Package 'autonomics'

December 11, 2023

Type Package

Title Generifying and intuifying cross-platform omics analysis

Version 1.10.2

Description
This package offers a generic and intuitive solution for cross-platform omics data analysis. It has functions for import, preprocessing, exploration, contrast analysis and visualization of omics data.
It follows a tidy, functional programming paradigm.

License GPL-3

Encoding UTF-8

LazyData true

VignetteBuilder knitr

biocViews DataImport, DimensionReduction, GeneExpression, MassSpectrometry, Preprocessing, PrincipalComponent, RNASeq, Software, Transcription

BugReports https://bitbucket.org/graumannlabtools/autonomics

URL https://github.com/bhagwataditya/autonomics

RoxygenNote 7.2.4

Depends R (>= 4.0)

Imports abind, assertive.base, assertive.files, assertive.numbers, assertive.sets, BiocFileCache, BiocGenerics, bit64, colorspace, data.table, dplyr, edgeR, ggplot2, ggrepel, graphics, grDevices, grid, gridExtra, limma, magrittr, matrixStats, methods, MultiAssayExperiment, parallel, pcaMethods, rappdirs, rlang, R.utils, readxl, S4Vectors, scales, stats, stringi, SummarizedExperiment, tidyr, tools, utils

Suggests affy, AnnotationDbi, BiocManager, BiocStyle, diagram, GenomicRanges, GEOquery, hgu95av2.db, ICSNP, knitr, lme4, lmerTest, MASS, mixOmics, mpm, nlme, org.Hs.eg.db, org.Mm.eg.db, RCurl, remotes, rmarkdown, ropls, Rsubread, rtracklayer, seqinr, statmod, testthat

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R topics documented:

`.read_maxquant` *Read/Analyze proteingroups/phosphosites*

Description

Read/Analyze proteingroups/phosphosites

Usage

```
.read_maxquant(
  file,
  quantity = guess_maxquant_quantity(file),
  sfile = NULL,
  sfileby = NULL,
  subgroupvar = "subgroup",
  select_subgroups = NULL,
  invert_subgroups = character(0),
  pepcountpattern = MAXQUANT_PATTERNS_PEPCOUNTS[1],
  verbose = TRUE
)
```

```
read_proteingroups(
  file,
  quantity = guess_maxquant_quantity(file),
  sfile = NULL,
  sfileby = NULL,
  select_subgroups = NULL,
  contaminants = FALSE,
  reverse = FALSE,
  fastafile = NULL,
  invert_subgroups = character(0),
  impute = stri_detect_regex(quantity, "[Ii]ntensity"),
  pepcountpattern = MAXQUANT_PATTERNS_PEPCOUNTS[1],
  subgroupvar = NULL,
  formula = NULL,
  block = NULL,
  contrastdefs = NULL,
  pca = FALSE,
  fit = NULL,
  verbose = TRUE,
  plot = TRUE
)

read_phosphosites(
  file,
  proteinfile = paste0(dirname(file), "/proteinGroups.txt"),
  quantity = guess_maxquant_quantity(file),
  sfile = NULL,
  sfileby = NULL,
  select_subgroups = NULL,
  contaminants = FALSE,
  reverse = FALSE,
  min_localization_prob = 0.75,
  fastafile = NULL,
  invert_subgroups = character(0),
  pca = FALSE,
  fit = NULL,
  subgroupvar = NULL,
  formula = NULL,
  block = NULL,
  contrastdefs = NULL,
  verbose = TRUE,
  plot = TRUE
)
```

Arguments

file	proteingroups/phosphosites file

quantity	string: "Ratio normalized", "Ratio", "LFQ intensity", "Reporter intensity corrected", "Reporter intensity", "Intensity labeled", "Intensity"
sfile	sample file
sfileby	sample file mergeby column
subgroupvar	subgroup svar
select_subgroups	subgroups to be selected (character vector)
invert_subgroups	subgroups to be inverted (character vector)
pepcountpattern	value in MAXQUANT_PATTERNS_PEPCOUNTS
verbose	whether to message
contaminants	whether to return contaminants
reverse	whether to return reverse peptides
fastafile	NULL or fastafile (to deconvolute proteingroups)
impute	whether to impute consistent nondetects
formula	desgnmat formula
block	block svar
contrastdefs	contrastdef vector/matrix/list
pca	whether to pca
fit	fit model: NULL, 'limma', 'lm', 'lme', 'lmer','wilcoxon'
plot	whether to plot
proteinfile	proteingroups file
min_localization_prob	min site localization probability (number)

Value

SummarizedExperiment

Examples

```
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, pca=TRUE, fit='limma')
```

`.read_metabolon` *Read metabolon*

Description

Read metabolon

Usage

```
.read_metabolon(
  file,
  sheet = "OrigScale",
  fid_var = "(COMP|COMP_ID)",
  sid_var = "(CLIENT_IDENTIFIER|Client ID)",
  sfile = NULL,
  sfileby = NULL,
  by = NULL,
  subgroupvar = "Group"
)

read_metabolon(
  file,
  sheet = "OrigScale",
  fid_var = "(COMP|COMP_ID)",
  sid_var = "(CLIENT_IDENTIFIER|Client ID)",
  sfile = NULL,
  sfileby = NULL,
  by = NULL,
  subgroupvar = "Group",
  fname_var = "BIOCHEMICAL",
  impute = FALSE,
  add_kegg_pathways = FALSE,
  add_smiles = FALSE,
  pca = FALSE,
  fit = NULL,
  formula = NULL,
  block = NULL,
  contrastdefs = NULL,
  verbose = TRUE,
  plot = TRUE
)
```

Arguments

`file`	metabolon xlsx filepath
`sheet`	xls sheet number or name

fid_var	feature_id fvar
sid_var	sampleid svar
sfile	sample file
sfileby	sample file mergeby column
by	metabolon file mergeby column
subgroupvar	subgroup svar
fname_var	featurename fvar
impute	whether to impute
add_kegg_pathways	whether to add kegg pathways
add_smiles	whether to add smiles
pca	whether to pca
fit	fit model: NULL, 'limma', 'lm', 'lme', 'lmer', 'wilcoxon'
formula	designmat formula
block	block svar
contrastdefs	contrastdef vector/matrix/list
verbose	whether to msg
plot	whether to plot

Value

SummarizedExperiment

Examples

```
file <- download_data('atkin18.metabolon.xlsx')
read_metabolon(file, pca = TRUE, fit = 'limma', block='SUB')
```

.read_rectangles *Read omics data from rectangular file*

Description

Read omics data from rectangular file

Usage

```
.read_rectangles(
  file,
  sheet = 1,
  fid_rows,
  fid_cols,
  sid_rows,
  sid_cols,
  expr_rows,
  expr_cols,
  fvar_rows = NULL,
  fvar_cols = NULL,
  svar_rows = NULL,
  svar_cols = NULL,
  fdata_rows = NULL,
  fdata_cols = NULL,
  sdata_rows = NULL,
  sdata_cols = NULL,
  transpose = FALSE,
  verbose = TRUE
)

read_rectangles(
  file,
  sheet = 1,
  fid_rows,
  fid_cols,
  sid_rows,
  sid_cols,
  expr_rows,
  expr_cols,
  fvar_rows = NULL,
  fvar_cols = NULL,
  svar_rows = NULL,
  svar_cols = NULL,
  fdata_rows = NULL,
  fdata_cols = NULL,
  sdata_rows = NULL,
  sdata_cols = NULL,
  transpose = FALSE,
  sfile = NULL,
  sfileby = NULL,
  subgroupvar = character(0),
  verbose = TRUE
)
```

Arguments

file	string: name of text (txt, csv, tsv, adat) or excel (xls, xlsx) file
sheet	integer/string: only relevant for excel files
fid_rows	numeric vector: featureid rows
fid_cols	numeric vector: featureid cols
sid_rows	numeric vector: sampleid rows
sid_cols	numeric vector: sampleid cols
expr_rows	numeric vector: expr rows
expr_cols	numeric vector: expr cols
fvar_rows	numeric vector: fvar rows
fvar_cols	numeric vector: fvar cols
svar_rows	numeric vector: svar rows
svar_cols	numeric vector: svar cols
fdata_rows	numeric vector: fdata rows
fdata_cols	numeric vector: fdata cols
sdata_rows	numeric vector: sdata rows
sdata_cols	numeric vector: sdata cols
transpose	TRUE or FALSE (default)
verbose	TRUE (default) or FALSE
sfile	sample file
sfileby	sample file mergeby column
subgroupvar	subgroupvar in sfile

Value

SummarizedExperiment

Examples

```
# RNASEQ
   file <- download_data('billing16.rnacounts.txt')
   read_rectangles(file,fid_rows   = 2:58736,   fid_cols   = 1,
                   sid_rows   = 1,         sid_cols   = 4:14,
                   expr_rows  = 2:58736,   expr_cols  = 4:14,
                   fvar_rows  = 1,         fvar_cols  = 1:3,
                   fdata_rows = 2:58736,   fdata_cols = 1:3,
                   transpose  = FALSE)
# LCMSMS PROTEINGROUPS
   file <- download_data('billing19.proteingroups.txt')
   read_rectangles(file,fid_rows   = 2:9044,  fid_cols   = 383,
                   sid_rows   = 1,       sid_cols   = seq(124, 316, by = 6),
                   expr_rows  = 2:9044,  expr_cols  = seq(124, 316, by = 6),
                   fvar_rows  = 1,       fvar_cols  = c(2, 6, 7, 383),
```

```
                  fdata_rows = 2:9044,  fdata_cols = c(2, 6, 7, 383),
                  transpose  = FALSE)
# SOMASCAN
   file <- download_data('billing16.somascan.adat')
   read_rectangles(file,fid_rows   = 21,       fid_cols   = 19:1146,
                  sid_rows   = 30:40,    sid_cols   = 4,
                  expr_rows  = 30:40,    expr_cols  = 19:1146,
                  fvar_rows  = 21:28,    fvar_cols  = 18,
                  svar_rows  = 29,       svar_cols  = 1:17,
                  fdata_rows = 21:28,    fdata_cols = 19:1146,
                  sdata_rows = 30:40,    sdata_cols = 1:17,
                  transpose  = TRUE)
# METABOLON
   file <- download_data('halama18.metabolon.xlsx')
   read_rectangles(file, sheet = 2,
                  fid_rows   = 11:401,    fid_cols   = 5,
                  sid_rows   = 3,         sid_cols   = 15:86,
                  expr_rows  = 11:401,    expr_cols  = 15:86,
                  fvar_rows  = 10,        fvar_cols  = 1:14,
                  svar_rows  = 1:10,      svar_cols  = 14,
                  fdata_rows = 11:401,    fdata_cols = 1:14,
                  sdata_rows = 1:10,      sdata_cols = 15:86,
                  transpose  = FALSE)
```

