = gene_exp_matrix,
    cnv_data = gene_cnv_matrix
)
```

---

run_genomic_enrich *Running genomic enrichment analysis*

Description

Running genomic enrichment analysis

Usage

```
run_genomic_enrich(
  model_results,
  species = "hsa",
  pvalueCutoff = 0.1,
  pAdjustMethod = "BH",
  qvalueCutoff = 0.1,
  ont = "all",
  BPPARAM = BiocParallel::SerialParam(),
  extracted_data = NULL,
  ...
)
```

Arguments

model_results	Model integration results, typically a list containing different types of genomic results
species	Species to select for the enrichment analysis. Default is 'hsa' (Homo sapiens).
pvalueCutoff	P-value cutoff for significant enrichment. Default is 0.1.
pAdjustMethod	Method for adjusting p-values. Default is 'BH' (Benjamini & Hochberg).
qvalueCutoff	Q-value cutoff for significant enrichment. Default is 0.1.
ont	Ontology to use for the enrichment analysis. Default is 'all'.
BPPARAM	A BiocParallelParam object specifying parallelization options. Default is BiocParallel::SerialParam().
extracted_data	Pre-extracted data for enrichment analysis. If NULL, function will extract relevant data from model_results.
...	Additional arguments to be passed to the internal enrichment function.

Value

A list containing enrichment results. If CNV and methylation data are available, it returns a nested list with results for each data type.

Examples

```
# Example usage:
library(MultiAssayExperiment)
data(mmultiassay_ov)
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:200,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
#multiomics_integration <- run_multiomics(mmultiassay_ov)
#gen_enr <- run_genomic_enrich(multiomics_integration, qvalueCutoff = 1,
#pvalueCutoff = 0.05, pAdjustMethod = 'none')
```

---

run_genomic_integration

Integration of expression, Copy Number Variations and methylation data

---

Description

This function will perform an integration of expression data and Copy Number Variations data

Usage

```
run_genomic_integration(
  expression,
  cnv_data,
  methylation,
  sequencing_data = TRUE,
  normalize = TRUE,
  norm_method = "TMM",
  interactions = NULL,
  class = NULL,
  scale = TRUE,
  run_deg = TRUE,
  BPPARAM = SerialParam(),
  ...
)
```

Arguments

expression	Matrix or data.frame containing the expression values for each model. Rows represent samples, while each column represents the different response variables of the models.
cnv_data	Matrix or data.frame containing the Copy Number variation status for the models. Rows represent samples, while columns represent the different covariates. If **interactions** are not provided, they will be automatically generated and for each gene contained in **expression** the model will look for the same gene in **cnv_data**
methylation	Matrix or data.frame containing the methylation values for the models. Rows represent samples, while columns represent the different covariates. If **interactions** are not provided, they will be automatically generated and for each gene contained in **expression** the model will look for the same gene in **methylation**
sequencing_data	logical. Are expression data obtained from RNA sequencing ? Default is set to TRUE
normalize	logical.Should expression data be normalized ? Default is set to TRUE
norm_method	Normalization method to be used for expression data. One of "TMM" (default), "TMMwsp", "RLE", "upperquartile", "none".
interactions	A list of character vectors containing the interactions between response variable and covariates. The names of the list should match the response variables while the character contained in each element of the list should match the covariates. If NULL (default), the interactions will be automatically defined according to response variable's colnames.
class	Character vector specifying the classes for differential expression analysis.
scale	Logical. Should the data be scaled? Default is set to TRUE.
run_deg	Logical. Should differential expression analysis be performed? Default is set to TRUE.

BPPARAM	A BiocParallelParam object specifying the parallel backend to be used.
...	Additional arguments to be passed to internal functions.

Value

A list or a MultiClass object if **class** is provided containing the results of the Genomic integration

Examples

```
# Example usage_multi:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
meth_matrix <- t(as.matrix(assay(mmultiassay_ov[["methylation"]])))
gene_exp_matrix <- t(as.matrix(assay(mmultiassay_ov[["gene_exp"]])))
gene_cnv_matrix <- t(as.matrix(assay(mmultiassay_ov[["cnv_data"]])))
genomic_integration <- run_genomic_integration(
    expression = gene_exp_matrix,
    cnv_data = gene_cnv_matrix, methylation = meth_matrix
)
```

---

run_met_integration *Integration of expression and methylation*

Description

This function will perform an integration of expression data and methylation data

Usage

