

# Package ‘autonomics’

May 29, 2024

**Type** Package

**Title** Unified statistical Modeling of Omics Data

**Version** 1.12.0

**Description** This package unifies access to Statistical Modeling of Omics Data.

Across linear modeling engines (lm, lme, lmer, limma, and wilcoxon).

Across coding systems (treatment, difference, deviation, etc).

Across model formulae (with/without intercept, random effect, interaction or nesting).

Across omics platforms (microarray, rnaseq, msproteomics, affinity proteomics, metabolomics).

Across projection methods (pca, pls, sma, lda, spls, opl).

It provides a fast enrichment analysis implementation.

And an intuitive contrastogram visualisation to summarize contrast effects in complex designs.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**VignetteBuilder** knitr

**biocViews** Software, DataImport, Preprocessing, DimensionReduction,  
PrincipalComponent, Regression, DifferentialExpression,  
GeneSetEnrichment, Transcriptomics, Transcription,  
GeneExpression, RNASeq, Microarray, Proteomics, Metabolomics,  
MassSpectrometry,

**BugReports** <https://github.com/bhagwataditya/autonomics>

**URL** <https://github.com/bhagwataditya/autonomics>

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vsn

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---

.extract\_p\_features    *Extract coefficient features*

---

**Description**

Extract coefficient features

**Usage**

```
.extract_p_features(
  object,
  coefs,
  p = 0.05,
  fit = fits(fdt(object)),
  combiner = "|",
  verbose = TRUE
)
```

```
.extract_fdr_features(  
  object,  
  coefs,  
  fdr = 0.05,  
  fit = fits(fdt(object)),  
  combiner = "|",  
  verbose = TRUE  
)  
  
.extract_effectsize_features(  
  object,  
  coefs,  
  effectsize = 1,  
  fit = fits(fdt(object)),  
  combiner = "|",  
  verbose = TRUE  
)  
  
.extract_sign_features(  
  object,  
  coefs,  
  sign,  
  fit = fits(fdt(object))[1],  
  combiner = "|",  
  verbose = TRUE  
)  
  
.extract_n_features(  
  object,  
  coefs,  
  combiner = "|",  
  n,  
  fit = fits(fdt(object))[1],  
  verbose = TRUE  
)  
  
extract_coef_features(  
  object,  
  fit = fits(fdt(object))[1],  
  coefs = default_coefs(fdt(object), fit = fit),  
  combiner = "|",  
  p = 1,  
  fdr = 1,  
  effectsize = 0,  
  sign = c(-1, +1),  
  n = 4,  
  verbose = TRUE
```

)

**Arguments**

object	SummarizedXExperiment
coefs	subset of coefs(object)
p	p threshold
fit	subset of fits(fdt(object))
combiner	' ' or '&': how to combine multiple fits/coefs
verbose	TRUE or FALSE
fdr	fdr threshold
effectsize	effectsize threshold
sign	effect sign
n	number of top features (Inf means all)

**Value**

SummarizedExperiment

**Examples**

```
# Read and Fit
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% fit_limma()
fdt(object) %<>% add_adjusted_pvalues('fdr')

# Single coef
object0 <- object
object %<>% .extract_p_features(      coefs = 't1', p = 0.05)
object %<>% .extract_fdr_features(    coefs = 't1', fdr = 0.05)
object %<>% .extract_effectsize_features(coefs = 't1', effectsize = 1)
object %<>% .extract_sign_features(   coefs = 't1', sign = -1)
object %<>% .extract_n_features(     coefs = 't1', n = 1)
object <- object0
object %<>% extract_coef_features(coefs = 't1', p = 0.05, fdr = 0.05, effectsize = 1, sign = -1, n = 1)

# Multiple coefs
object <- object0
object %<>% .extract_p_features(      coefs = c('t1', 't2'), p = 0.05)
object %<>% .extract_fdr_features(    coefs = c('t1', 't2'), fdr = 0.01)
object %<>% .extract_effectsize_features(coefs = c('t1', 't2'), effectsize = 1)
object %<>% .extract_sign_features(   coefs = c('t1', 't2'), sign = -1)
object %<>% .extract_n_features(     coefs = c('t1', 't2'), n = 1)
object <- object0
object %<>% extract_coef_features(coefs = c('t1', 't2'), p = 0.05, fdr = 0.01, effectsize = 1, sign = -1, n = 1)
```



---

.merge *Clean Merge*

---

### Description

Clean Merge

### Usage

```
.merge(dt1, dt2, by)
```

### Arguments

dt1	data.table
dt2	data.table
by	string

### Examples

```
require(data.table)
dt1 <- data.table(feature_id = c('PG1', 'PG2'), gene = c('G1', 'G2'))
dt2 <- data.table(feature_id = c('PG1', 'PG2'), protein = c('P1', 'P2'))
dt1 %<>% .merge(dt2, by = 'feature_id')
dt1
```

---

.read\_diann\_precursors  
*Read diann*

---

### Description

Read diann

### Usage

```
.read_diann_precursors(file, Lib.PG.Q = 0.01, verbose = TRUE)
```

```
.read_diann_proteingroups(file, Lib.PG.Q = 0.01)
```

```
read_diann_proteingroups(  
  file,  
  Lib.PG.Q = 0.01,  
  simplify_snames = TRUE,  
  contaminants = character(0),  
  impute = FALSE,  
)
```

```

plot = FALSE,
pca = plot,
pls = plot,
fit = if (plot) "limma" else NULL,
formula = ~subgroup,
block = NULL,
coefs = NULL,
contrasts = NULL,
palette = NULL,
verbose = TRUE
)

read_diann(...)

```

### Arguments

file	'report.tsv' file
Lib.PG.Q	Lib.PG.Q cutoff
verbose	TRUE or FALSE
simplify_snames	TRUE or FALSE: simplify (drop common parts in) samplenames ?
contaminants	character vector: contaminant uniprot
impute	TRUE or FALSE: impute group-specific NA values?
plot	TRUE or FALSE
pca	TRUE or FALSE: run pca ?
pls	TRUE or FALSE: run pls ?
fit	model engine: 'limma', 'lm', 'lme(r)', 'wilcoxon' or NULL
formula	model formula
block	model blockvar: string or NULL
coefs	model coefficients of interest: character vector or NULL
contrasts	coefficient contrasts of interest: character vector or NULL
palette	color palette: named string vector
...	used to maintain deprecated functions

### Value

data.table or SummarizedExperiment

### Examples

```

# Read
file <- download_data('dilution.report.tsv')
.read_diann_precursors(file)      # precursors longdt
.read_diann_proteingroups(file)  # proteingroups longdt
fdt(read_diann_proteingroups(file)) # proteingroups sumexp

```

```
# Compare
PR <- .read_diann_precursors(file)
PG <- .read_diann_proteingroups(file)
PG[intensity==top1] # matches      : 24975 (85%) proteingroups
PG[intensity!=top1] # doesnt match : 4531 (15%) proteingroups
RUN <- 'IPT_HeLa_1_DIAstd_Slot1-40_1_9997'
PR[uniprot=='Q96JP5;Q96JP5-2' & run == RUN, 1:6] # match: 8884 == 8884
PR[uniprot=='P36578' & run == RUN, 1:6] # no match: 650887 != 407978
PR[intensity != top1][feature_id == unique(feature_id)[1]][run == unique(run)[1]][1:2, 1:6]
PR[intensity != top1][feature_id == unique(feature_id)[2]][run == unique(run)[1]][1:2, 1:6]
PR[intensity != top1][feature_id == unique(feature_id)[3]][run == unique(run)[1]][1:3, 1:6]
```

---

.read\_maxquant\_proteingroups

*Read proteingroups/phosphosites as-is*

---

## Description

Read proteingroups/phosphosites as-is

## Usage

```
.read_maxquant_proteingroups(
  file,
  quantity = guess_maxquant_quantity(file),
  verbose = TRUE
)

.read_maxquant_phosphosites(
  file,
  profile,
  quantity = guess_maxquant_quantity(file),
  verbose = TRUE
)
```

## Arguments

file	proteingroups / phosphosites file
quantity	string
verbose	TRUE / FALSE
profile	proteingroups file

## Value

data.table

**Examples**

```
profile <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
fosfile <- system.file('extdata/billing19.phosphosites.txt', package = 'autonomics')
prodt <- .read_maxquant_proteingroups(file = profile)
fosdt <- .read_maxquant_phosphosites( file = fosfile, profile = profile)
```

---

<code>.read_metabolon</code>	<i>Read metabolon xlsxfile</i>
------------------------------	--------------------------------

---

**Description**

Read metabolon xlsxfile

**Usage**

```
.read_metabolon(  
  file,  
  sheet = "OrigScale",  
  fidvar = "BIOCHEMICAL",  
  sidvar = "(CLIENT_IDENTIFIER|Client ID)",  
  sfile = NULL,  
  by.x = "sample_id",  
  by.y = NULL,  
  subgroupvar = "Group",  
  verbose = TRUE  
)
```

```
read_metabolon(  
  file,  
  sheet = "OrigScale",  
  fidvar = "BIOCHEMICAL",  
  sidvar = "(CLIENT_IDENTIFIER|Client ID)",  
  sfile = NULL,  
  by.x = "sample_id",  
  by.y = NULL,  
  subgroupvar = "Group",  
  fnamevar = "BIOCHEMICAL",  
  kegg_pathways = FALSE,  
  smiles = FALSE,  
  impute = TRUE,  
  plot = FALSE,  
  pca = plot,  
  pls = plot,  
  label = "feature_id",  
  fit = if (plot) "limma" else NULL,  
  formula = ~subgroup,  
  block = NULL,
```

```
  coefs = NULL,  
  contrasts = NULL,  
  palette = NULL,  
  verbose = TRUE  
)
```

### Arguments

<code>file</code>	metabolon xlsx file
<code>sheet</code>	excel sheet (number or string)
<code>fidvar</code>	featureid var
<code>sidvar</code>	samplid var
<code>sfile</code>	sample file
<code>by.x</code>	'file' mergeby column
<code>by.y</code>	'sfile' mergeby column
<code>subgroupvar</code>	subgroup var
<code>verbose</code>	TRUE or FALSE
<code>fnamevar</code>	featurename fvar
<code>kegg_pathways</code>	TRUE or FALSE: add kegg pathways?
<code>smiles</code>	TRUE or FALSE: add smiles?
<code>impute</code>	TRUE or FALSE: impute group-specific NA values?
<code>plot</code>	TRUE or FALSE
<code>pca</code>	TRUE or FALSE
<code>pls</code>	TRUE or FALSE
<code>label</code>	fvar
<code>fit</code>	model engine: 'limma', 'lm', 'lme(r)', 'wilcoxon' or NULL
<code>formula</code>	model formula
<code>block</code>	model blockvar: string or NULL
<code>coefs</code>	model coefficients of interest: character vector or NULL
<code>contrasts</code>	coefficient contrasts of interest: character vector or NULL
<code>palette</code>	NULL or colorvector

### Value

SummarizedExperiment

### Examples

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')  
read_metabolon(file, plot = TRUE, block = 'Subject')
```

---

`.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 <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')  
read_rectangles( file, fid_rows = 2:25,    fid_cols = 2,  
                 sid_rows = 1,          sid_cols = 5:28,  
                 expr_rows = 2:25 ,    expr_cols = 5:28,  
                 fvar_rows = 1,        fvar_cols = 1:4,  
                 fdata_rows = 2:25 ,  fdata_cols = 1:4,    transpose = FALSE)
```

```

# LCMSMS PROTEINGROUPS
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
read_rectangles( file,
  fid_rows = 2:21,    fid_cols = 383,
  sid_rows = 1,      sid_cols = seq(124, 316, by = 6),
  expr_rows = 2:21,  expr_cols = seq(124, 316, by = 6),
  fvar_rows = 1,     fvar_cols = c(2, 6, 7, 383),
  fdata_rows = 2:21, fdata_cols = c(2, 6, 7, 383),
  transpose = FALSE )

# SOMASCAN
file <- system.file('extdata/atkin.somascan.adat', package = 'autonomics')
read_rectangles(file, fid_rows = 30,    fid_cols = 23:42,
  sid_rows = 42:108,  sid_cols = 4,
  expr_rows = 42:108, expr_cols = 23:42,
  fvar_rows = 28:40,  fvar_cols = 22,
  svar_rows = 41,     svar_cols = 1:21,
  fdata_rows = 28:40, fdata_cols = 23:42,
  sdata_rows = 42:108, sdata_cols = 1:21, transpose = TRUE)

# METABOLON
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
read_rectangles(file, sheet = 2,
  fid_rows = 11:30,   fid_cols = 2,
  sid_rows = 4,       sid_cols = 15:81,
  expr_rows = 11:30,  expr_cols = 15:81,
  fvar_rows = 10,     fvar_cols = 1:14,
  svar_rows = 1:10,   svar_cols = 14,
  fdata_rows = 11:30, fdata_cols = 1:14,
  sdata_rows = 1:10,  sdata_cols = 15:81,
  transpose = FALSE )