`.read_rnaseq_bams` *Read rnaseq*

Description

Read/analyze rnaseq counts / bamfiles

Usage

```
.read_rnaseq_bams(
  dir,
  paired,
  genome,
  nthreads = detectCores(),
  sfile = NULL,
  sfileby = NULL,
  subgroupvar = NULL,
  ffile = NULL,
  ffileby = NULL,
  fnamevar = NULL,
  verbose = TRUE
)

.read_rnaseq_counts(
  file,
```

```
  fid_col = 1,
  sfile = NULL,
  sfileby = NULL,
  ffile = NULL,
  ffileby = NULL,
  subgroupvar = NULL,
  verbose = TRUE
)

read_rnaseq_bams(
  dir,
  paired,
  genome,
  nthreads = detectCores(),
  sfile = NULL,
  sfileby = NULL,
  subgroupvar = NULL,
  block = NULL,
  ffile = NULL,
  ffileby = NULL,
  fnamevar = NULL,
  formula = NULL,
  min_count = 10,
  pseudocount = 0.5,
  genesize = NULL,
  cpm = TRUE,
  tmm = cpm,
  log2 = TRUE,
  pca = FALSE,
  fit = NULL,
  voom = !is.null(fit),
  contrastdefs = NULL,
  verbose = TRUE,
  plot = TRUE
)

read_rnaseq_counts(
  file,
  fid_col = 1,
  sfile = NULL,
  sfileby = NULL,
  subgroupvar = NULL,
  block = NULL,
  ffile = NULL,
  ffileby = NULL,
  fnamevar = NULL,
  formula = NULL,
  min_count = 10,
```

```
  pseudocount = 0.5,
  genesize = NULL,
  cpm = TRUE,
  tmm = cpm,
  log2 = TRUE,
  pca = FALSE,
  fit = NULL,
  voom = !is.null(fit),
  contrastdefs = NULL,
  verbose = TRUE,
  plot = TRUE
)
```

Arguments

dir	read_rnaseq_bams: bam/samfile dir
paired	read_rnaseq_bams: whether paired end reads
genome	read_rnaseq_bams: mm10"/"hg38"/etc. or GTF file
nthreads	read_rnaseq_bams: nthreads used by Rsubread::featureCounts()
sfile	sample file
sfileby	sample file mergeby column
subgroupvar	subgroup svar
ffile	feature file
ffileby	feature file mergeby column
fnamevar	featurename fvar
verbose	whether to message
file	read_rnaseq_counts: count file
fid_col	featureid fvar
block	block svar
formula	designmat formula
min_count	min feature count required in some samples
pseudocount	added pseudocount to prevent -Inf log2 values
genesize	genesize fvar for tpm
cpm	whether to compute cpm
tmm	whether to tmm-scale library sizes
log2	whether to log2 transform
pca	whether to pca
fit	fit model: NULL, 'limma', 'lm', 'lme', 'lmer', 'wilcoxon'
voom	whether to compute voom precision weights
contrastdefs	contrastdef vector/matrix/list
plot	whether to plot

Value

SummarizedExperiment

Author(s)

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Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, pca= TRUE, fit='limma')

# requires Rsubread
# file <- download_data('billing16.bam.zip')
# object <- read_rnaseq_bams(file, paired=TRUE, genome='hg38', pca=TRUE,
#                            fit='limma', plot=TRUE)
```

.read_somascan *Read somascan*

Description

Read data from somascan adat file

Usage

```
.read_somascan(
  file,
  fidvar = "SeqId",
  sidvar = "SampleId",
  sfile = NULL,
  sfileby = NULL,
  by = NULL,
  subgroupvar = "SampleGroup"
)

read_somascan(
  file,
  fidvar = "SeqId",
  sidvar = "SampleId",
  sfile = NULL,
  sfileby = NULL,
  by = NULL,
  subgroupvar = "SampleGroup",
  fname_var = "EntrezGeneSymbol",
  sample_type = "Sample",
  feature_type = "Protein",
```

```
  sample_quality = c("FLAG", "PASS"),
  feature_quality = c("FLAG", "PASS"),
  rm_na_svars = FALSE,
  rm_single_value_svars = FALSE,
  pca = FALSE,
  fit = NULL,
  formula = NULL,
  block = NULL,
  contrastdefs = NULL,
  verbose = TRUE,
  plot = TRUE
)
```

Arguments

file	*.adat file path (string)
fidvar	featureid fvar (string)
sidvar	sampleid svar (string)
sfile	sample file
sfileby	sample file mergeby column
by	metabolon file mergeby column
subgroupvar	subgroup svar (string)
fname_var	featurename fvar (string)
sample_type	subset of c('Sample','QC','Buffer','Calibrator')
feature_type	subset of c('Protein', 'Hybridization Control Elution', 'Rat Protein')
sample_quality	subset of c('PASS', 'FLAG', 'FAIL')
feature_quality	subset of c('PASS', 'FLAG', 'FAIL')
rm_na_svars	whether to rm NA svars
rm_single_value_svars	whether to rm single value svars
pca	whether to pca
fit	fit model: NULL, 'limma', 'lm', 'lme', 'lmer','wilcoxon'
formula	design formula (using svars)
block	block var
contrastdefs	contrastdef vector/matrix/list
verbose	whether to msg
plot	whether to plot

Value

Summarizedexperiment

Examples

```
file <- download_data('atkin18.somascan.adat')
read_somascan(file, pca = TRUE, fit = 'limma', block = 'Subject_ID')
```

`add_smiles` *Add smiles*

Description

Add smiles

Usage

```
add_smiles(object)
```

Arguments

`object`	character/factor vector with pubchem ids

Value

character/factor vector

References

https://pubchemdocs.ncbi.nlm.nih.gov/pug-rest-tutorial

Examples

```
file <- download_data('atkin18.metabolon.xlsx')
object <- read_metabolon(file, plot=FALSE)
add_smiles(object[1:10, ])
```

`analysis` *Get/set analysis*

Description

Get/set analysis

Usage

```
analysis(object)

## S4 method for signature 'SummarizedExperiment'
analysis(object)

analysis(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,list'
analysis(object) <- value
```

Arguments

object	SummarizedExperiment
value	list

Value

analysis details (get) or updated object (set)

Examples

```
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
analysis(object)
```

---

analyze *Analyze*

Description

Analyze

Usage

```
analyze(
  object,
  pca = FALSE,
  fit = NULL,
  subgroupvar = default_subgroupvar(object),
  formula = default_formula(object, subgroupvar, fit),
  block = NULL,
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  contrastdefs = contrast_coefs(object, formula),
  verbose = TRUE,
  plot = TRUE
)
```

Arguments

object	SummarizedExperiment
pca	whether to perform pca
fit	NULL, 'limma', 'lm', 'lme', 'lmer', or 'wilcoxon'
subgroupvar	subgroup svar
formula	model formula
block	block svar
weightvar	NULL or name of weight matrix in assays(object)
contrastdefs	contrastdefs vector/matrix/list
verbose	whether to msg
plot	whether to plot

Value

SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('atkin18.metabolon.xlsx')
object <- read_metabolon(file, plot=FALSE)
object %<>% analyze(pca=TRUE, subgroupvar = 'Group', fit='limma')
```

---

assert_is_valid_sumexp

Assert that x is a valid SummarizedExperiment

Description

Assert that x is a valid SummarizedExperiment

Assert that x is a valid SummarizedExperiment

Usage

```
assert_is_valid_sumexp(x, .xname = get_name_in_parent(x))

assert_is_valid_sumexp(x, .xname = get_name_in_parent(x))
```

Arguments

x	SummarizedExperiment
.xname	see assertive.base::get_name_in_parent

Value

TRUE or FALSE

TRUE or FALSE

Examples

```
# VALID
    file <- download_data('halama18.metabolon.xlsx')
    x <- read_metabolon(file, plot = FALSE)
    assert_is_valid_sumexp(x)
# NOT VALID
    rownames(SummarizedExperiment::colData(x)) <- NULL
    # assert_is_valid_sumexp(x)
# VALID
    file <- download_data('halama18.metabolon.xlsx')
    x <- read_metabolon(file, plot = FALSE)
    assert_is_valid_sumexp(x)
# NOT VALID
    rownames(SummarizedExperiment::colData(x)) <- NULL
    # assert_is_valid_sumexp(x)
```

AUTONOMICS_DATASETS *Data used in examples/vignette/tests/longtests*

Description

Data used in examples/vignette/tests/longtests

Usage

```
AUTONOMICS_DATASETS
```

Format

An object of class `character` of length 13.

Examples

```
AUTONOMICS_DATASETS
```

`biplot` *Biplot*

Description

Biplot

Usage

```
biplot(
  object,
  x = pca1,
  y = pca2,
  color = NULL,
  group = NULL,
  label = NULL,
  feature_label = feature_name,
  ...,
  fixed = list(shape = 15, size = 3),
  nloadings = 0
)

plot_biplot(...)
```

Arguments

`object`	SummarizedExperiment
`x`	pca1, etc.
`y`	pca2, etc.
`color`	svar mapped to color (symbol)
`group`	svar mapped to group
`label`	svar mapped to label (symbol)
`feature_label`	fvar mapped to (loadings) label
`...`	additional svars mapped to aesthetics
`fixed`	fixed plot aesthetics
`nloadings`	number of loadings per half-axis to plot

Value

ggplot object

Examples

```
require(magrittr)
file <- download_data('atkin18.metabolon.xlsx')
object <- read_metabolon(file, plot = FALSE)
object %<>% pca(ndim=4)
biplot(object)
biplot(object, color=SUB, group=SUB)
biplot(object, color=SUB, nloadings=1)
biplot(object, pca3, pca4, color=SUB, nloadings=1)
```

---

center *Center samples*

Description

Center samples

Usage

```
center(
  object,
  selector = rep(TRUE, nrow(object)) == TRUE,
  fun = "median",
  verbose = TRUE
)
```

Arguments

object	SummarizedExperiment
selector	logical vector (length = nrow(object))
fun	aggregation function (string)
verbose	TRUE/FALSE

Value

SummarizedExperiment

Examples

```
require(magrittr)
require(matrixStats)
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE, impute=FALSE)
fdata(object)$housekeeping <- FALSE
fdata(object)$housekeeping[order(rowVars(values(object)))[1:100]] <- TRUE
values(object)[, object$subgroup=='Adult'] %<>% add(5)
plot_sample_densities(object)
plot_sample_densities(center(object))
plot_sample_densities(center(object, housekeeping))
```

contrastdefs *Get/set contrastdefs*

Description

Get/set contrastdefs

Usage

```
contrastdefs(object)

## S4 method for signature 'SummarizedExperiment'
contrastdefs(object)

contrastdefs(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,list'
contrastdefs(object) <- value
```

Arguments

object	SummarizedExperiment
value	list

Value

contrastdefs (get) or SummarizedExperiment (set)

Examples

```
file <- download_data('billing16.proteingroups.txt')
inv <- c('EM_E', 'BM_E', 'BM_EM')
object <- read_proteingroups(
            file, invert_subgroups=inv, fit='limma', plot=FALSE)
contrastdefs(object)
```

contrast_subgroup_cols *Row/Col contrasts*

Description

Row/Col contrasts

Usage

```
contrast_subgroup_cols(object, subgroupvar)

contrast_subgroup_rows(object, subgroupvar)
```

Arguments

object	SummarizedExperiment
subgroupvar	subgroup svar

Value

matrix

Examples

```
file <- download_data('halama18.metabolon.xlsx')
object <- read_metabolon(file, plot=FALSE)
subgroup_matrix(object, subgroupvar = 'Group')
contrast_subgroup_cols(object, subgroupvar = 'Group')
contrast_subgroup_rows(object, subgroupvar = 'Group')
```

---

counts *Get/Set counts*

Description

Get / Set counts matrix

Usage

```
counts(object)

## S4 method for signature 'SummarizedExperiment'
counts(object)

counts(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
counts(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
counts(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,`NULL`'
counts(object) <- value
```

Arguments

object	SummarizedExperiment
value	count matrix (features x samples)

Value

count matrix (get) or updated object (set)

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, plot=FALSE)
counts(object) <- values(object)
counts(object)[1:3, 1:3]
```

---

counts2cpm *Convert between counts and cpm*

Description

Convert between counts and cpm

Usage