```
run_met_integration(
  expression,
  methylation,
  sequencing_data = TRUE,
  normalize = TRUE,
  norm_method = "TMM",
  class = NULL,
  run_deg = TRUE,
  BPPARAM = SerialParam(),
  ...
)
```

Arguments

expression	Matrix or data.frame containing the expression values for each model. Rows represent samples, while each column represents the different response variables of the models.

methylation	Matrix or data.frame containing the methylation values for the models. Rows represent samples, while columns represent the different covariates. If **interactions** are not provided, they will be automatically generated and for each gene contained in **expression** the model will look for the same gene in **methylation**
sequencing_data	logical. Are expression data obtained from RNA sequencing ? Default is set to TRUE
normalize	logical.Should expression data be normalized ? Default is set to TRUE
norm_method	Normalization method to be used for expression data. One of "TMM" (default), "TMMwsp", "RLE", "upperquartile", "none".
class	Character vector specifying the classes for differential expression analysis.
run_deg	Logical. Should differential expression analysis be performed? Default is set to TRUE.
BPPARAM	A BiocParallelParam object specifying the parallel backend to be used.
...	Additional arguments to be passed to internal functions.

Value

A list or a MultiClass object if **class** is provided containing the results of the Methylation integration

Examples

```
# Example usage_multi:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
meth_matrix <- t(as.matrix(assay(mmultiassay_ov[["methylation"]])))
gene_exp_matrix <- t(as.matrix(assay(mmultiassay_ov[["gene_exp"]])))
met_integration <- run_met_integration(
    expression = gene_exp_matrix,
    methylation = meth_matrix
)
```

---

run_multiomics *Complete Multi-Omics integration*

Description

This function will perform a complete Multi-Omics integration on a MultiAssayExperiment

Usage

```
run_multiomics(
  data,
  interactions_met = NULL,
  interactions_miRNA_target = NULL,
  interactions_tf = NULL,
  interactions_tf_miRNA = NULL,
  RNAseq = TRUE,
  miRNAseq = TRUE,
  normalize_miRNA_expr = TRUE,
  normalize_gene_expr = TRUE,
  norm_method_gene_expr = "TMM",
  norm_method_miRNA_expr = "TMM",
  class = NULL,
  BPPARAM = SerialParam()
)
```

Arguments

data	A MultiAssayExperiment. It can be generated exploiting the **generate_multiassay** function.
interactions_met	**interactions** as for **run_met_integration**
interactions_miRNA_target	miRNA-target interactions as requested by **run_tf_integration**
interactions_tf	TF-target interactions as requested by **run_tf_integration**
interactions_tf_miRNA	TF-target interactions as requested by **run_tf_integration**
RNAseq	logical. Are gene expression data obtained from RNA sequencing ? Default is set to TRUE
miRNAseq	logical. Are miRNA expression data obtained from miRNA sequencing ? Default is set to TRUE
normalize_miRNA_expr	logical.Should miRNA expression data be normalized ? Default is set to TRUE
normalize_gene_expr	logical.Should gene expression data be normalized ? Default is set to TRUE
norm_method_gene_expr	Normalization method to be used for gene expression data. One of "TMM" (default), "TMMwsp", "RLE", "upperquartile", "none".
norm_method_miRNA_expr	Normalization method to be used for miRNA expression data. One of "TMM" (default), "TMMwsp", "RLE", "upperquartile", "none".
class	Character vector specifying the classes for differential expression analysis.
BPPARAM	A BiocParallelParam object specifying the parallel backend to be used.

Value

A MultiOmics object containing the results of all the possible integration models

Examples

```
# Example usage_multiomics:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
multiomics_integration <- run_multiomics(data = mmultiassay_ov)
```

`run_shiny` *Start a Shiny application for integrated multi-omics data analysis.*

Description

The `run_shiny` function launches an interactive Shiny application that allows users to explore and analyze integrated multi-omics data through various visualizations and analyses.

Usage

```
run_shiny(multiomics_integration)
```

Arguments

`multiomics_integration`
: An object representing the integration of multi-omics data, compatible with the `extract_model_res` function.

Details

The `run_shiny` function extracts model results from `multiomics_integration`, performs preprocessing operations to prepare the data for the Shiny user interface, creates the user interface and server for the Shiny application.

Value

No return value. The function starts an interactive Shiny application.

References

Description of the multi-omics data model and integrated analysis techniques used.

See Also

`extract_model_res`

Examples