```

---

*.read\_rnaseq\_bams*      *Read rnaseq counts/bams*

---

## Description

Read rnaseq counts/bams

## Usage

```

.read_rnaseq_bams(
  dir,
  paired,
  genome,
  nthreads = detectCores(),
  sfile = NULL,
  by.y = NULL,
  ensdb = NULL,
  verbose = TRUE
)

```



```
.read_rnaseq_counts(  
  file,  
  fid_col = 1,  
  sfile = NULL,  
  by.y = NULL,  
  ensdb = NULL,  
  verbose = TRUE  
)  
  
read_rnaseq_bams(  
  dir,  
  paired,  
  genome,  
  nthreads = detectCores(),  
  sfile = NULL,  
  by.y = NULL,  
  block = NULL,  
  formula = ~subgroup,  
  min_count = 10,  
  pseudo = 0.5,  
  ensdb = NULL,  
  tpm = FALSE,  
  cpm = TRUE,  
  log2 = TRUE,  
  plot = FALSE,  
  label = "feature_id",  
  pca = plot,  
  pls = plot,  
  fit = if (plot) "limma" else NULL,  
  voom = cpm,  
  coefs = NULL,  
  contrasts = NULL,  
  palette = NULL,  
  verbose = TRUE  
)  
  
read_rnaseq_counts(  
  file,  
  fid_col = 1,  
  sfile = NULL,  
  by.y = NULL,  
  formula = ~subgroup,  
  block = NULL,  
  min_count = 10,  
  pseudo = 0.5,  
  tpm = FALSE,  
  ensdb = NULL,
```

```

cpm = !tpm,
log2 = TRUE,
plot = FALSE,
label = "feature_id",
pca = plot,
pls = plot,
fit = if (plot) "limma" else NULL,
voom = cpm,
coefs = NULL,
contrasts = NULL,
palette = NULL,
verbose = TRUE
)

```

### Arguments

<code>dir</code>	read_rnaseq_bams: bam/sam dir
<code>paired</code>	read_rnaseq_bams: TRUE/FALSE : paired end reads ?
<code>genome</code>	read_rnaseq_bams: 'mm10', 'hg38', etc. or GTF file
<code>nthreads</code>	read_rnaseq_bams: nthreads used by Rsubread::featureCounts()
<code>sfile</code>	sample file
<code>by.y</code>	sample file mergeby column
<code>ensdb</code>	EnsDb with genesizes : e.g. AnnotationHub::AnnotationHub[['AH64923']]
<code>verbose</code>	TRUE or FALSE: message?
<code>file</code>	count file
<code>fid_col</code>	featureid column (number or string)
<code>block</code>	model blockvar: string or NULL
<code>formula</code>	model formula
<code>min_count</code>	min feature count required in some samples
<code>pseudo</code>	pseudocount added to prevent -Inf log2 values
<code>tpm</code>	TRUE or FALSE : add tpm to assays ( counts / libsize / genelength ) ?
<code>cpm</code>	TRUE or FALSE: add cpm to assays ( counts / effectivelibsize ) ?
<code>log2</code>	TRUE or FALSE: log2 transform ?
<code>plot</code>	TRUE or FALSE: plot?
<code>label</code>	fvar
<code>pca</code>	TRUE or FALSE: perform and plot pca?
<code>pls</code>	TRUE or FALSE: run pls ?
<code>fit</code>	model engine: 'limma', 'lm', 'lme(r)', 'wilcoxon' or NULL
<code>voom</code>	model weights to be computed? TRUE/FALSE
<code>coefs</code>	model coefficients of interest: string vector or NULL
<code>contrasts</code>	model coefficient contrasts of interest: string vector or NULL
<code>palette</code>	color palette : named string vector

**Value**

SummarizedExperiment

**Author(s)**

Aditya Bhagwat, Shahina Hayat

**Examples**

```
# read_rnaseq_bams
  if (requireNamespace('Rsubread')){
    dir <- download_data('billing16.bam.zip')
    object <- read_rnaseq_bams(dir, paired = TRUE, genome = 'hg38')
    object <- read_rnaseq_bams(dir, paired = TRUE, genome = 'hg38', plot = TRUE)
  }
# read_rnaseq_counts
  file <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
  object <- read_rnaseq_counts(file, fit = 'limma', coefs = 'E15')
  object <- read_rnaseq_counts(file, fit = 'limma', coefs = 'E15', voom = FALSE)
  object <- read_rnaseq_counts(file, fit = 'limma', coefs = 'E15', voom = FALSE, cpm = FALSE)
  object <- read_rnaseq_counts(file, fit = 'limma', coefs = 'E15', voom = FALSE, cpm = FALSE, log2 = FALSE)
  object <- read_rnaseq_counts(file, plot = TRUE)

# read_rnaseq_counts(tpm = TRUE)
  ## Not run:
  ah <- AnnotationHub::AnnotationHub()
  ensdb <- ah[['AH64923']]
  object <- read_rnaseq_counts(file, fit = 'limma', coefs = 'E02', tpm = TRUE, ensdb = ensdb)

## End(Not run)
```

---

.read\_somascan                      *Read somascan adatfile*

---

**Description**

Read somascan adatfile

**Usage**

```
.read_somascan(
  file,
  fidvar = "Target",
  sidvar = "SampleId",
  sfile = NULL,
  by.x = NULL,
  by.y = NULL,
  subgroupvar = "SampleGroup",
  verbose = TRUE
```

```

)

read_somascan(
  file,
  fidvar = "Target",
  sidvar = "SampleId",
  sfile = NULL,
  by.x = NULL,
  by.y = 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,
  plot = FALSE,
  label = "feature_id",
  pca = plot,
  pls = plot,
  fit = if (plot) "limma" else NULL,
  formula = ~subgroup,
  block = NULL,
  coefs = NULL,
  contrasts = NULL,
  palette = NULL,
  verbose = TRUE
)

```

### Arguments

file	somascan (adat) file
fidvar	featureid var
sidvar	sampleid var
sfile	sample file
by.x	'file' mergeby column
by.y	'sfile' mergeby column
subgroupvar	subgroup var: string
verbose	TRUE or FALSE: message?
fname_var	featurename var: 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	TRUE or FALSE: rm NA svars?
rm_single_value_svars	TRUE or FALSE: rm single value svars?
plot	TRUE or FALSE: plot ?
label	fvar
pca	TRUE or FALSE: run pca?
pls	TRUE or FALSE: run pls?
fit	model engine: 'limma', 'lm', 'lme(r)', 'wilcoxon' or NULL
formula	model formula
block	model blockvar
coefs	model coefficients of interest: character vector or NULL
contrasts	coefficient contrasts of interest: character vector or NULL
palette	character vector or NULL

**Value**

Summarizedexperiment

**Examples**

```
file <- system.file('extdata/atkin.somascan.adat', package = 'autonomics')
read_somascan(file, plot = TRUE, block = 'Subject')
```

---

abstract\_fit

*Abstract model fit*

---

**Description**

Abstract model fit

**Usage**

```
abstract_fit(
  object,
  sep = guess_fitsep(fdt(object)),
  fit = fits(fdt(object)),
  coef = coefs(fdt(object), fit = fit),
  significancevar = "p",
  significance = 0.05
)
```

**Arguments**

object	SummarizedExperiment
sep	string
fit	character vector
coef	character vector
significancevar	'p' or 'fdr'
significance	fraction : pvalue cutoff

**Value**

SummarizedExperiment

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file, fit = 'limma', coef = 't3')
fdt(object)
fdt(abstract_fit(object))
```

---

add\_adjusted\_pvalues *Add adjusted pvalues*

---

**Description**

Add adjusted pvalues

**Usage**

```
add_adjusted_pvalues(
  featuredt,
  method,
  fit = fits(featuredt),
  coefs = default_coefs(featuredt, fit = fit),
  verbose = TRUE
)
```

**Arguments**

featuredt	fdt(object)
method	'fdr', 'bonferroni', ... (see 'p.adjust.methods')
fit	'limma', 'lm', 'lme', 'lmer'
coefs	coefficient (string)
verbose	TRUE or FALSE

**Value**

SummarizedExperiment

**Examples**

```

file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
fdt(object) %<>% extract(, 1:2)
object %<>% fit_limma(coef = 'Adult')
object %<>% extract(order(fdt(.)$`p~Adult~limma`), )
  fdt(object)
(fdt(object) %<>% add_adjusted_pvalues('fdr'))
(fdt(object) %<>% add_adjusted_pvalues('fdr'))      # smart enough not to add second column
(fdt(object) %>% add_adjusted_pvalues('bonferroni'))

```

---

add_assay_means	<i>Add assay means</i>
-----------------	------------------------

---

**Description**

Add assay means

**Usage**

```
add_assay_means(object, assay = assayNames(object)[1], bin = TRUE)
```

**Arguments**

object	SummarizedExperiment or NULL
assay	string
bin	TRUE or FALSE

**Value**

SummarizedExperiment

**Examples**

```

file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
fdt(object) %<>% extract(, 1:2)
fdt(object)
object %<>% add_assay_means(SummarizedExperiment::assayNames(.))
fdt(object)

```

---

add\_facetvars            *Add facetvars*

---

**Description**

Add facetvars

**Usage**

```
add_facetvars(  
  object,  
  fit = fits(fdt(object))[1],  
  coefs = default_coefs(fdt(object), fit = fit)  
)
```

**Arguments**

object	SummarizedExperiment
fit	string
coefs	string vector

**Value**

SummarizedExperiment

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')  
object <- read_metabolon(file, fit = 'limma')  
fdt(object)  
fdt(add_facetvars(object))
```

---

add\_opentargets\_by\_uniprot  
                          *Add opentargets annotations*

---

**Description**

Add opentargets annotations

**Usage**

```
add_opentargets_by_uniprot(  
  object,  
  cols = c("genesymbol", "genename", "function"),  
  verbose = TRUE  
)
```



**Arguments**

object	SummarizedExperiment
cols	character vector
verbose	TRUE or FALSE

**Value**

SummarizedExperiment

**Examples**

```
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
object %<>% add_opentargets_by_uniprot()
```

---

add_psp	<i>Add psp</i>
---------	----------------

---

**Description**

Add PhosphoSitePlus literature counts

**Usage**

```
add_psp(
  object,
  pspfile = file.path(R_user_dir("autonomics", "cache"), "phosphositeplus",
    "Phosphorylation_site_dataset.gz")
)
```

**Arguments**

object	SummarizedExperiment
pspfile	phosphositeplus file

**Details**

Go to [www.phosphosite.org](http://www.phosphosite.org)  
 Register and Login.  
 Download Phosphorylation\_site\_dataset.gz'.  
 Save into: file.path(R\_user\_dir('autonomics','cache'),'phosphositeplus')

**Value**

SummarizedExperiment

**Examples**

```
fosfile <- system.file('extdata/billing19.phosphosites.txt', package = 'autonomics')
profile <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_phosphosites(fosfile = fosfile, profile = profile)
fdt(object)
object %<>% add_psp()
fdt(object)
```