```
counts2cpm(x, libsize = scaledlibsizes(x))

cpm2counts(x, libsize)
```

Arguments

x	count/cpm matrix
libsize	(scaled) libsize vector

Value

cpm/tpm/count matrix

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, cpm=FALSE, log2=FALSE, plot=FALSE)
libsize <- scaledlibsizes(values(object))
tpm <- counts2tpm(counts(object), genesize = 1)
cpm <- counts2cpm(counts(object), libsize)
counts  <- cpm2counts(cpm, libsize)
sum(counts(object) - counts)
```

counts2tpm *counts to tpm*

Description

counts to tpm

Usage

```
counts2tpm(x, genesize)
```

Arguments

x	count matrix
genesize	genesize vector (kilobase)

Value

tpm matrix

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, cpm=FALSE, log2=FALSE, plot=FALSE)
counts2tpm(counts(object), genesize=1)[1:3, 1:3]
```

cpm *Get/Set cpm*

Description

Get / Set cpm matrix

Usage

```
cpm(object)

## S4 method for signature 'SummarizedExperiment'
cpm(object)

cpm(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
cpm(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
cpm(object) <- value
```

Arguments

object	SummarizedExperiment
value	cpm matrix (features x samples)

Value

cpm matrix (get) or updated object (set)

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, plot=FALSE)
cpm(object) <- values(object)
cpm(object)[1:3, 1:3]
```

---

create_design *Create design*

Description

Create design matrix for statistical analysis

Usage

```
create_design(
  object,
  subgroupvar = if ("subgroup" %in% svars(object)) "subgroup" else NULL,
  formula = default_formula(object, subgroupvar, fit = "limma"),
  verbose = TRUE
)
```

Arguments

object	SummarizedExperiment
subgroupvar	subgroup svar
formula	formula with svars
verbose	whether to message

Value

design matrix

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, plot=FALSE)
unique(create_design(object))

object$subgroup <- 'billing19'
unique(create_design(object))

file <- download_data('atkin18.somascan.adat')
object <- read_somascan(file, plot=FALSE)
unique(create_design(object))
create_design(object, formula= ~ 0 + SampleGroup + Sex + T2D + age + bmi)
object$subgroup <- 'atkin18'
unique(create_design(object))
```

`create_sfile` *Create sfile*

Description

Create sfile

Usage

```
create_sfile(object, sfile, verbose = TRUE)
```

Arguments

`object`	SummarizedExperiment
`sfile`	sample file
`verbose`	TRUE/FALSE

Value

sample file path

Examples

```
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
create_sfile(object, paste0(tempfile(), '.tsv'))
```

default_sfile *Default sfile*

Description

Default sfile

Usage

```
default_sfile(file)
```

Arguments

file	data file

Value

sample file

Examples

```
file <- download_data('billing19.proteingroups.txt')
default_sfile(file)
```

default_subgroupvar *Create default formula*

Description

Create default formula

Usage

```
default_subgroupvar(object)

default_formula(object, subgroupvar = default_subgroupvar(object), fit)
```

Arguments

object	SummarizedExperiment
subgroupvar	string
fit	'limma', 'lm', 'lme', 'lmer'

Value

formula

Examples

```
file <- download_data('atkin18.metabolon.xlsx')
object <-.read_metabolon(file)
default_subgroupvar(object)
default_formula(object, fit = 'limma')
default_formula(object, fit = 'lm')
```

`download_data` *Download autonomics example data*

Description

Download autonomics example data

Usage

```
download_data(
  filename,
 url = paste0("https://bitbucket.org/graumannlabtools/autonomics/downloads/", filename),
  verbose = TRUE
)
```

Arguments

`filename`	file name
`url`	web url

- Billing 2016: stemcell comparison: E, EM, BM
  - `'billing16.bam.zip'`
  - `'billing16.rnacounts.txt'`
  - `'billing16.somascan.adat'`
  - `'billing16.proteingroups.txt'`
- Atkin 2018: hypoglycemia: t0, t1, t2, t3
  - `'atkin18.somascan.adat'`
  - `'atkin18.metbolon.xlsx'`
- Halama 2018: glutaminase inhibition: 4 conc, 4 timepoints
  - `'halama18.metabolon.xlsx'`
- Billing 2019: stemcell differentiation: E00, E01, E02, E05, EM15, EM30, M00
  - `'billing19.rnacounts.txt'`
  - `'billing19.proteingroups.txt'`
  - `'billing19.phosphosites.txt'`
- Fukuda 2020: zebrafish development: X30dpt, Adult
  - `'fukuda20.proteingroups.txt'`

`verbose`	TRUE / FALSE

Value

local file path

Examples

```
# atkin18 - hypoglycemia - pubmed 30525282
    download_data('atkin18.somascan.adat')          # somascan  intensities
    download_data('atkin18.metabolon.xlsx')         # metabolon intensities

# billing16 - stemcell characterization - pubmed 26857143
    download_data('billing16.proteingroups.txt')  # proteingroup ratios
    download_data('billing16.somascan.adat')      # somascan  intensities
    download_data('billing16.rnacounts.txt')      # rnaseq    counts
    download_data('billing16.bam.zip')            # rnaseq    alignments

# billing19 - stemcell differentiation - pubmed 31332097
    # download_data('billing19.proteingroups.txt')    # proteingroup ratios
    # download_data('billing19.phosphosites.txt')     # phosphosite  ratios
    # download_data('billing19.rnacounts.txt')        # rnaseq       counts

# fukuda20 - heart regeneration - pubmed PXD016235
    download_data('fukuda20.proteingroups.txt')     # proteingroup LFQ

# halama18 - glutaminase inhibition - pubmed 30525282
    download_data('halama18.metabolon.xlsx')        # metabolon intensities
```

`download_gtf` *Download GTF file*

Description

Download GTF file with feature annotations

Usage

```
download_gtf(
  organism,
  release = 100,
 gtffile = sprintf("%s/gtf/%s", rappdirs::user_cache_dir(appname = "autonomics"),
    basename(make_gtf_url(organism, release) %>% substr(1, nchar(.) - 3)))
)
```

Arguments

`organism`	'Homo sapiens', 'Mus musculus' or 'Rattus norvegicus'
`release`	GTF release (number)
`gtffile`	string: path to local GTF file

Value

gtffile path

Examples

```
organism <- 'Homo sapiens'
# download_gtf(organism)
```

---

dt2mat *'data.table' to 'matrix'*

Description

Convert between 'data.table' and 'matrix'

Usage

```
dt2mat(x)

mat2dt(x, idvar)
```

Arguments

x	data.table / matrix
idvar	idvar string

Value

matrix / data.table

Examples

```
x <- data.table::data.table(
        gene    = c('ENSG001', 'ENSG002', 'ENSG003'),
        sampleA = c(1787, 10, 432),
        sampleB = c(1143,  3, 268))
dt2mat(x)
mat2dt(dt2mat(x), 'gene')
```

explore_imputations *Explore imputations*

Description

Explore imputations

Usage

```
explore_imputations(object, subgroup, xbiplot = pca1, ybiplot = pca2, ...)
```

Arguments

object	SummarizedExperiment
subgroup	subgroup (sym)
xbiplot	biplot x axis. Default pca1 (symbol)
ybiplot	biplot y axis. Default pca2 (symbol)
...	aesthetic mappings

Value

ggplot object

Examples

```
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, impute = FALSE, pca = TRUE, plot = FALSE)
explore_imputations(object, subgroup=subgroup)
explore_transformations(object, subgroup=subgroup)
```

explore_transformations *Explore transformations*

Description

Explore transformations

Usage

```
explore_transformations(
  object,
  subgroup = subgroup,
  transformations = c("quantnorm", "zscore", "invnorm"),
  method = "pca",
  xdim = 1,
  ydim = 2,
  ...
)
```

Arguments

object	SummarizedExperiment
subgroup	subgroup (sym)
transformations	vector
method	'pca', 'pls', 'sma', or 'lda'
xdim	number (default 1)
ydim	number (default 2)
...	passed to plot_data

Value

grid object

Examples

```
file <- download_data('billing16.proteingroups.txt')
invert <- c('EM_E', 'EM_BM', 'BM_E')
object <- read_proteingroups(file, invert_subgroups = invert, plot=FALSE)
explore_transformations(object)
```

---

extract_features *Extract features*

Description

Extract features

Usage

```
extract_features(object, extractor)
```

Arguments

object	SummarizedExperiment
extractor	logical/numeric vector

Value

SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
(object %<>% extract_features(c(5,4)))
```

---

extract_rectangle *Extract rectangle from omics file, data.table, or matrix*

Description

Extract rectangle from omics file, data.table, or matrix

Usage

```
extract_rectangle(x, ...)

## S3 method for class 'character'
extract_rectangle(
  x,
  rows = seq_len(nrows(x, sheet = sheet)),
  cols = seq_len(ncols(x, sheet = sheet)),
  verbose = FALSE,
  transpose = FALSE,
  drop = FALSE,
  sheet = 1,
  ...
)

## S3 method for class 'data.table'
extract_rectangle(
  x,
  rows = seq_len(nrow(x)),
  cols = seq_len(ncol(x)),
  transpose = FALSE,
  drop = FALSE,
  ...
)
```

```
## S3 method for class 'matrix'
extract_rectangle(
  x,
  rows = seq_len(nrow(x)),
  cols = seq_len(ncol(x)),
  transpose = FALSE,
  drop = FALSE,
  ...
)
```

Arguments

x	omics datafile or datatable
...	allow for S3 method dispatch
rows	numeric vector
cols	numeric vector
verbose	logical
transpose	logical
drop	logical
sheet	numeric or string

Value

matrix

Examples

```
# FROM FILE: extract_rectangle.character
#=======================================
# exprs
   require(magrittr)
   x <- download_data('halama18.metabolon.xlsx')
   extract_rectangle(x, rows = 11:401, cols = 15:86, sheet = 2) %>%
   extract(1:3, 1:3)

# fids
   extract_rectangle(x, rows = 11:401, cols = 5, sheet = 2)     %>%
   extract(1:3, )

# sids
   extract_rectangle(x, rows = 2, cols = 15:86, sheet = 2)      %>%
   extract(,1:3)

# fdata
   extract_rectangle(x, rows = 10:401, cols = 1:14,  sheet = 2) %>%
   extract(1:3, 1:3)

# sdata
```

```
   extract_rectangle(x, rows = 1:10,   cols = 14:86, sheet = 2,
   transpose = TRUE) %>% extract(1:3, 1:3)

# FROM MATRIX: extract_rectangle.matrix
#=====================================
# exprs
   x <-download_data('halama18.metabolon.xlsx') %>%
       extract_rectangle(sheet = 2)
   extract_rectangle(x, rows = 11:401, cols = 15:86, sheet = 2) %>%
   extract(1:3, 1:3)

# fids
   extract_rectangle(x, rows = 11:401, cols = 5,     sheet = 2) %>%
   extract(1:3, )

# sids
   extract_rectangle(x, rows = 2,      cols = 15:86, sheet = 2) %>%
   extract(,1:3)

# fdata
   extract_rectangle(x, rows = 10:401, cols = 1:14,  sheet = 2) %>%
   extract(1:3, 1:3)

# sdata
   extract_rectangle(x, rows = 1:10,   cols = 14:86, sheet = 2,
   transpose = TRUE) %>% extract(1:3, 1:3)
```

`fdata` *Get/Set fdata*

Description

Get/Set feature data

Usage

```
fdata(object)

## S4 method for signature 'SummarizedExperiment'
fdata(object)

fdata(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,data.frame'
fdata(object) <- value
```

Arguments

`object`	SummarizedExperiment, eSet, or EList
`value`	data.frame

Value

feature dataframe (get) or updated object (set)

Examples

```
require(magrittr)
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
head(fdata(object)) # Getter
fdata(object) %<>% cbind(z=1)
head(fdata(object)) # Setter
```