```
# Example usage:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
# multiomics_integration <- run_multiomics(data = mmultiassay_ov)
# app <- run_shiny(multiomics_integration)
```

`run_tf_enrich` *Running TF enrichment analysis*

Description

Running TF enrichment analysis

Usage

```
run_tf_enrich(
  model_results,
  species = "hsa",
  pvalueCutoff = 0.1,
  qvalueCutoff = 0.1,
  pAdjustMethod = "BH",
  ont = "all",
  BPPARAM = BiocParallel::SerialParam(),
  extracted_data = NULL,
  ...
)
```

Arguments

`model_results`	Model integration results, typically a list containing TF data.
`species`	Species to select for the enrichment analysis. Default is 'hsa' (Homo sapiens).
`pvalueCutoff`	P-value cutoff for significant enrichment. Default is 0.1.
`qvalueCutoff`	Q-value cutoff for significant enrichment. Default is 0.1.
`pAdjustMethod`	Method for adjusting p-values. Default is 'BH' (Benjamini & Hochberg).
`ont`	Ontology to use for the enrichment analysis. Default is 'all'.
`BPPARAM`	A BiocParallelParam object specifying parallelization options. Default is BiocParallel::SerialParam().
`extracted_data`	Pre-extracted data for enrichment analysis. If NULL, function will extract relevant data from model_results.
`...`	Additional arguments to be passed to the internal enrichment function.

Value

A list containing TF enrichment results.

Examples

```
# Example usage:
library(MultiAssayExperiment)
data(mmultiassay_ov)
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:200,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
#multiomics_integration <- run_multiomics(mmultiassay_ov)
#run_tf_enrich(multiomics_integration, qvalueCutoff = 1, pvalueCutoff = 0.05,
#pAdjustMethod = 'none')
```

---

run_tf_integration *Integration of expression and Transcription Factors / Generic Regulators*

Description

This function will perform an integration of gene/miRNA expression data and Transcription Factors expression. Moreover, every type of regulator can be provided to the function as covariate through the **tf_expression** argument. Interactions for TF-target, miRNA-target and TF-miRNA integration will be automatically downloaded by the function as defined by the **type** argument. Other types of interactions should be provided through the **interactions** argument.

Usage

```
run_tf_integration(
  expression,
  tf_expression = expression,
  interactions = NULL,
  type = "none",
  sequencing_data = TRUE,
  species = "hsa",
  normalize = TRUE,
  norm_method = "TMM",
  normalize_cov = TRUE,
  norm_method_cov = "TMM",
  class = NULL,
  run_deg = TRUE,
  BPPARAM = SerialParam(),
  ...
)
```

Arguments

expression	Matrix or data.frame containing the expression values for each model. Rows represent samples, while each column represents the different response variables of the models.
tf_expression	Matrix or data.frame containing the expression values for the models. Rows represent samples, while columns represent the different covariates. If not provided, it will be set equal to **expression**.
interactions	A list of character vectors containing the interactions between response variable and covariates. The names of the list should match the response variables while the character contained in each element of the list should match the covariates. If NULL (default), the interactions will be automatically downloaded according to the **type** argument.
type	A character defining the type of regulation under analysis. Should be one of "tf_miRNA", "tf", "miRNA_target".
sequencing_data	logical. Are expression data obtained from RNA sequencing ? Default is set to TRUE
species	species information for interactions download. Fully supported species are "hsa" (default) and "mmu".
normalize	logical.Should expression data be normalized ? Default is set to TRUE
norm_method	Normalization method to be used for expression data. One of "TMM" (default), "TMMwsp", "RLE", "upperquartile", "none".
normalize_cov	Same as **normalize** but for covariates.
norm_method_cov	Same as **norm_method** but for covariates.
class	Character vector specifying the classes for differential expression analysis.
run_deg	Logical. Should differential expression analysis be performed? Default is set to TRUE.
BPPARAM	A BiocParallelParam object specifying the parallel backend to be used.
...	Additional arguments to be passed to internal functions.

Value

A list or a MultiClass object if **class** is provided containing the results of the transcriptional integration

Examples

```
# Example usage_multi:
library(MultiAssayExperiment)
data("mmultiassay_ov")
tmp <- lapply(experiments(mmultiassay_ov), function(x) x[1:20,])
mmultiassay_ov <- MultiAssayExperiment(experiments = tmp)
gene_exp_matrix <- t(as.matrix(assay(mmultiassay_ov[["gene_exp"]])))
tf_integration <- run_tf_integration(expression = gene_exp_matrix, type="tf")
```

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