---

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 <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
# add_smiles(object[1:10, ]) # seems down
```

altenrich

*Alternative Enrichment Analysis***Description**

Alternative Enrichment Analysis

**Usage**

```

altenrich(
  object,
  pathwaydt,
  genevar = "gene",
  genesep = "[ ,;]",
  coef = default_coefs(fdt(object))[1],
  fit = fits(fdt(object))[1],
  significancevar = "p",
  significance = 0.05,
  effectsizesize = 0,
  n = 3,
  genes = FALSE,
  verbose = TRUE
)

```

**Arguments**

object	SummarizedExperiment
pathwaydt	data.table, e.g. <code>read_msigt</code>
genevar	gene fvar
genesep	string or NULL
coef	string in <code>coefs(fdt(object))</code>
fit	'limma', 'lm', 'lme', 'lmer', 'wilcoxon'
significancevar	'p' or 'fdr'
significance	significance cutoff
effectsizesize	effectsizesize cutoff
n	no of detected genes required (for geneset to be examined)
genes	whether to record genes
verbose	whether to msg

**Details**

This is an alternative enrichment analysis implementation. It is more modular: uses four times `.enrichment(VERBOSE)?` as backend. But also four times slower than `enrichment`, so not recommended. It is retained for testing purposes.

This alternative enrichment implementation

**See Also**

[enrichment()]

---

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 <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')  
object <- read_maxquant_proteingroups(file)  
analysis(object)
```

---

analyze

*Analyze*


---

**Description**

Analyze

**Usage**

```
analyze(
  object,
  pca = TRUE,
  pls = TRUE,
  fit = "limma",
  formula = default_formula(object),
  drop = varlevels_dont_clash(object, all.vars(formula)),
  codingfun = contr.treatment,
  contrasts = NULL,
  coefs = colnames(create_design(object, formula = formula, drop = drop)),
  block = NULL,
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  plot = pca & !is.null(fit),
  label = "feature_id",
  palette = NULL,
  verbose = TRUE
)
```

**Arguments**

object	SummarizedExperiment
pca	TRUE / FALSE: perform pca ?
pls	TRUE / FALSE: perform pls ?
fit	linmod engine: 'limma', 'lm', 'lme(r)', 'lmer', 'wilcoxon'
formula	model formula
drop	TRUE / FALSE : drop varname in designmat ?
codingfun	factor coding function <ul style="list-style-type: none"> <li>• <code>contr.treatment</code>: intercept = <math>y_0</math>, <math>\text{coef}_i = y_i - y_0</math></li> <li>• <code>contr.treatment.explicit</code>: intercept = <math>y_0</math>, <math>\text{coef}_i = y_i - y_0</math></li> <li>• <code>code_control</code>: intercept = <math>y_{\text{mean}}</math>, <math>\text{coef}_i = y_i - y_0</math></li> <li>• <code>contr.diff</code>: intercept = <math>y_0</math>, <math>\text{coef}_i = y_i - y_{(i-1)}</math></li> <li>• <code>code_diff</code>: intercept = <math>y_{\text{mean}}</math>, <math>\text{coef}_i = y_i - y_{(i-1)}</math></li> <li>• <code>code_diff_forward</code>: intercept = <math>y_{\text{mean}}</math>, <math>\text{coef}_i = y_i - y_{(i+)}</math></li> <li>• <code>code_deviation</code>: intercept = <math>y_{\text{mean}}</math>, <math>\text{coef}_i = y_i - y_{\text{mean}}</math> (drop last)</li> <li>• <code>code_deviation_first</code>: intercept = <math>y_{\text{mean}}</math>, <math>\text{coef}_i = y_i - y_{\text{mean}}</math> (drop first)</li> </ul>

- code\_helmert: intercept = ymean, coefi = yi - mean(y0:(yi-1))
- code\_helmert\_forward: intercept = ymean, coefi = yi - mean(y(i+1):yp)

contrasts	model coefficient contrasts of interest: string vector or NULL
coefs	model coefficients of interest: string vector or NULL
block	model blockvar
weightvar	NULL or name of weight matrix in assays(object)
plot	TRUE / FALSE
label	fvar
palette	NULL or colorvector
verbose	TRUE / FALSE: message?

**Value**

SummarizedExperiment

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% analyze()
```

---

annotate_maxquant	<i>Annotate maxquant</i>
-------------------	--------------------------

---

**Description**

Annotate maxquant data.table

**Usage**

```
annotate_maxquant(
  dt,
  uniprothdrs,
  contaminanthdrs,
  maxquanthdrs,
  restapi = FALSE,
  verbose = TRUE
)
```

### Arguments

dt data.table : output of read\_maxquant\_(proteingroups|phosphosites)  
 uniprothdrs data.table : output of read\_uniprot dt  
 contaminanthdrs data.table : output of read\_uniprot dt  
 maxquanthdrs data.table : output of read\_uniprot dt  
 restapi logical(1) : use uniprot restapi to complete missing annotations ?  
 verbose logical(1) : message ?

### Details

Uncollapse, annotate, curate, recollapse, name

### Value

data.table

### Examples

```
# Fukuda 2020: contaminants + maxquanthdrs
#-----
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
dt <- .read_maxquant_proteingroups(file)
dt[, 1:2]
uniprothdrs <- NULL
contaminanthdrs <- read_contaminantdt()
maxquanthdrs <- parse_maxquant_hdrs(dt$`Fasta headers`); dt$`Fasta headers` <- NULL
dt %<>% annotate_maxquant(uniprothdrs, contaminanthdrs, maxquanthdrs)
dt[, 1:9]
dt[reverse== '+', 1:9]
dt[contaminant== '+', 1:9]

# Billing 2019: uniprothdrs + contaminants + maxquanthdrs
#-----
profile <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
fosfile <- system.file('extdata/billing19.phosphosites.txt', package = 'autonomics')
upfile <- system.file('extdata/uniprot_hsa_20140515.fasta', package = 'autonomics')
prodt <- .read_maxquant_proteingroups(profile); prodt[, 1:2]
fosdt <- .read_maxquant_phosphosites(fosfile, profile); fosdt[, 1:3]
uniprothdrs <- read_uniprot dt(upfile)
contaminanthdrs <- read_contaminantdt()
maxquanthdrs <- parse_maxquant_hdrs(prodt$`Fasta headers`)
annotate_maxquant(prodt, uniprothdrs, contaminanthdrs, maxquanthdrs)[, 1:8]
annotate_maxquant(fosdt, uniprothdrs, contaminanthdrs, maxquanthdrs)[, 1:8]
```

---

annotate\_uniprot\_rest *Annotate uniprot/ensp*

---

### Description

Annotate uniprot/ensp

### Usage

```
annotate_uniprot_rest(x, columns = UNIPROTCOLS, verbose = TRUE)
```

### Arguments

x	character vector
columns	character vector
verbose	TRUE or FALSE

### Value

data.table(dbid, uniprot, reviewed, protein, gene, canonical, isoform, fragment, existence, organism, full)

### Examples

```
annotate_uniprot_rest( x = c('P00761', 'Q32MB2') )
annotate_uniprot_rest( x = c('ENSBTAP00000006074', 'ENSP00000377550') )
```

---

assert\_is\_valid\_sumexp

*Assert that x is a valid SummarizedExperiment*

---

### Description

Assert that x is a valid SummarizedExperiment

### Usage

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

### Arguments

x	SummarizedExperiment
.xname	see get_name_in_parent



**Value**

TRUE or FALSE

**Examples**

```
# VALID
  file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
  x <- read_metabolon(file)
  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 19.

**Examples**

AUTONOMICS\_DATASETS

---

bin                      *Bin continuous variable*

---

**Description**

Bin continuous variable

**Usage**

```
bin(object, ...)  
  
## S3 method for class 'logical'  
bin(object, ...)  
  
## S3 method for class 'character'  
bin(object, ...)  
  
## S3 method for class 'factor'  
bin(object, ...)  
  
## S3 method for class 'numeric'  
bin(object, probs = c(0, 0.33, 0.66, 1), ...)  
  
## S3 method for class 'SummarizedExperiment'  
bin(object, fvar, probs = c(0, 0.33, 0.66, 1), ...)
```

**Arguments**

object	numeric or SummarizedExperiment
...	(S3 dispatch)
probs	numeric
fvar	string or NULL

**Value**

factor vector

**Examples**

```
# Numeric vector  
object <- rnorm(10, 5, 1)  
bin(object)  
  
# SummarizedExperiment  
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')  
fdt(object <- read_maxquant_proteingroups(file))  
fdt(bin(object, 'pepcounts'))
```

---

biplot

*Biplot*

---

**Description**

Biplot

**Usage**

```

biplot(
  object,
  method = biplot_methods(object)[1],
  by = biplot_by(object, method)[1],
  dims = biplot_dims(object, method, by)[1:2],
  color = "subgroup",
  shape = NULL,
  size = NULL,
  alpha = NULL,
  group = NULL,
  linetype = NULL,
  label = NULL,
  feature_label = "feature_id",
  fixed = list(shape = 15, size = 3),
  nx = 0,
  ny = 0,
  colorpalette = make_svar_palette(object, color),
  alphapalette = make_alpha_palette(object, alpha),
  title = paste0(method, guess_fitsep(fdt(object)), by),
  theme = ggplot2::theme(plot.title = element_text(hjust = 0.5), panel.grid =
    element_blank())
)

```

**Arguments**

object	SummarizedExperiment
method	'pca', 'pls', 'lda', 'spls', 'opls', 'sma'
by	svar
dims	numeric vector: e.g. 1:2
color	svar
shape	svar
size	svar
alpha	svar
group	svar
linetype	svar
label	svar
feature_label	fvar
fixed	fixed plot aesthetics
nx	number of x features to plot
ny	number of y features to plot
colorpalette	character vector
alphapalette	character vector
title	string
theme	ggplot2::theme output

**Value**

ggplot object

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% pca(ndim = 4)
object %<>% pls(ndim = 4)
biplot(object)
biplot(object, nx = 1)
biplot(object, dims = 3:4, nx = 1)
biplot(object, method = 'pls')
biplot(object, method = 'pls', dims = 3:4)
biplot(object, method = 'pls', dims = 3:4, group = 'Subject')
```

---

biplot\_corrections      *Biplot batch corrections*

---

**Description**

Biplot batch corrections

**Usage**

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

**Arguments**

object	SummarizedExperiment
method	'pca', 'pls', 'lda', or 'sma'
by	svar
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 <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file, pca = TRUE, plot = FALSE)
biplot_corrections(object, color = 'subgroup', covariates = c('Sex', 'Diabetes', 'Subject', 'Time'))
```

---

biplot_covariates	<i>Biplot covariates</i>
-------------------	--------------------------

---

**Description**

Biplot covariates

**Usage**

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

**Arguments**

object	SummarizedExperiment
method	'pca', 'pls', 'lda', or 'sma'
by	svar
block	svar
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 <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file, pca = TRUE)
biplot_covariates(object, covariates = 'subgroup', ndim = 12, dimcols = 3)
biplot_covariates(object, covariates = c('Sex', 'Diabetes', 'Subject', 'Time'))
biplot_covariates(object, covariates = c('Sex', 'Diabetes', 'Subject', 'Time'), ndim = 2)
biplot_covariates(object, covariates = c('subgroup'), dimcols = 3)
```

---

block2lme

*Put block in lme-compatible format*

---

**Description**

Put block in lme-compatible format

**Usage**

```
block2lme(block, ...)