---

filter_exprs_replicated_in_some_subgroup

Filter features with replicated expression in some subgroup

Description

Filter features with replicated expression in some subgroup

Usage

```
filter_exprs_replicated_in_some_subgroup(
  object,
  subgroupvar = "subgroup",
  comparator = if (contains_ratios(object)) "!=" else ">",
  lod = 0,
  verbose = TRUE
)
```

Arguments

object	SummarizedExperiment
subgroupvar	subgroup svar
comparator	'>' or '!='
lod	number: limit of detection
verbose	TRUE or FALSE

Value

Filtered SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('atkin18.metabolon.xlsx')
object <- read_metabolon(file, plot=FALSE)
object %<>% filter_exprs_replicated_in_some_subgroup(subgroupvar = 'Group')
filter_exprs_replicated_in_some_subgroup(object, character(0))
filter_exprs_replicated_in_some_subgroup(object, NULL)
```

---

filter_features *Filter features on condition*

Description

Filter features on condition

Usage

```
filter_features(object, condition, verbose = FALSE)
```

Arguments

object	SummarizedExperiment
condition	filter condition
verbose	logical

Value

filtered eSet

Examples

```
file <- download_data('atkin18.metabolon.xlsx')
object <- read_metabolon(file, plot=FALSE)
filter_features(object,   SUPER_PATHWAY=='Lipid',  verbose = TRUE)
```

filter_medoid *Filter medoid sample*

Description

Filter medoid sample

Usage

```
filter_medoid(object, by = NULL, verbose = FALSE)
```

Arguments

object	SummarizedExperiment
by	svar
verbose	whether to message

Value

SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, plot=FALSE)
object %<>% filter_medoid(by = 'subgroup', verbose=TRUE)
```

filter_replicated *Filter for replicated features*

Description

Filter for replicated features

Usage

```
filter_replicated(object, comparator = `>`, lod = 0, n = 2, verbose = TRUE)
```

Arguments

object	SummarizedExperiment
comparator	string
lod	number: limit of detection
n	number: number of replicates above lod
verbose	TRUE/FALSE

Value

SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
object %<>% filter_replicated()
```

`filter_samples` *Filter samples on condition*

Description

Filter samples on condition

Usage

```
filter_samples(object, condition, verbose = FALSE, record = TRUE)
```

Arguments

`object`	SummarizedExperiment
`condition`	filter condition
`verbose`	TRUE or FALSE (default)
`record`	TRUE (default) or FALSE

Value

filtered SummarizedExperiment

Examples

```
file <- download_data('atkin18.metabolon.xlsx')
object <- read_metabolon(file, plot=FALSE)
filter_samples(object, Group != 't0', verbose = TRUE)
```

fit_limma *Fit model and test for differential expression*

Description

Fit model and test for differential expression

Usage

```
fit_limma(
  object,
  subgroupvar = if ("subgroup" %in% svars(object)) "subgroup" else NULL,
  formula = default_formula(object, subgroupvar, "limma"),
  contrastdefs = contrast_coefs(object, formula),
  block = NULL,
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  verbose = TRUE,
  plot = FALSE
)

fit_lm(
  object,
  subgroupvar = if ("subgroup" %in% svars(object)) "subgroup" else NULL,
  formula = default_formula(object, subgroupvar, fit = "lm"),
  block = NULL,
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  contrastdefs = NULL,
  verbose = TRUE,
  plot = FALSE
)

fit_lme(
  object,
  subgroupvar = if ("subgroup" %in% svars(object)) "subgroup" else NULL,
  formula = default_formula(object, subgroupvar, fit = "lme"),
  block = NULL,
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  contrastdefs = NULL,
  verbose = TRUE,
  plot = FALSE
)

fit_lmer(
  object,
  subgroupvar = if ("subgroup" %in% svars(object)) "subgroup" else NULL,
  formula = default_formula(object, subgroupvar, fit = "lmer"),
  block = NULL,
```

```
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  contrastdefs = NULL,
  verbose = TRUE,
  plot = FALSE
)

fit_wilcoxon(
  object,
  subgroupvar = if ("subgroup" %in% svars(object)) "subgroup" else NULL,
  formula = default_formula(object, subgroupvar, fit = "wilcoxon"),
  contrastdefs = contrast_coefs(object, formula = formula),
  block = NULL,
  weightvar = NULL,
  verbose = TRUE,
  plot = FALSE
)
```

Arguments

object	SummarizedExperiment
subgroupvar	subgroup variable
formula	modeling formula
contrastdefs	contrastdef vector / matrix / list • c("t1-t0", "t2-t1", "t3-t2") • matrix(c("WT.t1-WT.t0", "WT.t2-WT.t1", "WT.t3-WT.t2"), c("KD.t1-KD.t0", "KD.t2-KD.t1", "KD.t3-KD.t2"), nrow=2, byrow=TRUE) • list(matrix(c("WT.t1-WT.t0", "WT.t2-WT.t1", "WT.t3-WT.t2"), c("KD.t1-KD.t0", "KD.t2-KD.t1", "KD.t3-KD.t2"), nrow=2, byrow=TRUE), matrix(c("KD.t0-WT.t0", "KD.t1-WT.t1", "KD.t2-WT.t2", "KD.t3-WT.t3"), nrow=1, byrow=TRUE))
block	block svar (or NULL)
weightvar	NULL or name of weight matrix in assays(object)
verbose	whether to msg
plot	whether to plot

Value

Updated SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('atkin18.somascan.adat')
object <- read_somascan(file, plot=FALSE)
object %<>% fit_limma(subgroupvar = 'SampleGroup')
object %<>% fit_lm(   subgroupvar = 'SampleGroup')
plot_venn(is_sig(object, contrast='t3-t2'))
```

```
S4Vectors::metadata(object)$limma <- S4Vectors::metadata(object)$lm <- NULL
object %<>% fit_limma(   subgroupvar = 'SampleGroup', block = 'Subject_ID')
object %<>% fit_wilcoxon(subgroupvar = 'SampleGroup', block = 'Subject_ID')
# object %<>% fit_lme(   subgroupvar = 'SampleGroup', block = 'Subject_ID')
# object %<>% fit_lmer(  subgroupvar = 'SampleGroup', block = 'Subject_ID')
plot_venn(is_sig(object, contrast='t3-t2'))
```

`flevels` *Get fvar levels*

Description

Get fvar levels

Usage

```
flevels(object, fvar)
```

Arguments

`object`	SummarizedExperiment
`fvar`	feature variable

Value

fvar values

Examples

```
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
head(flevels(object, 'feature_name'))
```

`fnames` *Get/Set fnames*

Description

Get/Set feature names

Usage

```
fnames(object)

## S4 method for signature 'SummarizedExperiment'
fnames(object)

fnames(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,character'
fnames(object) <- value
```

Arguments

object	SummarizedExperiment, eSet, or EList
value	character vector with feature names

Value

feature name vector (get) or updated object (set)

Examples

```
require(magrittr)
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
fnames(object) %<>% paste0('PG', .)
object
```

---

formula2str *formula to string*

Description

formula to string

Usage

```
formula2str(formula)
```

Arguments

formula	formula

Value

string

Examples

```
formula2str(~0+subgroup)
```

`fvalues` *Get fvalues*

Description

Get fvar values

Usage

```
fvalues(object, fvar)
```

Arguments

`object`	SummarizedExperiment
`fvar`	feature variable

Value

fvar values

Examples

```
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
head(fvalues(object, 'feature_name'))
fvalues(object, NULL)
```

`fvars` *Get/Set fvars*

Description

Get/Set feature variables

Usage

```
fvars(object)

## S4 method for signature 'SummarizedExperiment'
fvars(object)

fvars(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,character'
fvars(object) <- value
```

Arguments

object	SummarizedExperiment
value	character vector with feature variables

Value

feature variables vector (get) or updated object (set)

Examples

```
require(magrittr)
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
fvars(object)[1] %<>% paste0('1')
fvars(object)[1]
```

---

guess_maxquant_quantity

Guess maxquant quantity from snames

Description

character vector, dataframe, or SummarizedExperiment.

Usage

```
guess_maxquant_quantity(x, ...)

## S3 method for class 'character'
guess_maxquant_quantity(x, ...)

## S3 method for class 'data.frame'
guess_maxquant_quantity(x, ...)

## S3 method for class 'SummarizedExperiment'
guess_maxquant_quantity(x, ...)
```

Arguments

x	character vector, dataframe, or SummarizedExperiment
...	used for proper S3 method dispatch

Value

string: value from names(MAXQUANT_PATTERNS_QUANTITY)

Examples

```
# file
    file <- download_data('fukuda20.proteingroups.txt')
    guess_maxquant_quantity(file)

# character vector
    x <- "Ratio M/L normalized STD(L)_E00(M)_E01(H)_R1"
    guess_maxquant_quantity(x)

    x <- "Ratio M/L STD(L)_E00(M)_E01(H)_R1"
    guess_maxquant_quantity(x)

    x <- "LFQ intensity E00.R1"
    guess_maxquant_quantity(x)

    x <- "Reporter intensity corrected 0 STD(0)E00(1)E01(2)_R1"
    guess_maxquant_quantity(x)

    x <- "Reporter intensity 0 STD(0)E00(1)E01(2)_R1"
    guess_maxquant_quantity(x)

    x <- "Intensity H STD(L)_E00(M)_E01(H)_R1"
    guess_maxquant_quantity(x)

# dataframe
    file <- download_data('fukuda20.proteingroups.txt')
    x <- data.table::fread(file)
    guess_maxquant_quantity(x)

# SummarizedExperiment
    file <- download_data('fukuda20.proteingroups.txt')
    object <- read_proteingroups(file, plot=FALSE)
    guess_maxquant_quantity(file)
```

---

guess_sep *Guess separator*

Description

Guess separator

Usage

```
guess_sep(x, ...)

## S3 method for class 'character'
guess_sep(x, separators = c(".", "_"), verbose = FALSE, ...)

## S3 method for class 'factor'
```

```
guess_sep(x, ...)

## S3 method for class 'SummarizedExperiment'
guess_sep(x, var = "sample_id", separators = c(".", "_"), verbose = FALSE, ...)
```

Arguments

x	character vector or SummarizedExperiment
...	used for proper S3 method dispatch
separators	character vector: possible separators to look for
verbose	TRUE or FALSE
var	svar or fvar

Value

separator (string) or NULL (if no separator could be identified)

Examples

```
# charactervector
   x <- c('PERM_NON.R1[H/L]', 'PERM_NON.R2[H/L]', 'PERM_NON.R3[H/L]')
   guess_sep(x)

   x <- c('WT untreated 1', 'WT untreated 2', 'WT treated 1')
   guess_sep(x)

   x <- c('group1', 'group2', 'group3.R1')
   guess_sep(x)

# SummarizedExperiment
   # file <- download_data('halama18.metabolon.xlsx')
   # object <- read_metabolon(file, plot=FALSE)
   # guess_sep(object)

   # file <- download_data('billing16.proteingroups.txt')
   # object <- read_proteingroups(file, plot=FALSE)
   # guess_sep(object)
```

---

impute_systematic_nondetects

Impute systematic nondetects

Description

Impute systematic nondetects

Usage

```
impute_systematic_nondetects(
  object,
  subgroup = subgroup,
  fun = halfnormimpute,
  plot = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

object	SummarizedExperiment
subgroup	subgroup svar
fun	imputation function
plot	TRUE or FALSE
verbose	TRUE or FALSE
...	passed to ‘fun‘

Value

SummarizedExperiment

Examples

```
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, impute = FALSE, plot = FALSE)
impute_systematic_nondetects(object)
```

---

invert *Invert*

Description

For character vectors: invert collapsed strings. For SummarizedExperiments: invert expressions , subgroups, and sample ids

Usage

```
invert(x, ...)