## S3 method for class 'list'
block2lme(block, verbose = TRUE, ...)

## S3 method for class 'formula'
block2lme(block, verbose = TRUE, ...)

## S3 method for class 'character'
block2lme(block, verbose = TRUE, ...)

formula2lmer(formula, block)

formula2lm(formula, block)

block_vars(formula)
```

**Arguments**

block	block: character vector or formula
...	required for s3 dispatch
verbose	TRUE or FALSE
formula	formula

**Examples**

```
# lme: ensure lme-compatible block specification
block2lme( block = list(subject = ~1, batch = ~1))
block2lme( block = ~1|subject)
block2lme( block = c('subject', 'batch'))

# lm: integrate block into formula as random effect
formula2lm( formula = ~ subgroup, block = c('subject', 'batch') )

# lmer: integrate block into formula as fixed effect
formula2lmer( formula = ~ subgroup, block = c('subject', 'batch') )
formula2lmer( formula = ~ subgroup + (1|subject) + (1|batch) )
```

---

center	<i>Center samples</i>
--------	-----------------------

---

**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(matrixStats)
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
fdt(object)$housekeeping <- FALSE
fdt(object)$housekeeping[order(rowVars(values(object)))[1:5]] <- TRUE
```

```

values(object)[, object$subgroup=='Adult'] %<>% magrittr::add(5)
plot_sample_densities(object)
plot_sample_densities(center(object))
plot_sample_densities(center(object, housekeeping))

```

---

code

*Contrast Code Factor*


---

## Description

Contrast Code Factor for General Linear Model

## Usage

```

code(object, ...)

## S3 method for class 'factor'
code(object, codingfun, verbose = TRUE, ...)

## S3 method for class 'data.table'
code(object, codingfun, vars = names(object), verbose = TRUE, ...)

contr.treatment.explicit(n)

code_control(n)

contr.diff(n)

code_diff(n)

code_diff_forward(n)

code_deviation(n)

code_deviation_first(n)

code_helmert(n)

code_helmert_forward(n)

```

## Arguments

object	factor vector
...	used for s3 dispatch
codingfun	factor coding function

- `contr.treatment`: intercept =  $y_0$ , coefi =  $y_i - y_0$
- `contr.treatment.explicit`: intercept =  $y_0$ , coefi =  $y_i - y_0$



	<ul style="list-style-type: none"> <li>• <code>code_control</code>: intercept = ymean, coefi = yi - y0</li> <li>• <code>contr.diff</code>: intercept = y0, coefi = yi - y(i-1)</li> <li>• <code>code_diff</code>: intercept = ymean, coefi = yi - y(i-1)</li> <li>• <code>code_diff_forward</code>: intercept = ymean, coefi = yi - y(i+)</li> <li>• <code>code_deviation</code>: intercept = ymean, coefi = yi - ymean (drop last)</li> <li>• <code>code_deviation_first</code>: intercept = ymean, coefi = yi - ymean (drop first)</li> <li>• <code>code_helmert</code>: intercept = ymean, coefi = yi - mean(y0:(yi-1))</li> <li>• <code>code_helmert_forward</code>: intercept = ymean, coefi = yi - mean(y(i+1):yp)</li> </ul>
<code>verbose</code>	TRUE or FALSE
<code>vars</code>	svars
<code>n</code>	character vector

## Details

A General Linear Model contains:

- \* An Intercept Coefficient: expressing some form of sample average
- \* For each numeric variable: a slope coefficient
- \* For each k-leveled factor: (k-1) Contrast Coefficients.

The interpretation of (intercept and contrast) coefficients depends on the contrast coding function used. Several contrast coding functions are available in 'stats' and 'codingMatrices' But their (function and coefficient) namings are a bit confusing and unsystematic. Instead, the functions below offer an intuitive interface (to the otherwise powerful stats/codingMatrices packages). The names of these functions reflect the contrast coding used (treatment, backward, sum, or helmert contrasts). They also reflect the intercept interpretation (either first factor's first level or grand mean). They all produce intuitive coefficient names (e.g. 't1-t0' rather than just 't1'). They all have unit scaling (a coefficient of 1 means a backward of 1).

## Value

(explicitly coded) factor vector

## Examples

```
# Coding functions
x <- factor(paste0('t', 0:3))
xlevels <- levels(x)
contr.treatment(      xlevels)
contr.treatment.explicit(xlevels)
contr.diff(           xlevels)
code_control(         xlevels)
code_diff(            xlevels)
code_diff_forward(    xlevels)
code_deviation(       xlevels)
code_deviation_first( xlevels)
code_helmert(         xlevels)
code_helmert_forward( xlevels)

# Code
```

```

x %<>% code(contr.treatment)
x %<>% code(contr.treatment.explicit)
x %<>% code(contr.diff)
x %<>% code(code_control)
x %<>% code(code_diff)
x %<>% code(code_diff_forward)
x %<>% code(code_deviation)
x %<>% code(code_deviation_first)
x %<>% code(code_helmert)
x %<>% code(code_helmert_forward)

# Model
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% fit_limma(codingfun = contr.treatment) # default
object %<>% fit_limma(codingfun = contr.treatment.explicit)
object %<>% fit_limma(codingfun = contr.diff)
object %<>% fit_limma(codingfun = code_control)
object %<>% fit_limma(codingfun = code_diff)
object %<>% fit_limma(codingfun = code_diff_forward)
object %<>% fit_limma(codingfun = code_deviation)
object %<>% fit_limma(codingfun = code_deviation_first)
object %<>% fit_limma(codingfun = code_helmert)
object %<>% fit_limma(codingfun = code_helmert_forward)

```

---

coefs

*Get coefs*


---

## Description

Get coefs

## Usage

```
coefs(featuredt, ...)
```

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

```
coefs(featuredt, ...)
```

```
## S3 method for class 'data.table'
```

```
coefs(featuredt, fit = fits(featuredt), svars = NULL, ...)
```

## Arguments

featuredt	data.table or factor
...	required for s3 dispatch
fit	string: 'limma', 'lm', 'lme', 'lmer'
svars	NULL or charactervector (svar for which to return coefs)

**Value**

character vector

**Examples**

```
# Factor
x <- factor(c('A', 'B', 'C'))
coefs(x)
coefs(code(x, contr.treatment.explicit))
coefs(code(x, code_control))

# SummarizedExperiment
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file, fit = 'limma')
coefs(fdt(object))
```

---

collapsed\_entrezg\_to\_symbol  
*Collapsed entrezg to genesymbol*

---

**Description**

Collapsed entrezg to genesymbol

**Usage**

```
collapsed_entrezg_to_symbol(x, sep, orgdb)
```

**Arguments**

x	charactervector
sep	string
orgdb	OrgDb

**Value**

character vector

**Examples**

```
if (requireNamespace('org.Hs.eg.db', quiet = TRUE)){
  x <- c('7448/3818/727', '5034/9601/64374')
  orgdb <- org.Hs.eg.db::org.Hs.eg.db
  collapsed_entrezg_to_symbol(x, sep = '/', orgdb = orgdb)
}
```

---

CONTAMINANTSURL	<i>Contaminants URL</i>
-----------------	-------------------------

---

**Description**

Contaminants URL

**Usage**

CONTAMINANTSURL

**Format**

An object of class character of length 1.

**Examples**

CONTAMINANTSURL

---

contrast_subgroup_cols	<i>Row/Col contrasts</i>
------------------------	--------------------------

---

**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 <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object$subgroup <- paste0(object$Diabetes, '.', object$Time)
subgroup_matrix(object, subgroupvar = 'subgroup')
contrast_subgroup_cols(object, subgroupvar = 'subgroup')
contrast_subgroup_rows(object, subgroupvar = 'subgroup')
```

---

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 <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
object <- read_rnaseq_counts(file)
counts(object)[1:3, 1:3]
counts(object) <- values(object)
```

---

counts2cpm	<i>Convert between counts and cpm/tpm</i>
------------	---

---

**Description**

Convert between counts and cpm/tpm

**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 <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
object <- read_rnaseq_counts(file)
libsize <- scaledlibsizes(counts(object))
tpm <- counts2tpm(counts(object), genesize = 1)
cpm <- counts2cpm(counts(object), libsize)
counts <- cpm2counts(cpm, libsize)
sum(counts(object) - counts)
```

---

counts2tpm	<i>counts to tpm</i>
------------	----------------------

---

**Description**

counts to tpm

**Usage**

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

**Arguments**

x	count matrix
genesize	genesize vector (kilobase)

**Value**

tpm matrix

**Examples**

```
file <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
object <- read_rnaseq_counts(file)
counts(object)[1:3, 1:3]
counts2tpm(counts(object), genesize = 1)[1:3, 1:3]
```

---

count_in	<i>Count/Collapse in/outside intersection</i>
----------	---

---

**Description**

Count/Collapse in/outside intersection

**Usage**

```
count_in(x, ...)

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

## S3 method for class 'factor'
count_in(x, y, ...)

## S3 method for class 'list'
count_in(x, y, ...)

collapse_in(x, ...)

## S3 method for class 'character'
collapse_in(x, y, sep, ...)

## S3 method for class 'factor'
collapse_in(x, y, sep, ...)

## S3 method for class 'list'
collapse_in(x, y, sep, ...)

count_out(x, ...)

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

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

```
count_out(x, y, ...)

## S3 method for class 'list'
count_out(x, y, ...)
```

### Arguments

x	character OR list
...	used for S3 dispatch
y	character
sep	string

### Value

number OR numeric

### Examples

```
# Sets
contrast1 <- c('a', 'b', 'c', 'd')
pathway <- c('c', 'd', 'e', 'f')
contrast2 <- c('e', 'f', 'g', 'h')

# Count outside
count_out(contrast1, pathway)
count_out(list(contrast1 = contrast1, contrast2 = contrast2), pathway)

# Count inside
count_in(contrast1, pathway)
count_in(list(contrast1 = contrast1, contrast2 = contrast2), pathway)

# Collapse inside
collapse_in(contrast1, pathway, sep = ' ')
collapse_in(list(contrast1 = contrast1, contrast2 = contrast2), pathway, sep = ' ')
```

---

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 <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
object <- read_rnaseq_counts(file)
cpm(object)[1:3, 1:3]
cpm(object) <- values(object)

```

---

create_design	<i>Create design</i>
---------------	----------------------

---

### Description

Create design matrix for statistical analysis

### Usage

```

create_design(object, ...)

## S3 method for class 'SummarizedExperiment'
create_design(
  object,
  formula = default_formula(object),
  drop = varlevels_dont_clash(object, all.vars(formula)),
  codingfun = contr.treatment,
  verbose = TRUE,
  ...
)

## S3 method for class 'data.table'
create_design(

```

```

object,
formula = default_formula(object),
drop = varlevels_dont_clash(object, all.vars(formula)),
codingfun = contr.treatment,
verbose = TRUE,
...
)

```

## Arguments

object	SummarizedExperiment or data.frame
...	required to s3ify
formula	formula with svars
drop	whether to drop predictor names
codingfun	factor coding function <ul style="list-style-type: none"> <li>• <code>contr.treatment</code>: intercept = <math>y_0</math>, coefi = <math>y_i - y_0</math></li> <li>• <code>contr.treatment.explicit</code>: intercept = <math>y_0</math>, coefi = <math>y_i - y_0</math></li> <li>• <code>code_control</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - y_0</math></li> <li>• <code>contr.diff</code>: intercept = <math>y_0</math>, coefi = <math>y_i - y_{(i-1)}</math></li> <li>• <code>code_diff</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - y_{(i-1)}</math></li> <li>• <code>code_diff_forward</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - y_{(i+)}</math></li> <li>• <code>code_deviation</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - y_{\text{mean}}</math> (drop last)</li> <li>• <code>code_deviation_first</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - y_{\text{mean}}</math> (drop first)</li> <li>• <code>code_helmert</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - \text{mean}(y_0:(y_i-1))</math></li> <li>• <code>code_helmert_forward</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - \text{mean}(y_{(i+1):y_p})</math></li> </ul>
verbose	whether to message

## Value

design matrix

## Examples

```

file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
unique(create_design(object))
unique(create_design(object, ~ Time))
unique(create_design(object, ~ Time, codingfun = contr.treatment.explicit))
unique(create_design(object, ~ Time, codingfun = contr.diff))
unique(create_design(object, ~ Time + Diabetes))
unique(create_design(object, ~ Time / Diabetes))
unique(create_design(object, ~ Time * Diabetes))

```

---

DATADIR *Download autonomics example data*

---

**Description**

Download autonomics example data

**Usage**

DATADIR