## S3 method for class 'character'
invert(x, sep = guess_sep(x), ...)

## S3 method for class 'SummarizedExperiment'
invert(
```

```
  x,
  subgroups = slevels(x, "subgroup"),
  sep = guess_sep(x, "subgroup"),
  ...
)
```

Arguments

x	character vector or SummarizedExperiment
...	to enable S3 method dispatch
sep	string: collapsed string separator
subgroups	character vector: subgroup levels to be inversed

Value

character vector or SummarizedExperiment

Examples

```
# character
    x <- c('Ctrl_A', 'Ctrl_B')
    invert(x)

# SummarizedExperiment
    file <- download_data('fukuda20.proteingroups.txt')
    object <- read_proteingroups(file, plot=FALSE)
    invert(object)
```

---

is_imputed *Get/set is_imputed*

Description

Get/Set is_imputed

Usage

```
is_imputed(object)

## S4 method for signature 'SummarizedExperiment'
is_imputed(object)

is_imputed(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
is_imputed(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,`NULL`'
is_imputed(object) <- value
```

Arguments

object	SummarizedExperiment
value	matrix

Value

matrix (get) or updated object (set)

Examples

```
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
sum(is_imputed(object))
```

---

is_sig *Is significant?*

Description

Is significant?

Usage

```
is_sig(
  object,
  fit = intersect(names(metadata(object)), TESTS),
  contrast = if (is_scalar(fit)) colnames(metadata(object)[[fit]]) else 1,
  quantity = "fdr"
)
```

Arguments

object	SummarizedExperiment
fit	subset of autonomics::TESTS
contrast	subset of colnames(metadata(object)[[fit]])
quantity	value in dimnames(metadata(object)[[fit]])[3]

Value

matrix: -1 (downregulated), +1 (upregulatd), 0 (not fdr significant)

Examples

```
require(magrittr)
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
object %<>% fit_lm()
object %<>% fit_limma()
issig <- is_sig(object, fit = c('lm','limma'), contrast = 'Adult-X30dpt')
plot_venn(issig)
```

---

limma *Get/set limma results*

Description

Get/Set limma results

Usage

```
limma(object)

## S4 method for signature 'SummarizedExperiment'
limma(object)

limma(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,array'
limma(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,`NULL`'
limma(object) <- value
```

Arguments

object	SummarizedExperiment
value	list

Value

limma results (get) or updated object (set)

Examples

```
file <- download_data('billing16.proteingroups.txt')
inv <- c('EM_E', 'BM_E', 'BM_EM')
object <- read_proteingroups(
          file, invert_subgroups=inv, fit='limma', plot=FALSE)
dim(limma(object))
dim(limma(object[1:5, ]))
```

log2counts *Get/Set log2counts*

Description

Get / Set log2counts matrix

Usage

```
log2counts(object)

## S4 method for signature 'SummarizedExperiment'
log2counts(object)

log2counts(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
log2counts(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
log2counts(object) <- value
```

Arguments

object	SummarizedExperiment
value	log2count matrix (features x samples)

Value

log2count matrix (get) or updated object (set)

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, plot=FALSE)
log2counts(object) <- values(object)
log2counts(object)[1:3, 1:3]
```

log2countsratios *Get/Set log2countsratios*

Description

Get / Set log2countsratios matrix

Usage

```
log2countsratios(object)

## S4 method for signature 'SummarizedExperiment'
log2countsratios(object)

log2countsratios(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
log2countsratios(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
log2countsratios(object) <- value
```

Arguments

object	SummarizedExperiment
value	log2countsratios matrix (features x samples)

Value

log2countsratios matrix (get) or updated object (set)

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, plot=FALSE)
log2countsratios(object) <- values(object)
log2countsratios(object)[1:3, 1:3]
```

log2cpm *Get/Set log2cpm*

Description

Get / Set log2cpm matrix

Usage

```
log2cpm(object)

## S4 method for signature 'SummarizedExperiment'
log2cpm(object)

log2cpm(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
log2cpm(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
log2cpm(object) <- value
```

Arguments

object	SummarizedExperiment
value	log2cpm matrix (features x samples)

Value

log2cpm matrix (get) or updated object (set)

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, plot=FALSE)
log2cpm(object) <- values(object)
log2cpm(object)[1:3, 1:3]
```

`log2cpmratios` *Get/Set log2cpmratios*

Description

Get / Set log2cpmratios matrix

Usage

```
log2cpmratios(object)

## S4 method for signature 'SummarizedExperiment'
log2cpmratios(object)

log2cpmratios(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
log2cpmratios(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
log2cpmratios(object) <- value
```

Arguments

`object`	SummarizedExperiment
`value`	log2cpmratios matrix (features x samples)

Value

log2cpmratios matrix (get) or updated object (set)

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, plot=FALSE)
log2cpmratios(object) <- values(object)
log2cpmratios(object)[1:3, 1:3]
```

log2tpm *Get/Set log2tpm*

Description

Get / Set log2tpm matrix

Usage

```
log2tpm(object)

## S4 method for signature 'SummarizedExperiment'
log2tpm(object)

log2tpm(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
log2tpm(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
log2tpm(object) <- value
```

Arguments

object	SummarizedExperiment
value	log2tpm matrix (features x samples)

Value

log2tpm matrix (get) or updated object (set)

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, plot=FALSE)
log2tpm(object) <- values(object)
log2tpm(object)[1:3, 1:3]
```

`log2tpmratios` *Get/Set log2tpmratios*

Description

Get / Set log2tpmratios matrix

Usage

```
log2tpmratios(object)

## S4 method for signature 'SummarizedExperiment'
log2tpmratios(object)

log2tpmratios(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
log2tpmratios(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
log2tpmratios(object) <- value
```

Arguments

`object`	SummarizedExperiment
`value`	log2tpmratios matrix (features x samples)

Value

log2tpmratios matrix (get) or updated object (set)

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, plot=FALSE)
log2tpmratios(object) <- values(object)
log2tpmratios(object)[1:3, 1:3]
```

log2transform *Transform values*

Description

Transform values

Usage

```
log2transform(object, verbose = FALSE)

exp2(object, verbose = FALSE)

zscore(object, verbose = FALSE)

quantnorm(object, verbose = FALSE)

invnorm(object, verbose = FALSE)
```

Arguments

object	SummarizedExperiment
verbose	TRUE or FALSE

Value

Transformed sumexp

Examples

```
require(magrittr)
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE, impute=FALSE)

object                       %>% plot_sample_densities()
invnorm(object)              %>% plot_sample_densities()

object                       %>% plot_sample_densities()
quantnorm(object)            %>% plot_sample_densities()

object                       %>% plot_sample_densities()
zscore(object)               %>% plot_sample_densities()

object                       %>% plot_sample_densities()
exp2(object)                 %>% plot_sample_densities()
log2transform(exp2(object))  %>% plot_sample_densities()
```

make_volcano_dt *Create volcano datatable*

Description

Create volcano datatable

Usage

```
make_volcano_dt(
  object,
  fit,
  contrastdefmat = contrastdefs(object)[[1]],
  ntop = 3
)
```

Arguments

object	SummarizedExperiment
fit	'limma', 'lme', 'lm', 'wilcoxon'
contrastdefmat	contrastdef matrix
ntop	no of top features to be annotated

Value

data.table

Examples

```
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, fit='limma', plot=FALSE)
make_volcano_dt(object, fit = 'limma')
```

matrix2sumexp *Convert matrix into SummarizedExperiment*

Description

Convert matrix into SummarizedExperiment

Usage

```
matrix2sumexp(
  x,
  sdt = NULL,
  sdtby = if (is.null(sdt)) NULL else names(sdt)[1],
  subgroupvar = NULL,
  fdt = NULL,
  fdtby = if (is.null(fdt)) NULL else names(fdt)[1],
  fnamevar = NULL,
  verbose = TRUE
)
```

Arguments

x	matrix
sdt	sample data.table / data.frame / DataFrame
sdtby	sample data mergeby column
subgroupvar	string / NULL
fdt	feature data.table / data.frame / DataFrame
fdtby	feature data mergeby column
fnamevar	string / NULL
verbose	TRUE/FALSE

Value

SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('atkin18.metabolon.xlsx')
x <- values(read_metabolon(file, plot=FALSE))
object <- matrix2sumexp(x)
object %<>% pca()
biplot(object, nloadings=0, color=subgroup)
```

MAXQUANT_PATTERNS_PEPCOUNTS

maxquant peptide count patterns

Description

maxquant peptide count patterns

Usage

```
MAXQUANT_PATTERNS_PEPCOUNTS
```

Format

An object of class `character` of length 3.

Examples

```
MAXQUANT_PATTERNS_PEPCOUNTS
```

MAXQUANT_PATTERNS_QUANTITY *maxquant quantity patterns*

Description

maxquant quantity patterns

Usage

```
MAXQUANT_PATTERNS_QUANTITY
```

Format

An object of class `character` of length 7.

Examples

```
MAXQUANT_PATTERNS_QUANTITY
```

---

merge_sdata *Merge sample/feature data*

Description

Merge sample/feature data

Usage

```
merge_sdata(
  object,
  dt,
  by.x = "sample_id",
  by.y = names(dt)[1],
  verbose = TRUE
)

merge_fdata(
  object,
  dt,
  by.x = "feature_id",
  by.y = names(dt)[1],
  verbose = TRUE
)
```

Arguments

object	SummarizedExperiment
dt	data.frame, data.table, DataFrame
by.x	object mergevar
by.y	df mergevar
verbose	TRUE/FALSE

Value

SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('halama18.metabolon.xlsx')
object <- read_metabolon(file, plot=FALSE)
object %<>% merge_sdata( data.frame(sample_id = object$sample_id,
                                    number = seq_along(object$sample_id)))
head(sdata(object))
```

---

merge_sfile *Merge sample/feature file*

Description

Merge sample/feature file

Usage

```
merge_sfile(
  object,
  sfile = NULL,
  by.x = "sample_id",
  by.y = NULL,
  stringsAsFactors = TRUE,
  verbose = TRUE
)

merge_ffile(
  object,
  ffile = NULL,
  by.x = "feature_id",
  by.y = NULL,
  stringsAsFactors = TRUE,
  verbose = TRUE
)
```

Arguments

object	SummarizedExperiment
sfile	sample file path
by.x	object mergevar
by.y	file mergevvar
stringsAsFactors	TRUE or FALSE
verbose	TRUE (default) or FALSE
ffile	ffile path

Value

SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('billing19.proteingroups.txt')
select <-  c('E00','E01', 'E02','E05','E15','E30', 'M00')
select %<>% paste0('_STD')
object <- read_proteingroups(file, select_subgroups = select, plot=FALSE)
sfile <- paste0(tempdir(),'/', basename(tools::file_path_sans_ext(file)))
sfile %<>% paste0('.samples.txt')
invisible(create_sfile(object, sfile))
merge_sfile(object, sfile)
```

message_df *message dataframe*

Description

message dataframe using sprintf syntax. Use place holder '

Usage

```
message_df(format_string, x)
```

Arguments

format_string	sprintf style format string
x	data.frame

Value

nothing returned

Examples

```
x <- data.frame(feature_id = c('F001', 'F002'), symbol = c('FEAT1', 'FEAT2'))
message_df('\t%s', x)

x <- c(rep('PASS', 25), rep('FAIL', 25))
message_df(format_string = '%s', table(x))
```

nfactors *stri_split and extract*

Description

stri_split and extract

Usage

```
nfactors(x, sep = guess_sep(x))

split_extract(x, i, sep = guess_sep(x))
```