```
download_data(
  filename = NULL,
  localdir = file.path(DATADIR, split_extract_fixed(filename, ".", 1)),
  verbose = TRUE,
  force = FALSE
)
```

**Arguments**

filename	file name		
	'atkin.somascan.adat'	Halama, 2018	effects of hypoglycemia
	'atkin.metabolon.xlsx'		
	'billing16.bam.zip'	Billing, 2016	stemcell comparison
	'billing16.rnacounts.txt'		
	'billing16.somascan.adat'		
	'billing16.proteingroups.txt'		
	'billing19.rnacounts.txt'	Billing, 2016	stemcell differentiation
	'billing19.proteingroups.txt'		
	'billing19.phosphosites.txt'		
	'ddglucose.proteingroups.txt'	Omics Module	glycolysis inhibitor
	'fukuda20.proteingroups.txt'	Fukuda, 2020	zebrafish development
	'halama18.metabolon.xlsx'	Halama, 2018	glutaminase inhibitor
localdir	local dir to save file to		
verbose	TRUE / FALSE		
force	TRUE / FALSE		

**Format**

An object of class character of length 1.

**Value**

local file path

**Examples**

```

# Show available datasets
  download_data()

# atkin 2018 - hypoglycemia - pubmed 30525282
  # download_data('atkin.somascan.adat')      # somascan intensities
  # download_data('atkin.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

```

---

 default\_geom

*Default geom*


---

**Description**

Default geom

**Usage**

```
default_geom(object, x, block = NULL)
```

**Arguments**

object	SummarizedExperiment
x	svar
block	svar or NULL

**Value**

character vector

**Examples**

```

file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object$Age <- runif(min = 20, max = 60, n = ncol(object))
svars(object)
default_geom(object, x = 'Age')
default_geom(object, x = c('Age', 'Diabetes'))
default_geom(object, x = c('Age', 'Diabetes'), block = 'Subject')

```

---

default_sfile	<i>Default sfile</i>
---------------	----------------------

---

**Description**

Default sfile

**Usage**

```
default_sfile(file)
```

**Arguments**

file	data file
------	-----------

**Value**

sample file

**Examples**

```

file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
default_sfile(file)

```

---

default_subgroupvar	<i>Create default formula</i>
---------------------	-------------------------------

---

**Description**

Create default formula

**Usage**

```
default_subgroupvar(object)
```

```
default_formula(object)
```

**Arguments**

object            SummarizedExperiment

**Value**

formula

**Examples**

```
# Abundances
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
default_formula(object)
file <- download_data('billing16.proteingroups.txt')
object <- read_maxquant_proteingroups(file)
default_formula(object)
```

---

demultiplex

*Demultiplex snames*

---

**Description**

Demultiplex maxquant samplenames

**Usage**

```
demultiplex(x, verbose = FALSE)
```

**Arguments**

x                    character vector  
 verbose            TRUE or FALSE

**Details**

WT(L).KD(H).R1{H/L} -> KD\_WT.R1 WT(1).KD(2).R1{1} -> WT.R1 WT.R1 -> WT.R1

**Value**

character

**Examples**

```

# uniplexed / intensity / ratio
  demultiplex(c('KD.R1','OE.R1'))
  demultiplex(c('WT(L).KD(M).OE(H).R1{M}', 'WT(L).KD(M).OE(H).R1{H}'))
  demultiplex(c('WT(L).KD(M).OE(H).R1{M/L}', 'WT(L).KD(M).OE(H).R1{H/L}'))
# run / replicate
  demultiplex(c('WT(L).OE(H).R1{L}', 'WT(L).OE(H).R1{H}')) # run
  demultiplex(c('WT.R1(L).OE.R1(H){L}', 'WT.R1(L).OE.R1(H){H}')) # repl
# label / index
  demultiplex(c('WT(L).OE(H).R1{L}', 'WT(L).OE(H).R1{H}')) # label
  demultiplex(c('WT(1).OE(2).R1{1}', 'WT(1).OE(2).R1{2}')) # index
# with unused channels
  demultiplex('WT(1).KD(2).OE(3).R1{6}')

```

dequantify

*Dequantify maxquant names***Description**

Drop quantity ('Reporter intensity').  
 Encode channel as suffix.

**Usage**

```
dequantify(x, quantity = guess_maxquant_quantity(x), verbose = FALSE)
```

**Arguments**

x	character
quantity	'ratio', 'normalizedratio', 'LFQ intensity', 'intensity', 'labeledintensity' 'reporterintensity', 'correctedreporterintensity'
verbose	TRUE or FALSE

**Details**

Ratio H/L WT(L).KD(H).R1 -> WT(L).KD(H).R1{H/L}  
 Reporter intensity 0 WT(126).KD(127).R1 -> WT(1).KD(2).R1{1}

LFQ intensity WT.R1 -> WT.R1

**Value**

character

**Examples**

```

dequantify(c('Ratio H/L WT(L).KD(M).OE(H).R1',          # Ratios
             'Ratio M/L WT(L).KD(M).OE(H).R1'))
dequantify(c('Ratio H/L normalized WT(L).KD(M).OE(H).R1', # Norm. Ratios
             'Ratio M/L normalized WT(L).KD(M).OE(H).R1'))
dequantify(c('LFQ intensity WT.R1',                    # LFQ intensity
             'LFQ intensity KD.R1'))
dequantify(c('Reporter intensity 1 WT(126).KD(127).R1',  # Rep.intensities
             'Reporter intensity 2 WT(126).KD(127).R1'))

```

---

download\_contaminants *Downloads contaminants*

---

**Description**

Downloads contaminants

**Usage**

```
download_contaminants(url = CONTAMINANTSURL, overwrite = FALSE)
```

**Arguments**

url                    contaminants file url (string)  
 overwrite            TRUE or FALSE: overwrite existung download?

**Value**

filename (string)

**Examples**

```

download_contaminants()                    # download first time
download_contaminants(overwrite = TRUE)  # download each time

```

---

download\_gtf                    *Download GTF file*

---

**Description**

Download GTF file with feature annotations



**Usage**

```
download_gtf(
  organism,
  release = 100,
  gtffile = sprintf("%s/gtf/%s", R_user_dir("autonomics", "cache"),
    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)
```

---

download_mcclain21	<i>Download mcclain21 data</i>
--------------------	--------------------------------

---

**Description**

Download mcclain21 data

**Usage**

```
download_mcclain21(
  counts_or_samples = "counts",
  localdir = file.path(DATADIR, "mcclain21"),
  force = FALSE
)
```

**Arguments**

counts_or_samples	'counts' or 'samples'
localdir	dirname
force	TRUE or FALSE

**Details**

[Mc clain 2021: COVID19 transcriptomics](#):

**Examples**

```
download_mcclain21('counts')
download_mcclain21('samples')
```

---

```
download_tcga_example Download tcga example
```

---

**Description**

Download tcga example

**Usage**

```
download_tcga_example()
```

---

```
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')
```

---

enrichment	<i>Enrichment analysis</i>
------------	----------------------------

---

### Description

Are selected genes enriched in pathway?

### Usage

```
enrichment(
  object,
  pathwaydt,
  fit = fits(fdt(object))[1],
  coef = coefs(fdt(object), fit = fit)[1],
  var = abstractvar(fdt(object), fit = fit, coef = coef),
  levels = fdt(object)[[var]] %>% base::levels() %>% extract(-1),
  genevar = "gene",
  genesep = "[ ,;]",
  n = 3,
  verbose = TRUE,
  genes = FALSE
)
```

### Arguments

object	SummarizedExperiment
pathwaydt	pathway data.table
fit	string
coef	string
var	selection fvar
levels	selection levels
genevar	gene fvar
genesep	gene separator (string)
n	number
verbose	whether to msg
genes	whether to report genes

### Details

Four enrichment analyses per geneset using the Fisher Exact Test (see four pvalues). Results are returned in a data.table

	in	: genes in pathway
	in.det	: detected genes in pathway

```

    in.sel : up/downregulated genes in pathway
  in.up(.genes) : upregulated genes in pathway
in.down(.genes) : downregulated genes in pathway
    out : genes outside pathway
    det : detected genes (in + out)
    sel : up/downregulated genes (in + out)
    up : upregulated genes (in + out)
    down : downregulated genes (in + out)
  p.coef.upDET : prob to randomly select this many (or more) upregulated genes (among detected genes)
  p.coef.downDET : prob to randomly select this many (or more) downregulated genes (among detected genes)
  p.coef.selDET : prob to randomly select this many (or more) up OR downregulated genes (among detected genes)
  p.coef.selGEN : prob to randomly select this many (or more) up OR downregulated genes (among genome genes)
  p.detGEN : prob to randomly select this many (or more) detected genes (among genome genes)

```

### Examples

```

# Read
pathwaydt <- read_msigt(collections = 'C5:GO:BP')
file <- system.file('extdata/atkin.somascan.adat', package = 'autonomics')
object <- read_somascan(file, fit = 'limma', coefs = 't1')
fvars(object) %<>% gsub('EntrezGeneSymbol', 'gene', .)
object %<>% abstract_fit()
var <- abstractvar(fdt(object))
enrichdt1 <- enrichment(object, pathwaydt, var = var) # 2:n factor
enrichdt2 <- enrichment(object, pathwaydt, var = var, levels = c('flat', 'down', 'up')) # 1:n factor
enrichdt3 <- altenrich(object, pathwaydt) # alternative implementation
cols <- intersect(names(enrichdt1), names(enrichdt3))
all(enrichdt1[, cols, with = FALSE] == enrichdt3[, cols, with = FALSE]) # identical

```

---

ens2org

*taxon/ens to organism*

---

### Description

taxon/ens to organism

### Usage

```
ens2org(x)
```

```
taxon2org(x)
```

### Arguments

x character vector

### Value

character vector

**Examples**

```
taxon2org( x = c('9606', '9913') )  
ens2org( x = c('ENSP00000377550', 'ENSBTAP00000038329') )
```

---

entrezg\_to\_symbol      *Entrezg to genesymbol*

---

**Description**

Entrezg to genesymbol

**Usage**

```
entrezg_to_symbol(x, orgdb)
```

**Arguments**

x	charactervector
orgdb	OrgDb

**Value**

character vector

**Examples**

```
if (requireNamespace('org.Hs.eg.db', quiet = TRUE)){  
  orgdb <- org.Hs.eg.db::org.Hs.eg.db  
  entrezg_to_symbol(x = c('7448', '3818', '727'), orgdb)  
}
```

---

explore\_transformations  
*Explore transformations*

---

**Description**

Explore transformations

**Usage**

```

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

```

**Arguments**

object	SummarizedExperiment
subgroupvar	string
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 <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
subgroups <- sprintf('%s_STD', c('E00', 'E01', 'E02', 'E05', 'E15', 'E30', 'M00'))
object <- read_maxquant_proteingroups(file, subgroups = subgroups)
explore_transformations(object, transformations = c('quantnorm', 'zscore', 'invnorm'))

```

---

extract_rectangle	<i>Extract rectangle from omics file, data.table, or matrix</i>
-------------------	---

---

**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
#=====
x <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
extract_rectangle(x, rows = 11:30, cols = 15:81, sheet = 2)[ 1:3, 1:3 ] # exprs
extract_rectangle(x, rows = 11:30, cols = 2, sheet = 2)[ 1:3, ] # fids
extract_rectangle(x, rows = 4, cols = 15:81, sheet = 2)[ , 1:3 ] # sids
extract_rectangle(x, rows = 10:30, cols = 1:14, sheet = 2)[ 1:3, 1:3 ] # fdt
extract_rectangle(x, rows = 1:10, cols = 14:81, sheet = 2, transpose = TRUE)[1:3, 1:3] # sdt

# FROM MATRIX: extract_rectangle.matrix
#=====
x <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics') %>% extract_rectangle(sheet = 2)
extract_rectangle(x, rows = 11:30, cols = 15:81, sheet = 2)[ 1:3, 1:3 ] # exprs
extract_rectangle(x, rows = 11:30, cols = 2, sheet = 2)[ 1:3, ] # fids
extract_rectangle(x, rows = 4, cols = 15:81, sheet = 2)[ , 1:3 ] # sids
extract_rectangle(x, rows = 10:30, cols = 1:14, sheet = 2)[ 1:3, 1:3 ] # fdt
extract_rectangle(x, rows = 1:10, cols = 14:81, sheet = 2, transpose = TRUE)[1:3, 1:3] # sdt
```

fdata

*Get/Set sample/feature data***Description**

Get/Set sample/feature data

**Usage**

fdata(object)

sdata(object)

fdt(object)

sdt(object)

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

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

```
## S4 method for signature 'SummarizedExperiment'
fdt(object)
```



```

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

fdata(object) <- value

sdata(object) <- value

fdt(object) <- value

sdt(object) <- value

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

## S4 replacement method for signature 'SummarizedExperiment,data.table'
sdt(object) <- value

```

### Arguments

object	SummarizedExperiment
value	data.frame/data.table

### Value

data.frame/data.table (get) or updated object (set)

### Examples

```

# Read data
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
# sdt/fdt
sdt(object)[1:3, ]
fdt(object)[1:3, ]
sdt(object) %<>% cbind(b=1)
fdt(object) %<>% cbind(b=1)
sdt(object)
fdt(object)
# sdata/fdata
sdata(object)[1:3, ]

```

```
fdata(object)[1:3, ]
sdata(object) %<>% cbind(a=1)
fdata(object) %<>% cbind(a=1)
sdata(object)[1:3, ]
fdata(object)[1:3, ]
```

---

fdr2p

*fdr to p*


---

### Description

fdr to p

### Usage

```
fdr2p(fdr)
```

### Arguments

fdr                      fdr values

### Examples

```
# Read/Fit
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% fit_limma()
pcol <- pvar(fdt(object), fit = 'limma', coef = 't3')
object %<>% extract(order(fdt(.)[[pcol]]), )
object %<>% extract(1:10, )
fdt(object) %<>% extract(, 1)
object %<>% fit_limma(coefs = 't3')
# fdr2p
fdt(object)[[pcol]]
fdt(object)[[pcol]] %>% p.adjust(method = 'fdr')
fdt(object)[[pcol]] %>% p.adjust(method = 'fdr') %>% fdr2p()
```

---

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",
  assay = assayNames(object)[1],
  comparator = if (contains_ratios(object)) "!=" else ">",
  lod = 0,
  nsample = 2,
  nsubgroup = 1,
  verbose = TRUE
)
```

**Arguments**

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

**Value**

Filtered SummarizedExperiment

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% filter_exprs_replicated_in_some_subgroup()
filter_exprs_replicated_in_some_subgroup(object, character(0))
filter_exprs_replicated_in_some_subgroup(object, NULL)
```

---

filter_features	<i>Filter features on condition</i>
-----------------	-------------------------------------

---

**Description**

Filter features on condition

**Usage**

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

**Arguments**

object	SummarizedExperiment
condition	filter condition
verbose	logical

**Value**

filtered eSet

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
filter_features(object, SUPER_PATHWAY == 'Lipid')
```

---

filter_medoid	<i>Filter medoid sample</i>
---------------	-----------------------------

---

**Description**

Filter medoid sample

**Usage**

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

**Arguments**

object	SummarizedExperiment
by	svar
verbose	whether to message

**Value**

SummarizedExperiment

**Examples**

```
file <- system.file('extdata/billing19.rnaseq.txt', package = 'autonomics')
object <- read_rnaseq_counts(file, plot = FALSE)
object %<>% filter_medoid(by = 'subgroup', verbose=TRUE)
```

---

filter_samples	<i>Filter samples on condition</i>
----------------	------------------------------------

---

**Description**

Filter samples on condition

**Usage**

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

**Arguments**

object	SummarizedExperiment
condition	filter condition
verbose	TRUE/FALSE
record	TRUE/FALSE

**Value**

filtered SummarizedExperiment

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
filter_samples(object, subgroup != 't0', verbose = TRUE)
```

---

fit	<i>Fit model and test for differential expression</i>
-----	---

---

**Description**

Fit model and test for differential expression

**Usage**

```
fit(
  object,
  formula = default_formula(object),
  engine = "limma",
  drop = varlevels_dont_clash(object, all.vars(formula)),
  codingfun = contr.treatment,
  design = create_design(object, formula = formula, drop = drop, codingfun = codingfun),
  contrasts = NULL,
```

```

  coefs = if (is.null(contrasts)) colnames(design) else NULL,
  block = NULL,
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  statvars = c("effect", "p", "se", "t")[1:2],
  sep = FITSEP,
  suffix = paste0(sep, "limma"),
  verbose = TRUE,
  plot = FALSE
)

fit_limma(
  object,
  formula = default_formula(object),
  drop = varlevels_dont_clash(object, all.vars(formula)),
  codingfun = contr.treatment,
  design = create_design(object, formula = formula, drop = drop, codingfun = codingfun),
  contrasts = NULL,
  coefs = if (is.null(contrasts)) colnames(design) else NULL,
  block = NULL,
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  statvars = c("effect", "p"),
  sep = FITSEP,
  suffix = paste0(sep, "limma"),
  verbose = TRUE,
  plot = FALSE
)

.fit_limma(
  object,
  formula = default_formula(object),
  drop = varlevels_dont_clash(object, all.vars(formula)),
  codingfun = "treatment",
  design = create_design(object, formula = formula, drop = drop, codingfun = codingfun),
  contrasts = NULL,
  coefs = if (is.null(contrasts)) colnames(design) else NULL,
  block = NULL,
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  statvars = c("effect", "p", "se", "t")[1:2],
  sep = FITSEP,
  suffix = paste0(sep, "limma"),
  verbose = TRUE,
  plot = FALSE
)

fit_wilcoxon(
  object,
  formula = default_formula(object),
  drop = NULL,

```

```

codingfun = contr.treatment.explicit,
contrasts = NULL,
coefs = NULL,
block = NULL,
weightvar = NULL,
statvars = c("effect", "p"),
sep = FITSEP,
verbose = TRUE,
plot = FALSE
)

```

### Arguments

object	SummarizedExperiment
formula	modeling formula
engine	'limma', 'lm', 'lme', 'lmer', or 'wilcoxon'
drop	TRUE or FALSE
codingfun	factor coding function <ul style="list-style-type: none"> <li>• <code>contr.treatment</code>: intercept = <math>y_0</math>, coefi = <math>y_i - y_0</math></li> <li>• <code>contr.treatment.explicit</code>: intercept = <math>y_0</math>, coefi = <math>y_i - y_0</math></li> <li>• <code>code_control</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - y_0</math></li> <li>• <code>contr.diff</code>: intercept = <math>y_0</math>, coefi = <math>y_i - y_{(i-1)}</math></li> <li>• <code>code_diff</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - y_{(i-1)}</math></li> <li>• <code>code_diff_forward</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - y_{(i+)}</math></li> <li>• <code>code_deviation</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - y_{\text{mean}}</math> (drop last)</li> <li>• <code>code_deviation_first</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - y_{\text{mean}}</math> (drop first)</li> <li>• <code>code_helmert</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - \text{mean}(y_0:(y_i-1))</math></li> <li>• <code>code_helmert_forward</code>: intercept = <math>y_{\text{mean}}</math>, coefi = <math>y_i - \text{mean}(y_{(i+1):y_p})</math></li> </ul>
design	design matrix
contrasts	NULL or character vector: coefficient contrasts to test
coefs	NULL or character vector: model coefs to test
block	block svar (or NULL)
weightvar	NULL or name of weight matrix in <code>assays(object)</code>
statvars	character vector: subset of <code>c('effect', 'p', 'fdr', 't', 'se')</code>
sep	string: pvar separator (" <code>~</code> " in " <code>p~t2~limma</code> ")
suffix	string: pvar suffix (" <code>limma</code> " in " <code>p~t2~limma</code> ")
verbose	whether to msg
plot	whether to plot

### Value

Updated SummarizedExperiment

**Examples**

```

# Read
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)

# Standard
fdt(object) %<>% extract(, 'feature_id')
object %<>% fit_lm(      ~ subgroup)           #      statistics default
object %<>% fit_limma(  ~ subgroup)          #      bioinformatics default
summarize_fit(fdt(object))

# Blocked
fdt(object) %<>% extract(, 'feature_id')
object %<>% fit_limma(  ~ subgroup, block = 'Subject') #      simple random effects
object %<>% fit_lme(    ~ subgroup, block = 'Subject') #      powerful random effects
object %<>% fit_lmer(   ~ subgroup, block = 'Subject') #      more powerful random effects
summarize_fit(fdt(object))

# Alternative coding: e.g. grand mean intercept
fdt(object) %<>% extract(, 'feature_id')
object %<>% fit_limma(  ~ subgroup, block = 'Subject', codingfun = code_control)
object %<>% fit_lme(    ~ subgroup, block = 'Subject', codingfun = code_control)
object %<>% fit_lmer(   ~ subgroup, block = 'Subject', codingfun = code_control)
summarize_fit(fdt(object))

# Posthoc contrasts (only limma!)
fdt(object) %<>% extract(, 'feature_id')
object %<>% fit_limma(  ~ subgroup, block = 'Subject', codingfun = code_control, coefs = 't1-t0')
object %<>% fit_limma(  ~ 0 + subgroup, block = 'Subject', contrasts = 't1-t0')
# flexible, but only approximate
# stat.ethz.ch/pipermail/bioconductor/2014-February/057682.html

# Non-parametric: wilcoxon
fdt(object) %<>% extract(, 'feature_id')
object %<>% fit_wilcoxon( ~ subgroup)           # unpaired
object %<>% fit_wilcoxon( ~ subgroup, block = 'Subject') # paired

# Custom separator
fdt(object) %<>% extract(, 'feature_id')
fdt( fit_lm(      object, sep = '.'))
fdt( fit_limma(  object, block = 'Subject', sep = '.'))
fdt( fit_lme(    object, block = 'Subject', sep = '.'))
fdt( fit_lmer(   object, block = 'Subject', sep = '.'))
fdt( fit_wilcoxon(object, block = 'Subject', sep = '.'))
fdt( fit_wilcoxon(object, sep = '.'))

```



**Description**

fitcoefs

**Usage**

```
fitcoefs(object)
```

**Arguments**

object            SummarizedExperiment

**Value**

string vector

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
fitcoefs(object)
fitcoefs(fit_limma(object))
```

---

fits

*Get fit models*

---

**Description**

Get fit models

**Usage**

```
fits(featuredt)
```

**Arguments**

featuredt        feature data.table

**Value**

character vector

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file, fit = 'limma')
fits(fdt(object))
```

---

FITSEP	<i>Fit results separator</i>
--------	------------------------------

---

**Description**

Fit results separator

**Usage**

FITSEP

PPATTERN

**Format**

An object of class character of length 1.

An object of class character of length 1.

**Examples**

FITSEP

---

fitvars	<i>Get fit vars/dt</i>
---------	------------------------

---

**Description**

Get fit vars/dt

**Usage**

fitvars(object)

fitdt(object)

**Arguments**

object            SummarizedExperiment

**Value**

string vector

**Examples**

```

file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
fitvars(object)
fitdt(object)
fitvars(fit_limma(object))
fitdt(fit_limma(object))

```

fit\_lmx

*Fit lm, lme, or lmer***Description**

Fit lm, lme, or lmer

**Usage**

```

fit_lmx(
  object,
  fit,
  formula = default_formula(object),
  drop = varlevels_dont_clash(object, all.vars(formula)),
  codingfun = contr.treatment,
  coefs = colnames(create_design(object, formula = formula, drop = drop, codingfun =
    codingfun, verbose = FALSE)),
  block = NULL,
  opt = "optim",
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  statvars = c("effect", "p", "se", "t")[1:2],
  sep = FITSEP,
  verbose = TRUE,
  plot = FALSE
)

```