Arguments

x	string
sep	string
i	integer

Value

character

Examples

```
require(magrittr)
file <- download_data('halama18.metabolon.xlsx')
object <- read_metabolon(file, plot=FALSE)
x <- object$sample_id[1:5]
nfactors(x)
split_extract(x, 1:2)
split_extract(x, seq_len(nfactors(x)-1))
split_extract(x, nfactors(x))

# With NA values
split_extract(fdata(object)$PUBCHEM, 1, ';')
```

---

normimpute *Impute from half-normal distribution around 0*

Description

Impute from half-normal distribution around 0

Usage

```
normimpute(x, selector = is.na(x), mean = 0)

halfnormimpute(x, selector = is.na(x))

zeroimpute(x, selector = is.na(x))

translate(
  x,
  ref = c(min, mean, median, max)[[1]],
  pos = 3 * sd(x, na.rm = TRUE)
)
```

Arguments

x	NA-containing numeric vector
selector	which values to impute
mean	number
ref	reference : which reference value away from which to impute
pos	position : how many sds away to impute

Value

numeric vector of same length

Examples

```
require(data.table)
x <- rnorm(1e5)
idx <- runif(length(x))>0.9
x[idx] <- NA
dt1 <- data.table(value = normimpute(x), distr = 'norm')

x <- abs(rnorm(1e5)); x[idx] <- NA
dt2 <- data.table(value = halfnormimpute(x), distr = 'halfnorm')

x <- abs(rnorm(1e5)); x[idx] <- NA
dt3 <- data.table(value = zeroimpute(x), distr = 'zero')

x <- abs(rnorm(1e5)); x[idx] <- NA
dt4 <- data.table(value = translate(x), distr = 'translate')

require(ggplot2)
ggplot(rbind(dt1,dt2,dt3, dt4), aes(x=value, fill=distr)) +
geom_density(alpha=0.5)
```

---

occupancies *Get/Set occupancies*

Description

Get / Set phosphosite occupancies matrix

Usage

```
occupancies(object)

## S4 method for signature 'SummarizedExperiment'
occupancies(object)

occupancies(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
occupancies(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
occupancies(object) <- value
```

Arguments

object	SummarizedExperiment
value	occupancy matrix (features x samples)

Value

occpuancy matrix (get) or updated object (set)

Examples

```
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
occupancies(object)
occupancies(object) <- values(object)
occupancies(object)[1:3, 1:3]
```

---

pca *Add PCA, SMA, LDA, PLS*

Description

Perform a dimension reduction. Add sample scores, feature loadings, and dimension variances to object.

Usage

```
pca(object, ndim = 2, minvar = 0, verbose = TRUE, plot = FALSE, ...)

pls(
  object,
  subgroupvar = "subgroup",
  ndim = 2,
  minvar = 0,
  verbose = FALSE,
  plot = FALSE,
  ...
)

sma(object, ndim = 2, minvar = 0, verbose = TRUE, plot = FALSE, ...)

lda(
  object,
  subgroupvar = "subgroup",
  ndim = 2,
  minvar = 0,
  verbose = TRUE,
  plot = FALSE,
```

```
  ...
)
```

Arguments

object	SummarizedExperiment
ndim	number
minvar	number
verbose	TRUE (default) or FALSE
plot	TRUE/FALSE
...	passed to biplot
subgroupvar	subgroup svar

Value

SummarizedExperiment

Author(s)

Aditya Bhagwat, Laure Cougnaud (LDA)

Examples

```
file <- download_data('atkin18.metabolon.xlsx')
object <- read_metabolon(file, plot = FALSE)
pca(object, plot=TRUE, color = Group)  # Principal Component Analysis
pls(object, subgroupvar = 'Group')  # Partial Least Squares
lda(object, subgroupvar = 'Group')  # Linear Discriminant Analysis
sma(object)  # Spectral Map Analysis
pca(object, ndim=3)
pca(object, ndim=Inf, minvar=5)
```

---

plot_boxplots *Plot sample/feature boxplots*

Description

Plot sample/feature boxplots

Usage

```
plot_boxplots(
  object,
  x,
  fill,
  color = NULL,
  facet = NULL,
```

```
  highlight = NULL,
  fixed = list(na.rm = TRUE)
)

plot_sample_boxplots(
  object,
  x = sample_id,
  fill = sample_id,
  color = NULL,
  highlight = NULL,
  fixed = list(na.rm = TRUE)
)

plot_feature_boxplots(
  object,
  x = feature_id,
  fill = feature_id,
  color = NULL,
  highlight = NULL,
  fixed = list(na.rm = TRUE)
)

plot_subgroup_boxplots(
  object,
  subgroup,
  x = !!enquo(subgroup),
  fill = !!enquo(subgroup),
  color = NULL,
  highlight = NULL,
  facet = feature_id,
  fixed = list(na.rm = TRUE)
)
```

Arguments

object	SummarizedExperiment
x	svar mapped to x
fill	svar mapped to fill
color	svar mapped to color
facet	svar mapped to facet
highlight	fvar expressing which feature should be highlighted
fixed	fixed aesthetics
subgroup	subgroup svar symbol

Value

ggplot object

See Also

plot_sample_densities, plot_sample_violins

Examples

```
# data
    require(magrittr)
    file <- download_data('halama18.metabolon.xlsx')
    object <- read_metabolon(file, plot = FALSE)
    object %<>% extract(, order(.$Group))
    fdata(object) %<>% cbind(
                        control=.$feature_name %in% c('biotin','phosphate'))
# plot
    plot_boxplots(object[1:9,], x = feature_id, fill = feature_id)
    plot_boxplots(object[,1:9], x = sample_id,  fill = sample_id )
    plot_feature_boxplots(object[1:9, ])
    plot_sample_boxplots(object[, 1:12])
    plot_sample_boxplots(object[, 1:12], highlight = control)
    plot_subgroup_boxplots(object[1:2, ], subgroup = Group)
```

---

plot_contrastogram *Plot contrastogram*

Description

Plot contrastogram

Usage

```
plot_contrastogram(
  object,
  subgroupvar,
  formula = default_formula(object, subgroupvar, "limma"),
  colors = make_colors(slevels(object, subgroupvar), guess_sep(object)),
  curve = 0.1
)
```

Arguments

object	SummarizedExperiment
subgroupvar	subgroup svar
formula	formula
colors	named color vector (names = subgroups)
curve	arrow curvature

Value

list returned by plotmat

Examples

```
if (requireNamespace('diagram', quietly = TRUE)){
   file <- download_data('halama18.metabolon.xlsx')
   object <- read_metabolon(file, fit='limma', plot=FALSE)
   plot_contrastogram(object, subgroupvar = 'Group')
}
```

`plot_corrections` *Biplot batch corrections*

Description

Biplot batch corrections

Usage

```
plot_corrections(...)

biplot_corrections(
  object,
  method = "pca",
  color = subgroup,
  covariates = character(0),
  varcols = ceiling(sqrt(1 + length(covariates))),
  plot = TRUE
)
```

Arguments

`...`	used to maintain deprecated functions
`object`	SummarizedExperiment
`method`	'pca', 'pls', 'lda', or 'sma'
`color`	variable mapped to color (symbol)
`covariates`	covariates to be batch-corrected
`varcols`	number of covariate columns
`plot`	TRUE/FALSE: plot?

Value

grid object

See Also

biplot_covariates

Examples

```
file <- download_data('atkin18.metabolon.xlsx')
object <- read_metabolon(file, pca=TRUE, plot = FALSE)
biplot_corrections(
    object,  color = Group, covariates = c('SEX', 'T2D', 'SUB', 'SET'))
```

`plot_covariates` *Biplot covariates*

Description

Biplot covariates

Usage

```
plot_covariates(...)

biplot_covariates(
  object,
  method = "pca",
  covariates = "subgroup",
  ndim = 6,
  dimcols = 1,
  varcols = length(covariates),
  plot = TRUE
)
```

Arguments

`...`	used to maintain deprecated functions
`object`	SummarizedExperiment
`method`	'pca', 'pls', 'lda', or 'sma'
`covariates`	covariates: mapped to color or batch-corrected
`ndim`	number of dimensions to plot
`dimcols`	number of dimension columns
`varcols`	number of covariate columns
`plot`	TRUE or FALSE: whether to plot

Value

ggplot object

See Also

biplot_corrections

Examples

```
file <- download_data('atkin18.metabolon.xlsx')
object <- read_metabolon(file, pca = TRUE, plot = FALSE)
biplot_covariates(object, covariates = 'Group', ndim = 12, dimcols = 3)
biplot_covariates(object, covariates = c('SEX', 'T2D', 'SUB', 'SET'))
biplot_covariates(object, covariates = c('SEX', 'T2D', 'SUB', 'SET'), ndim=2)
biplot_covariates(object, covariates = c('Group'), dimcols = 3)
```

---

plot_data *Plot data*

Description

Plot data

Usage

```
plot_data(
  data,
  geom = geom_point,
  color = NULL,
  fill = !!enquo(color),
  ...,
  fixed = list(),
  theme = list()
)
```

Arguments

data	data.frame'
geom	geom_point, etc.
color	variable mapped to color (symbol)
fill	variable mapped to fill (symbol)
...	mapped aesthetics
fixed	fixed aesthetics (list)
theme	list with ggplot theme specifications

Value

ggplot object

Author(s)

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Examples

```
require(magrittr)
file <- download_data('halama18.metabolon.xlsx')
object <- read_metabolon(file, plot = FALSE)
object %<>% pca()
data <- sdata(object)
plot_data(data, x = pca1, y = pca2)
plot_data(data, x = pca1, y = pca2, color = TIME_POINT)
data$TIME <- as.numeric(substr(data$TIME_POINT, 2, 3))
plot_data(data, x = pca1, y = pca2, color = TIME)
plot_data(data, x = pca1, y = pca2, color = NULL)

fixed <- list(shape = 15, size = 3)
plot_data(data, x = pca1, y = pca2, fixed=fixed)
```

---

plot_densities *Plot sample/feature densities*

Description

Plot sample/feature densities

Usage

```
plot_densities(
  object,
  group,
  fill,
  color = NULL,
  fixed = list(alpha = 0.5, na.rm = TRUE)
)

plot_sample_densities(
  object,
  fill = sample_id,
  color = NULL,
  group = sample_id,
  fixed = list(alpha = 0.5, na.rm = TRUE),
  subsetter = if (ncol(object) < 100) {
     seq_len(ncol(object))
 } else {

    sample(ncol(object), 9)
 }
)

plot_feature_densities(
```

```
  object,
  fill = feature_id,
  color = NULL,
  group = feature_id,
  fixed = list(alpha = 0.5, na.rm = TRUE),
  subsetter = if (nrow(object) < 100) {
     seq_len(nrow(object))
 } else {

    sample(nrow(object), 9)
 }
)
```

Arguments

object	SummarizedExperiment
group	svar mapped to group
fill	svar mapped to fill
color	svar mapped to color
fixed	fixed aesthetics
subsetter	subsetter for showing a subset of samples/features

Value

ggplot object

See Also

plot_sample_violins, plot_sample_boxplots

Examples

```
# Read data
    require(magrittr)
    file <- download_data('atkin18.metabolon.xlsx')
    object <- read_metabolon(file, plot = FALSE)
    object %<>% extract(, order(.$Group))
# Plot distributions
    plot_sample_densities(object, fill = Group)
    plot_feature_densities(object)
```

`plot_detects` *Plot detections*

Description

Plot detections

Usage

```
plot_detects(...)

plot_detections(object, subgroup = subgroup, fill = !!enquo(subgroup))

plot_quantifications(...)

plot_summarized_detections(
  object,
  subgroup = subgroup,
  fill = !!enquo(subgroup),
  na_imputes = TRUE
)
```

Arguments

`...`	for backward compatibilty
`object`	SummarizedExperiment
`subgroup`	subgroup var (sym)
`fill`	fill var (sym)
`na_imputes`	whether to NA imputes prior to plottin (TRUE/FALSE)g

Details

`plot_detections` plots feature x sample detections. It shows per feature/sample nondetects (white), imputes (light colored), and detects (full color).

`plot_summarized_detections` gives an summarized view, plotting featuretype x subgroup detections. It visualizes the subgroup-wise nondetect structure often seen in mass spectrometry proteomics data (across e.g. different cell types)

Value

ggplot object

Examples

```
require(magrittr)
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, impute=FALSE, plot = FALSE)
plot_summarized_detections(object)
plot_detections(object)
plot_detections(impute_systematic_nondetects(object, plot=FALSE))

file <- download_data('halama18.metabolon.xlsx')
object <- read_metabolon(file, impute = FALSE, plot = FALSE)
plot_summarized_detections(object, Group)
plot_detections(object, Group)
```

---

plot_features *Plot features*

Description

Plot features

Usage

```
plot_features(
  object,
  geom,
  subgroup,
  x = !!enquo(subgroup),
  fill = !!enquo(subgroup),
  color = !!enquo(subgroup),
  ...,
  fixed = list(na.rm = TRUE),
  theme = list(axis.text.x = element_blank(), axis.title.x = element_blank(),
    axis.ticks.x = element_blank())
)

plot_feature_profiles(...)
```

Arguments

object	SummarizedExperiment
geom	geom_point, geom_boxplot, etc.
subgroup	subgroup svar
x	svar mapped to x
fill	svar mapped to fill
color	svar mapped to color
...	mapped aesthetics

fixed	fixed aesthetics
theme	ggplot theme specifications

Value

ggplot object

Examples

```
require(magrittr)
file <- download_data('halama18.metabolon.xlsx')
object <- read_metabolon(file, pca=TRUE, plot = FALSE)
idx <- order(abs(fdata(object)$pca1), decreasing=TRUE)[1:9]
object %<>% extract(idx, )
plot_feature_boxplots(object)
plot_subgroup_boxplots(object, subgroup=Group)
plot_feature_profiles( object, subgroup=Group)
```

---

plot_venn *Plot venn*

Description

Plot venn

Usage

```
plot_venn(isfdr)
```

Arguments

isfdr	matrix(nrow, ncontrast): -1 (down), +1 (up)

Value

nothing returned

Examples

```
require(magrittr)
file <- download_data('atkin18.somascan.adat')
object <- read_somascan(file, plot=FALSE)
object %<>% fit_wilcoxon(subgroupvar='SampleGroup', block = 'Subject_ID')
object %<>% fit_limma(   subgroupvar='SampleGroup', block = 'Subject_ID')
isfdr <- is_sig(object, contrast = 't3-t2')
plot_venn(isfdr)
```

plot_violins *Plot sample/feature violins*

Description

Plot sample/feature violins

Usage

```
plot_violins(
  object,
  x,
  fill,
  color = NULL,
  group = NULL,
  facet = NULL,
  highlight = NULL,
  fixed = list(na.rm = TRUE)
)

plot_sample_violins(
  object,
  x = sample_id,
  fill = sample_id,
  color = NULL,
  highlight = NULL,
  fixed = list(na.rm = TRUE)
)

plot_feature_violins(
  object,
  x = feature_id,
  fill = feature_name,
  color = NULL,
  highlight = NULL,
  fixed = list(na.rm = TRUE)
)

plot_subgroup_violins(
  object,
  subgroup,
  x = !!enquo(subgroup),
  fill = !!enquo(subgroup),
  color = NULL,
  highlight = NULL,
  facet = feature_id,
  fixed = list(na.rm = TRUE)
```

```
)
```

Arguments

object	SummarizedExperiment
x	svar mapped to x
fill	svar mapped to fill
color	svar mapped to color
group	svar mapped to group
facet	svar mapped to facets
highlight	fvar expressing which feature should be highlighted
fixed	fixed aesthetics
subgroup	subgroup svar

Value

ggplot object

See Also

plot_sample_densities, plot_sample_boxplots

Examples

```
# data
    require(magrittr)
    file <- download_data('halama18.metabolon.xlsx')
    object <- read_metabolon(file, plot = FALSE)
    object %<>% extract(, order(.$Group))
    control_features <- c('biotin','phosphate')
    fdata(object) %<>% cbind(control=.$feature_name %in% control_features)
# plot
    plot_violins(object[1:12, ], x=feature_id, fill=feature_id)
    plot_feature_violins(object[1:12, ])
    plot_sample_violins(object[, 1:12],  highlight = control)
    plot_subgroup_violins(object[1:4, ], subgroup = Group)
```

---

plot_volcano *Plot volcano*

Description

Plot volcano

Usage

```
plot_volcano(
  object,
  fit = intersect(names(metadata(object)), TESTS)[1],
  contrastdefs = autonomics::contrastdefs(object)[[1]],
  label = feature_name,
  ntop = 1
)
```

Arguments

object	SummarizedExperiment
fit	'limma', 'lme', 'lm', 'wilcoxon'
contrastdefs	contrastdef vector / matrix / list
label	fvar for labeling top features
ntop	number: n top features to be annotated

Value

ggplot object

Examples

```
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, fit='limma', plot=FALSE)
plot_volcano(object)
```

---

preprocess_rnaseq_counts

Preprocess RNAseq counts

Description

Preprocess RNAseq counts

Usage

```
preprocess_rnaseq_counts(
  object,
  subgroupvar = if ("subgroup" %in% svars(object)) "subgroup" else NULL,
  formula = default_formula(object, subgroupvar, "limma"),
  block = NULL,
  min_count = 10,
  pseudocount = 0.5,
  genesize = NULL,
  cpm = TRUE,
```

```
  tmm = cpm,
  voom = TRUE,
  log2 = TRUE,
  verbose = TRUE,
  plot = TRUE
)
```

Arguments

object	SummarizedExperiment
subgroupvar	subgroup svar
formula	designmat formula
block	blocK svar
min_count	min count required in some samples
pseudocount	added pseudocount to avoid log(x)=-Inf
genesize	genesize fvar to compute tpm
cpm	whether to compute counts per million (scaled) reads
tmm	whether to tmm normalize
voom	whether to voom weight
log2	whether to log2
verbose	whether to msg
plot	whether to plot

Value

SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('billing19.rnacounts.txt')
object <- .read_rnaseq_counts(file)
object$subgroup
object %<>% preprocess_rnaseq_counts()
```

---

proteingroups *Get/Set proteingroups*

Description

Get / Set proteingroups matrix

Usage

```
proteingroups(object)

## S4 method for signature 'SummarizedExperiment'
proteingroups(object)

proteingroups(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
proteingroups(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
proteingroups(object) <- value
```

Arguments

object	SummarizedExperiment
value	occupancy matrix (features x samples)

Value

occpuancy matrix (get) or updated object (set)

Examples

```
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
proteingroups(object)[1:3, 1:3]
```

---

read_affymetrix *Read affymetrix microarray*

Description

Read affymetrix microarray

Usage

```
read_affymetrix(celfiles)
```

Arguments

celfiles	string vector: CEL file paths

Value

RangedSummarizedExperiment

Examples

```
require(magrittr)
url <- paste0('http://www.bioconductor.org/help/publications/2003/',
              'Chiaretti/chiaretti2/T33.tgz')
localdir  <- file.path(rappdirs::user_cache_dir(appname = 'autonomics'), 'T33')
dir.create(localdir, showWarnings=FALSE)
localfile <- file.path(localdir, basename(url))
if (!file.exists(localfile)){
    download.file(url, destfile = localfile)
    untar(localfile, exdir = path.expand(localdir))
}
localfile %<>% substr(1, nchar(.)-4)
if (!requireNamespace("BiocManager", quietly = TRUE))  install.packages(
                                                          'BiocManager')
if (!requireNamespace("hgu95av2.db", quietly = TRUE))  BiocManager::install(
                                                          'hgu95av2.db')
# read_affymetrix(celfiles = list.files(localfile, full.names = TRUE))
# currently openblas issue: https://stackoverflow.com/questions/61629861/
```

`rm_singleton_samples` *Rm singleton samples*

Description

Rm singleton samples

Usage

```
rm_singleton_samples(object, svar = "subgroup", verbose = TRUE)
```

Arguments

`object`	SummarizedExperiment
`svar`	sample var
`verbose`	TRUE/FALSE

Value

SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('atkin18.somascan.adat')
object <- read_somascan(file, plot=FALSE)
object %<>% filter_samples(SampleGroup %in% c('t1', 't2'), verbose = TRUE)
rm_singleton_samples(object, 'Subject_ID')
```

scaledlibsizes *Get tmm-scaled libsizes*

Description

Get tmm-scaled libsizes

Usage

```
scaledlibsizes(counts)
```

Arguments

counts	counts matri

Value

scaled libsize vector

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, cpm=FALSE, log2=FALSE, plot=FALSE)
scaledlibsizes(counts(object))
```

sdata *Get/Set sdata*

Description

Get/Set sample data

Usage

```
sdata(object)

## S4 method for signature 'SummarizedExperiment'
sdata(object)

## S4 method for signature 'MultiAssayExperiment'
sdata(object)

sdata(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,data.frame'
sdata(object) <- value
```

```
## S4 replacement method for signature 'SummarizedExperiment,DataFrame'
sdata(object) <- value

## S4 replacement method for signature 'MultiAssayExperiment,data.frame'
sdata(object) <- value

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

Arguments

object	SummarizedExperiment, eSet, or EList
value	dataframe

Value

sample dataframe (get) or updated object (set)

Examples

```
require(magrittr)
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
head(sdata(object))
head(sdata(object) %<>% cbind(z=1))
```

---

slevels *Get slevels*

Description

Get svar levels

Usage

```
slevels(object, svar)

subgroup_levels(object)
```

Arguments

object	SummarizedExperiment, eSet, or eList
svar	sample var (character)

Value

svar values (character)

Examples

```
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
slevels(object, 'subgroup')
subgroup_levels(object)
```

---

snames *Get/Set snames*

Description

Get/Set sample names

Usage

```
snames(object)

## S4 method for signature 'SummarizedExperiment'
snames(object)

snames(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,character'
snames(object) <- value
```

Arguments

object	SummarizedExperiment
value	string vector with sample names

Value

sample names vector (get) or updated eSet (set)

Examples

```
require(magrittr)
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
head(snames(object))
head(snames(object) %<>% paste0('SAMPLE_', .))
```

split_by_svar *Split by svar*

Description

Split by svar

Usage

```
split_by_svar(object, svar = subgroup)
```

Arguments

object	SummarizedExperiment
svar	svar to split on

Value

list of SummarizedExperiment

Examples

```
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, impute=FALSE, plot = FALSE)
split_by_svar(object)
```

standardize_maxquant_snames *Standardize maxquant snames*

Description

Standardize maxquant sample names

Usage

```
standardize_maxquant_snames(x, ...)

## S3 method for class 'character'
standardize_maxquant_snames(
  x,
  quantity = guess_maxquant_quantity(x),
  verbose = FALSE,
  ...
)
```

```
## S3 method for class 'SummarizedExperiment'
standardize_maxquant_snames(
  x,
  quantity = guess_maxquant_quantity(x),
  verbose = FALSE,
  ...
)
```