```

fit_lm(
  object,
  formula = default_formula(object),
  drop = varlevels_dont_clash(object, all.vars(formula)),
  codingfun = contr.treatment,
  block = NULL,
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  statvars = c("effect", "p", "se", "t")[1:2],
  sep = FITSEP,
  coefs = colnames(create_design(object, formula = formula, drop = drop, codingfun =
    codingfun, verbose = FALSE)),
  contrasts = NULL,
  verbose = TRUE,

```

```

    plot = FALSE
  )

fit_lme(
  object,
  formula = default_formula(object),
  drop = varlevels_dont_clash(object, all.vars(formula)),
  codingfun = contr.treatment,
  block = NULL,
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  opt = "optim",
  statvars = c("effect", "p", "se", "t")[1:2],
  sep = FITSEP,
  coefs = colnames(create_design(object, formula = formula, drop = drop, codingfun =
    codingfun, verbose = FALSE)),
  contrasts = NULL,
  verbose = TRUE,
  plot = FALSE
)

fit_lmer(
  object,
  formula = default_formula(object),
  drop = varlevels_dont_clash(object, all.vars(formula)),
  codingfun = contr.treatment,
  block = NULL,
  weightvar = if ("weights" %in% assayNames(object)) "weights" else NULL,
  statvars = c("effect", "p", "se", "t")[1:2],
  sep = FITSEP,
  coefs = colnames(create_design(object, formula = formula, drop = drop, codingfun =
    codingfun, verbose = FALSE)),
  contrasts = NULL,
  verbose = TRUE,
  plot = FALSE
)

```

### Arguments

object	SummarizedExperiment
fit	'lm', 'lme', or 'lmer'
formula	formula
drop	TRUE or FALSE
codingfun	coding function
coefs	NULL or stringvector
block	NULL or svar
opt	optimizer used in fit_lme: 'optim' (more robust) or 'nlminb'

weightvar	NULL or svar
statvars	character vector: subset of c('effect', 'p', 'fdr', 't')
sep	string
verbose	TRUE or FALSE
plot	TRUE or FALSE
contrasts	unused. only to allow generic get(fitfun)(contrasts)

**Value**

SummarizedExperiment

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
fit_lm(  object, formula = ~subgroup)
fit_limma( object, formula = ~subgroup)
fit_limma( object, formula = ~subgroup, block = 'Subject' )
fit_lme(  object, formula = ~subgroup, block = 'Subject' )
fit_lmer( object, formula = ~subgroup, block = 'Subject' )
# fit_lme( object, formula = ~subgroup, block = ~1|Subject) # needs fine-tuning
# fit_lmer( object, formula = ~subgroup + (1|Subject))      # needs fine-tuning
```

---

fit_survival	<i>Fit/Plot survival</i>
--------------	--------------------------

---

**Description**

Fit/Plot survival

**Usage**

```
fit_survival(
  object,
  assay = assayNames(object)[1],
  percentile = 25,
  sep = FITSEP,
  samples = if (ncol(object) < 50) TRUE else FALSE,
  verbose = TRUE
)

.plot_survival(
  object,
  assay = assayNames(object)[1],
  percentile = 25,
  title = paste0(assay, " ", percentile, "%"),
  subtitle = NULL,
```

```

palette = c("#009999", "#ff5050")
)

plot_survival(
  object,
  assay = assayNames(object)[1],
  percentile = percentiles(object),
  title = paste0(assay, " ", percentile, "%"),
  subtitle = NULL,
  palette = c("#009999", "#ff5050"),
  n = 4,
  ncol = 4,
  nrow = length(percentile),
  file = NULL,
  width = 7 * ncol,
  height = 7 * nrow
)

```

### Arguments

object	SummarizedExperiment
assay	string
percentile	percentage (not greater than 50)
sep	fvar string separator : e.g. '~' gives p~surv~LR50
samples	TRUE or FALSE : record which samples in which stratum ?
verbose	TRUE or FALSE
title	string
subtitle	string
palette	color vector
n	number
ncol	number
nrow	number
file	filepath
width	number
height	number

### Value

ggsurvplot

### Examples

```

file <- download_tcga_example()
if (!is.null(file) & requireNamespace('survminer')){
# Read

```

```
object <- readRDS(file)
object %<>% extract(, .$sample_type == 'T')
object %<>% extract(c('UGT3A2', 'NSUN3', 'XRCC4', 'WNT10A'), )
# Fit
fdt(object)
fdt(fit_survival(object))
fdt(fit_survival(object, percentile = 50))
fdt(fit_survival(object, percentile = 50, sep = '.'))
# Plot
object %<>% fit_survival()
plot_survival(object)
p1 <- .plot_survival(object[1, ])
p2 <- .plot_survival(object[2, ])
}
```

---

fix\_xlgenes

*Fix excel genes*

---

## Description

Fix excel genes

## Usage

```
fix_xlgenes(x)
```

## Arguments

x                    character

## Value

character

## Examples

```
x <- c('FAM46B', '15-Sep', '2-Mar', 'MARCHF6')
x
fix_xlgenes(x)
```

---

flevels	<i>Get fvar levels</i>
---------	------------------------

---

**Description**

Get fvar levels

**Usage**

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

**Arguments**

object	SummarizedExperiment
fvar	feature variable

**Value**

fvar values

**Examples**

```
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
head(flevels(object, 'feature_id'))
```

---

fnames	<i>Get/Set fnames</i>
--------	-----------------------

---

**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**

```
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
fnames(object) %<>% paste0('protein_', .)
object
```

---

formula2str	<i>formula to string</i>
-------------	--------------------------

---

**Description**

formula to string

**Usage**

```
formula2str(formula)
```

**Arguments**

formula	formula
---------	---------

**Value**

string

**Examples**

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

---

fvalues	<i>Get fvalues</i>
---------	--------------------

---

**Description**

Get fvar values

**Usage**

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

**Arguments**

object	SummarizedExperiment
fvar	feature variable

**Value**

fvar values

**Examples**

```
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
head(fvalues(object, 'feature_id'))
fvalues(object, NULL)
```

---

fvars	<i>Get/Set fvars</i>
-------	----------------------

---

**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**

```
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
fvars(object)[1] %<>% paste0('1')
fvars(object)[1]
```

---

genome_to_orgdb	<i>Get corresponding orgdb</i>
-----------------	--------------------------------

---

**Description**

Get corresponding orgdb

**Usage**

```
genome_to_orgdb(genome)
```

**Arguments**

genome	'hg38', 'hg19', 'mm10', or 'mm9'
--------	----------------------------------

**Value**

OrgDb

**Examples**

```
if (requireNamespace('org.Hs.eg.db', quiet = TRUE)){
  class(genome_to_orgdb('hg38'))
}
```

---

group_by_level	<i>group by level</i>
----------------	-----------------------

---

## Description

group by level

## Usage

```
group_by_level(x, ...)  
  
## S3 method for class 'character'  
group_by_level(x, ...)  
  
## S3 method for class 'factor'  
group_by_level(x, ...)  
  
## S3 method for class 'data.table'  
group_by_level(x, var, idvar, ...)
```

## Arguments

x	named logical/character/factor
...	S3 dispatch
var	string
idvar	string

## Value

unnamed character

## Examples

```
t1 <- c( KLF5 = 'up', F11 = 'up', RIG = 'flat', ABT1 = 'down')  
dt <- data.table( gene = c( 'KL5', 'F11', 'RIG', 'ABT1' ),  
                 t1 = c( 'up', 'up', 'flat', 'down' ) )  
group_by_level(t1) # character  
group_by_level(factor(t1)) # factor  
group_by_level(dt, 't1', 'gene') # data.table
```

---

guess_fitsep	<i>guess_fitsep</i>
--------------	---------------------

---

**Description**

guess\_fitsep

**Usage**

```
guess_fitsep(featuredt)
```

**Arguments**

featuredt      data.table

**Value**

string

**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
guess_fitsep(fdt(object))
guess_fitsep(fdt(fit_limma(object)))
```

---

guess_maxquant_quantity	<i>Guess maxquant quantity from snames</i>
-------------------------	--

---

**Description**

Guess maxquant quantity from snames

**Usage**

```
guess_maxquant_quantity(x)
```

**Arguments**

x                      character vector

**Value**

string: value from names(MAXQUANT\_PATTERNS)

**Examples**

```

# file
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
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)

```

---

guess\_sep

*Guess separator*

---

**Description**

Guess separator

**Usage**

```

guess_sep(x, ...)

## S3 method for class 'numeric'
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**

```
# character vector
guess_sep(c('PERM_NON.R1[H/L]', 'PERM_NON.R2[H/L]'))
guess_sep(c('WT_untreated_1', 'WT_untreated_2'))
guess_sep(c('group1', 'group2.R1'))
# SummarizedExperiment
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
guess_sep(object)
```

---

has\_multiple\_levels    *Variable has multiple levels?*

---

**Description**

Variable has multiple levels?

**Usage**

```
has_multiple_levels(x, ...)
```

## S3 method for class 'character'

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

## S3 method for class 'factor'

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

## S3 method for class 'numeric'

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

## S3 method for class 'data.table'

```
has_multiple_levels(
  x,
  y,
```

```

    .xname = get_name_in_parent(x),
    .yname = get_name_in_parent(y),
    ...
  )

## S3 method for class 'SummarizedExperiment'
has_multiple_levels(
  x,
  y,
  .xname = get_name_in_parent(x),
  .yname = get_name_in_parent(y),
  ...
)

```

### Arguments

x	vector, data.table or SummarizedExperiment
...	required for s3 dispatch
.xname	string
y	string
.yname	string

### Value

TRUE or false

### Examples

```

# numeric
a <- numeric();           has_multiple_levels(a)
a <- c(1, 1);             has_multiple_levels(a)
a <- c(1, 2);             has_multiple_levels(a)
# character
a <- character();         has_multiple_levels(a)
a <- c('A', 'A');         has_multiple_levels(a)
a <- c('A', 'B');         has_multiple_levels(a)
# factor
a <- factor();            has_multiple_levels(a)
a <- factor(c('A', 'A')); has_multiple_levels(a)
a <- factor(c('A', 'B')); has_multiple_levels(a)
# data.table
dt <- data.table(a = factor());   has_multiple_levels(dt, 'b')
dt <- data.table(a = factor());   has_multiple_levels(dt, 'a')
dt <- data.table(a = factor());   has_multiple_levels(dt, 'a')
dt <- data.table(a = factor(c('A', 'A'))); has_multiple_levels(dt, 'a')
dt <- data.table(a = factor(c('A', 'B'))); has_multiple_levels(dt, 'a')
# sumexp
object <- matrix(1:9, nrow = 3)
rownames(object) <- sprintf('%d', 1:3)
colnames(object) <- sprintf('%s%d', 1:3)

```



```

object <- list(exprs = object)
object %<>% SummarizedExperiment::SummarizedExperiment()
object$subgroup <- c('A', 'A', 'A');           has_multiple_levels(object, 'group')
object$subgroup <- c('A', 'A', 'A');           has_multiple_levels(object, 'subgroup')
object$subgroup <- c('A', 'B', 'A');           has_multiple_levels(object, 'subgroup')

```

---

hdlproteins	<i>hdl proteomewatch proteins</i>
-------------	-----------------------------------

---

**Description**

hdl proteomewatch proteins

**Usage**

```
hdlproteins()
```

**Value**

string vector: HDLProteomeWatch protein entries

**Examples**

```
hdlproteins()
```

---

impute	<i>Impute</i>
--------	---------------

---

**Description**

Impute NA values

**Usage**

```
impute(object, ...)
```

```
## S3 method for class 'numeric'
```

```
impute(object, shift = 2.5, width = 0.3, verbose = TRUE, plot = FALSE, ...)
```

```
## S3 method for class 'matrix'
```

```
impute(
  object,
  shift = 2.5,
  width = 0.3,
  verbose = TRUE,
  plot = FALSE,