Arguments

x	character vector or SummarizedExperiment
...	allow for proper S3 method dispatch
quantity	maxquant quantity
verbose	TRUE (default) or FALSE

Details

Drop "Ratio normalized", "LFQ intensity" etc from maxquant sample names

Value

character vector or SummarizedExperiment

Examples

```
# character vector
   x <- "Ratio M/L normalized STD(L)_E00(M)_E01(H)_R1"
   standardize_maxquant_snames(x)

   x <- "Ratio M/L STD(L)_E00(M)_E01(H)_R1"
   standardize_maxquant_snames(x)

   x <-'LFQ intensity STD_R1'
   standardize_maxquant_snames(x)

   x <- 'LFQ intensity L STD(L)_E00(M)_E01(H)_R1'
   standardize_maxquant_snames(x)

   x <-'Reporter intensity 0 A(0)_B(1)_C(2)_D(3)_E(4)_F(5)_R1'
   standardize_maxquant_snames(x)

   x <- 'Reporter intensity corrected 0 A(0)_B(1)_C(2)_D(3)_E(4)_F(5)_R1'
   standardize_maxquant_snames(x)
```

subgroup_array *Get subgroup matrix*

Description

Arrange (subgroup)levels in matrix

Usage

```
subgroup_array(object, subgroupvar)

subgroup_matrix(object, subgroupvar)
```

Arguments

object	SummarizedExperiment
subgroupvar	subgroup svar

Value

matrix

Examples

```
file <- download_data('halama18.metabolon.xlsx')
object <- read_metabolon(file, plot=FALSE)
subgroup_matrix(object, 'Group')
```

subtract_baseline *Subtract baseline*

Description

Subtract baseline level within block

Usage

```
subtract_baseline(
  object,
  subgroupvar,
  subgroupctr = slevels(object, subgroupvar)[1],
  block = NULL,
  assaynames = setdiff(assayNames(object), "weights"),
  verbose = TRUE
)
```

```
subtract_pairs(
  object,
  subgroupvar,
  subgroupctr = slevels(object, subgroupvar)[1],
  block,
  assaynames = setdiff(assayNames(object), "weights"),
  verbose = TRUE
)

subtract_differences(object, block, subgroupvar, verbose = TRUE)
```

Arguments

object	SummarizedExperiment
subgroupvar	subgroup svar
subgroupctr	control subgroup
block	block svar (within which subtraction is performed)
assaynames	which assays to subtract for
verbose	TRUE/FALSE

Details

subtract_baseline subtracts baseline levels within block, using the medoid baseline sample if multiple exist.

subtract_pairs also subtracts baseline level within block. It cannot handle multiple baseline samples, but has instead been optimized for many blocks

subtract_differences subtracts differences between subsequent levels, again within block

Value

SummarizedExperiment

Examples

```
# read
    require(magrittr)
    file <- download_data('atkin18.metabolon.xlsx')
    object0 <- read_metabolon(file, plot=FALSE)
    pca(object0, plot=TRUE, color=SET)

# subtract_baseline: takes medoid of baseline samples if multiple
    object <- subtract_baseline(object0, block='SUB', subgroupvar='SET')
    pca(object, plot=TRUE, color=SET)

# subtract_pairs: optimized for many blocks
    object <- subtract_pairs(   object0, block='SUB', subgroupvar='SET')
```

```
    pca(object, plot=TRUE, color=SET)

# subtract differences
    object <- subtract_differences(object0, block='SUB', subgroupvar='SET')
    values(object) %<>% na_to_zero()
    pca(object, plot=TRUE, color=SET)
```

---

sumexp2mae *Create MultiAssayExperiment from SummarizedExperiment list*

Description

Create MultiAssayExperiment from SummarizedExperiment list

Usage

```
sumexp2mae(experiments)
```

Arguments

experiments	named list of SummarizedExperiments

Value

MultiAssayExperiment

Examples

```
require(magrittr)
somascanfile  <- download_data('atkin18.somascan.adat')
metabolonfile <- download_data('atkin18.metabolon.xlsx')
somascan <- read_somascan(somascanfile,   plot=FALSE)
metabolon<- read_metabolon(metabolonfile, plot=FALSE)
svars(somascan)  %<>% stringi::stri_replace_first_fixed(
                        'SampleGroup', 'subgroup')
svars(metabolon) %<>% stringi::stri_replace_first_fixed(
                        'Group',       'subgroup')
metabolon$replicate <- NULL
object   <- sumexp2mae(list(somascan=somascan, metabolon=metabolon))
```

`sumexp_to_wide_dt` *Convert SummarizedExperiment into data.table*

Description

Convert SummarizedExperiment into data.table

Usage

```
sumexp_to_wide_dt(
  object,
  fid = "feature_id",
  fvars = intersect("feature_name", autonomics::fvars(object)),
  assay = assayNames(object)[1]
)

sumexp_to_long_dt(
  object,
  fid = "feature_id",
  fvars = intersect("feature_name", autonomics::fvars(object)),
  sid = "sample_id",
  svars = intersect("subgroup", autonomics::svars(object)),
  assay = assayNames(object) %>% intersect(c(.[1], "is_imputed"))
)

sumexp_to_subrep_dt(object, subgroup = subgroup)
```

Arguments

`object`	sumexp
`fid`	fvar carrying feature id
`fvars`	additional fvars to include in table
`assay`	matrix in assays(object) to be used
`sid`	svar carrying sample id
`svars`	additional svars to include in table
`subgroup`	subgroup (sym)

Details

- `sumexp_to_wide_dt`: feature x sample
- `sumexp_to_subrep_dt`: feature.subgroup x replicate
- `sumexp_to_long_dt`: feature.sample

Value

data.table

Examples

```
# Stem cell comparison
    file <- download_data('billing16.proteingroups.txt')
    invert_subgroups <- c('EM_E', 'BM_E', 'EM_BM')
    object <- read_proteingroups(file, invert_subgroups = invert_subgroups,
                  plot=FALSE)
    sumexp_to_wide_dt(object)
    sumexp_to_long_dt(object)
    sumexp_to_subrep_dt(object)

# Glutaminase
   require(magrittr)
   file <- download_data('atkin18.metabolon.xlsx')
   object <- read_metabolon(file, plot=FALSE)
   sumexp_to_wide_dt(object)
   sumexp_to_long_dt(object)
   sumexp_to_subrep_dt(object, Group)

# Fukuda
   require(magrittr)
   file <- download_data('fukuda20.proteingroups.txt')
   object <- read_proteingroups(file, impute=FALSE, plot=FALSE)
   sumexp_to_long_dt(object)
   object %<>% impute_systematic_nondetects(plot=FALSE)
   sumexp_to_long_dt(object)
```

`summarize_fit` *Summarize fit*

Description

Summarize fit

Usage

```
summarize_fit(object, fit = intersect(names(metadata(object)), TESTS)[1])
```

Arguments

`object`	SummarizedExperiment
`fit`	'limma', 'lme', 'lm', 'lme', 'wilcoxon'

Value

data.table(contrast, nup, ndown)

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, fit='limma', plot=FALSE)
summarize_fit(object, 'limma')
```

---

svalues *Get/Set svalues*

Description

Get/Set svar values

Usage

```
svalues(object, svar)

subgroup_values(object)

sampleid_values(object)

svalues(object, svar) <- value

## S4 replacement method for signature 'SummarizedExperiment,character'
svalues(object, svar) <- value
```

Arguments

object	SummarizedExperiment
svar	sample var (character)
value	value vector

Value

character vector (get) or SummarizedExperiment (set)

Examples

```
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
svalues(object, 'subgroup')
subgroup_values(object)
```

svars *Get/Set svars*

Description

Get/Set sample variables

Usage

```
svars(object)

## S4 method for signature 'SummarizedExperiment'
svars(object)

## S4 method for signature 'MultiAssayExperiment'
svars(object)

svars(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,character'
svars(object) <- value

## S4 replacement method for signature 'MultiAssayExperiment,character'
svars(object) <- value
```

Arguments

object	SummarizedExperiment
value	string fector with variable names

Value

sample variable names (get) or updated SummarizedExperiment

Examples

```
require(magrittr)
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
svars(object)[1]
(svars(object)[1] %<>% paste0('1'))
```

TESTS *Statistical models supported in autonomics*

Description

Statistical models supported in autonomics

Usage

```
TESTS
```

Format

An object of class `character` of length 5.

Examples

```
TESTS
```

tpm *Get/Set tpm*

Description

Get / Set tpm matrix

Usage

```
tpm(object)

## S4 method for signature 'SummarizedExperiment'
tpm(object)

tpm(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
tpm(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
tpm(object) <- value
```

Arguments

`object`	SummarizedExperiment
`value`	tpm matrix (features x samples)

Value

tpm matrix (get) or updated object (set)

Examples

```
file <- download_data('billing19.rnacounts.txt')
object <- read_rnaseq_counts(file, plot=FALSE)
tpm(object) <- values(object)
tpm(object)[1:3, 1:3]
```

---

values *Get/Set expr values*

Description

Get/Set value matrix

Usage

```
values(object)

## S4 method for signature 'SummarizedExperiment'
values(object)

values(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
values(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
values(object) <- value
```

Arguments

object	SummarizedExperiment
value	ratio matrix (features x samples)

Value

value matrix (get) or updated object (set)

Examples

```
file <- download_data('billing16.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
values(object)[1:3, 1:3]
values(object) <- 0
values(object)[1:3, 1:3]
```

venn_detects *Venn detects*

Description

Venn diagram full/systematic/random detects

Usage

```
venn_detects(object, subgroup)
```

Arguments

object	SummarizedExperiment
subgroup	subgroup symbol

Value

NULL

Examples

```
file <- download_data('fukuda20.proteingroups.txt')
object <- read_proteingroups(file, impute=FALSE, plot = FALSE)
venn_detects(object, subgroup)
```

weights *Get/Set weights*

Description

Get/Set weight matrix

Usage

```
weights(object, ...)

## S4 method for signature 'SummarizedExperiment'
weights(object)

weights(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
weights(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
```

```
weights(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,`NULL`'
weights(object) <- value
```

Arguments

object	SummarizedExperiment
...	addtional params
value	ratio matrix (features x samples)

Value

weight matrix (get) or updated object (set)

Examples

```
file <- download_data('billing19.proteingroups.txt')
object <- read_proteingroups(file, plot=FALSE)
weights(object)[1:3, 1:2]
weights(object) <- 1; weights(object)[1:3, 1:2]
```

---

zero_to_na *Change nondetect representation*

Description

Change nondetect representation

Usage

```
zero_to_na(x, verbose = FALSE)

nan_to_na(x, verbose = FALSE)

na_to_zero(x, verbose = FALSE)

inf_to_na(x, verbose = FALSE)

minusinf_to_na(x, verbose = FALSE)
```

Arguments

x	matrix
verbose	logical(1)

Value

Updated matrix

Examples

```
require(magrittr)
matrix(c(0, 7), nrow=1)
matrix(c(0, 7), nrow=1)    %>% zero_to_na(verbose=TRUE)

matrix(c(NA, 7), nrow=1)
matrix(c(NA, 7), nrow=1)   %>% na_to_zero(verbose=TRUE)

matrix(c(NaN, 7), nrow=1)
matrix(c(NaN, 7), nrow=1)  %>% nan_to_na(verbose=TRUE)

matrix(c(Inf, 7), nrow=1)
matrix(c(Inf, 7), nrow=1)  %>% inf_to_na(verbose=TRUE)

matrix(c(-Inf, 7), nrow=1)
matrix(c(-Inf, 7), nrow=1) %>% minusinf_to_na(verbose=TRUE)
```

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