```

```

    n = min(9, ncol(object)),
    palette = make_colors(colnames(object)),
    ...
)

## S3 method for class 'SummarizedExperiment'
impute(
  object,
  assay = assayNames(object)[1],
  by = "subgroup",
  shift = 2.5,
  width = 0.3,
  frac = 0.5,
  verbose = TRUE,
  plot = FALSE,
  palette = make_colors(colnames(object)),
  n = min(9, ncol(object)),
  ...
)

```

### Arguments

object	numeric vector, SumExp
...	required for s3 dispatch
shift	number: sd units
width	number: sd units
verbose	TRUE or FALSE
plot	TRUE or FALSE
n	number of samples to plot
palette	color vector
assay	string
by	svar
frac	fraction: fraction of available samples should be greater than this value for a subgroup to be called available

### Details

Imputes NA values from  $N(\text{mean} - 2.5 \text{ sd}, 0.3 \text{ sd})$

### Value

numeric vector, matrix or SumExp

**Examples**

```

# Simple Design
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
impute(values(object)[, 1], plot = TRUE)[1:3]           # vector
impute(values(object),      plot = TRUE)[1:3, 1:3]     # matrix
impute(object, plot = TRUE)                           # sumexp

# Complex Design
subgroups <- sprintf('%s_STD', c('E00', 'E01', 'E02', 'E05', 'E15', 'E30', 'M00'))
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file, subgroups = subgroups)
impute(values(object)[1:3, 1  ])   # vector
impute(values(object)[1:3, 1:5  ]) # matrix
impute( object )                   # sumexp

```

---

invert_subgroups	<i>Invert subgroups</i>
------------------	-------------------------

---

**Description**

Invert expressions , subgroups, and sample ids

**Usage**

```

invert_subgroups(
  object,
  subgroups = slevels(object, "subgroup"),
  sep = guess_sep(object, "subgroup")
)

```

**Arguments**

object	SummarizedExperiment
subgroups	character vector: subgroup levels to be inverted
sep	string: collapsed string separator

**Value**

character vector or SummarizedExperiment

**Examples**

```

file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
invert_subgroups(object)

```

---

is\_collapsed\_subset    *Is collapsed subset*

---

### Description

Is collapsed subset

### Usage

```
is_collapsed_subset(x, y, sep = ";")
```

### Arguments

x	character vector
y	character vector
sep	string

### Value

character vector

### Examples

```
x <- c('H3BNX8;H3BRM5', 'G5E9Y3')
y <- c('P20674;H3BNX8;H3BV69;H3BRM5', 'G5E9Y3;Q8WWN8;B4DIT1')
is_collapsed_subset(x, y)
```

---

is\_diann\_report    *Is diann, fragpipe, proteingroups, phosphosites file?*

---

### Description

Is diann, fragpipe, proteingroups, phosphosites file?

### Usage

```
is_diann_report(x, .xname = get_name_in_parent(x))
is_fragpipe_tsv(x, .xname = get_name_in_parent(x))
is_maxquant_proteingroups(x, .xname = get_name_in_parent(x))
is_maxquant_phosphosites(x, .xname = get_name_in_parent(x))
assert_diann_report(x, .xname = get_name_in_parent(x))
```

```
assert_fragpipe_tsv(x, .xname = get_name_in_parent(x))  
  
assert_maxquant_proteingroups(x, .xname = get_name_in_parent(x))  
  
assert_maxquant_phosphosites(x, .xname = get_name_in_parent(x))
```

### Arguments

x	file
.xname	name of x

### Examples

```
file <- NULL  
is_diann_report(file)  
is_fragpipe_tsv(file)  
is_maxquant_proteingroups(file)  
is_maxquant_phosphosites(file)  
  
file <- 3  
is_diann_report(file)  
is_fragpipe_tsv(file)  
is_maxquant_proteingroups(file)  
is_maxquant_phosphosites(file)  
  
file <- 'blabla.tsv'  
is_diann_report(file)  
is_fragpipe_tsv(file)  
is_maxquant_proteingroups(file)  
is_maxquant_phosphosites(file)  
  
file <- download_data('multiorganism.combined_protein.tsv')  
is_diann_report(file)  
is_fragpipe_tsv(file)  
is_maxquant_proteingroups(file)  
is_maxquant_phosphosites(file)  
  
file <- download_data('dilution.report.tsv')  
is_diann_report(file)  
is_fragpipe_tsv(file)  
is_maxquant_proteingroups(file)  
is_maxquant_phosphosites(file)  
  
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')  
is_diann_report(file)  
is_fragpipe_tsv(file)  
is_maxquant_proteingroups(file)  
is_maxquant_phosphosites(file)  
  
file <- system.file('extdata/billing19.phosphosites.txt', package = 'autonomics')  
is_diann_report(file)
```

```
is_fragpipe_tsv(file)
is_maxquant_proteingroups(file)
is_maxquant_phosphosites(file)
```

---

is_fastadt	<i>Is fastadt</i>
------------	-------------------

---

### Description

Is fastadt

### Usage

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

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

### Arguments

x	fasta data.table
.xname	string

### Examples

```
fastafile <- system.file('extdata/uniprot_hsa_20140515.fasta', package = 'autonomics')
x <- read_uniprotDT(fastafile)
# is_fastadt(x) # slow
```

---

is_file	<i>Is a file?</i>
---------	-------------------

---

### Description

Is a file (and not a dir)

### Usage

```
is_file(file)
```

### Arguments

file	filepath
------	----------

### Details

This function distinguishes between dir and file. Others dont: is.file, fs::file\_exists, assertive::is\_existing\_file

**Examples**

```
dir <- tempdir(); dir.create(dir, showWarnings = FALSE)
file <- tempfile(); invisible(file.create(file))
is_file(dir)
is_file(file)
```

---

is_fraction	<i>Is fraction</i>
-------------	--------------------

---

**Description**

Is fraction

**Usage**

```
is_fraction(x, .xname = get_name_in_parent(x))
assert_is_fraction(x, .xname = get_name_in_parent(x))
```

**Arguments**

x	number
.xname	string

**Value**

TRUE or false

**Examples**

```
is_fraction(0.1)      # YES
is_fraction(1)       # YES
is_fraction(1.2)     # NO - more than 1
is_fraction(c(0.1, 0.2)) # NO - vector
```

---

is_imputed	<i>Get/set is_imputed</i>
------------	---------------------------

---

**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 <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file, impute = TRUE)
sum(is_imputed(object))

```

---

<code>is_positive_number</code>	<i>Is positive number</i>
---------------------------------	---------------------------

---

**Description**

Is positive number

**Usage**

```

is_positive_number(x, .xname = get_name_in_parent(x))

assert_positive_number(x, .xname = get_name_in_parent(x))

is_weakly_positive_number(x, .xname = get_name_in_parent(x))

assert_weakly_positive_number(x, .xname = get_name_in_parent(x))

```



**Arguments**

x	number
.xname	name of x

**Value**

TRUE or false

**Examples**

```
is_positive_number( 3)
is_positive_number(-3)
is_positive_number( 0)
is_weakly_positive_number(0)
assert_positive_number(3)
```

---

is_scalar_subset	<i>Is scalar subset</i>
------------------	-------------------------

---

**Description**

Is scalar subset

**Usage**

```
is_scalar_subset(
  x,
  y,
  .xname = get_name_in_parent(x),
  .yname = get_name_in_parent(y)
)

assert_scalar_subset(
  x,
  y,
  .xname = get_name_in_parent(x),
  .yname = get_name_in_parent(y)
)
```

**Arguments**

x	scalar
y	SummarizedExperiment
.xname	name of x
.yname	name of y

**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
is_scalar_subset('subgroup', svars(object))
is_scalar_subset('subject', svars(object))
assert_scalar_subset('subgroup', svars(object))
```

---

is\_sig

*Is significant?*


---

**Description**

Is significant?

**Usage**

```
is_sig(
  object,
  fit = fits(fdt(object))[1],
  contrast = coefs(fdt(object)),
  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**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
object %<>% fit_lm()
object %<>% fit_limma()
issig <- is_sig(object, fit = c('lm','limma'), contrast = 'Adult')
plot_contrast_venn(issig)
```

---

is_valid_formula	<i>Is valid formula</i>
------------------	-------------------------

---

### Description

Is valid formula

### Usage

```
is_valid_formula(
  x,
  y,
  .xname = get_name_in_parent(x),
  .yname = get_name_in_parent(y)
)

assert_valid_formula(
  x,
  y,
  .xname = get_name_in_parent(x),
  .yname = get_name_in_parent(y)
)
```

### Arguments

x	formula
y	SummarizedExperiment
.xname	string
.yname	string

### Value

TRUE or false

### Examples

```
object <- matrix(1:9, nrow = 3)
rownames(object) <- sprintf('%d', 1:3)
colnames(object) <- sprintf('%s%d', 1:3)
object <- list(exprs = object)
object %<>% SummarizedExperiment::SummarizedExperiment()
object$group <- 'group0'
object$subgroup <- c('A', 'B', 'C')
svars(object)
  is_valid_formula( 'condition', object) # not formula
  is_valid_formula( ~condition,  object) # not svar
  is_valid_formula( ~group,      object) # not multilevel
```

```

is_valid_formula( ~subgroup,    object) # TRUE
is_valid_formula( ~0+subgroup,  object) # TRUE
is_valid_formula( ~1,           object) # TRUE
assert_valid_formula( ~subgroup, object)

```

---

keep\_connected\_blocks *Keep fully connected blocks*

---

### Description

Keep fully connected blocks

### Usage

```
keep_connected_blocks(object, block, verbose = TRUE)
```

### Arguments

object	SummarizedExperiment
block	svar
verbose	TRUE or FALSE

### Examples

```

file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% keep_connected_blocks( block = 'Subject')

```

---

keep\_connected\_features

*Keep features with n+ connected blocks*

---

### Description

Keep features with n+ connected blocks

### Usage

```
keep_connected_features(object, block, n = 2, verbose = TRUE)
```

### Arguments

object	SummarizedExperiment
block	svar
n	number
verbose	TRUE or FALSE

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% keep_connected_blocks( block = 'Subject')
object %<>% keep_connected_features(block = 'Subject')
```

---

keep\_replicated\_features  
*Keep replicated features*

---

**Description**

Keep features replicated for each slevel

**Usage**

```
keep_replicated_features(object, formula = ~1, n = 3, verbose = TRUE)
```

**Arguments**

object	SummarizedExperiment
formula	formula
n	min replications required
verbose	TRUE or FALSE

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% keep_replicated_features()
object %<>% keep_replicated_features(~ subgroup)
```

---

label2index                    *Convert labels into indices*

---

**Description**

Convert labels into indices

**Usage**

```
label2index(x)
```

**Arguments**

x	'character'
---	-------------

**Examples**

```
label2index(x = 'Reporter intensity 0 WT(0).KD(1).OE(2).R1')
label2index(x = 'Reporter intensity 1 WT(1).KD(2).OE(3).R1')
label2index(x = 'Reporter intensity 0 WT(126).KD(127).OE(128).R1')
label2index(x = 'Reporter intensity 1 WT(126).KD(127).OE(128).R1')
label2index(x = 'Reporter intensity 1 Mix1')
```

---

LINMOD_ENGINES	<i>Linear Modeling Engines</i>
----------------	--------------------------------

---

**Description**

Linear Modeling Engines

**Usage**

```
LINMOD_ENGINES
```

**Format**

An object of class character of length 5.

**Examples**

```
LINMOD_ENGINES
```

---

list2mat	<i>list to matrix</i>
----------	-----------------------

---

**Description**

list to matrix

**Usage**

```
list2mat(x)
```

**Arguments**

x	list
---	------

**Value**

matrix

**Examples**

```
x <- list(roundfruit = c('apple', 'orange'), redfruit = c('apple', 'strawberry'))
list2mat(x)
```

---

list_files	<i>list_files</i>
------------	-------------------

---

**Description**

list.files for programming

**Usage**

```
list_files(dir, full.names)
```

**Arguments**

dir	directory
full.names	TRUE or FALSE

**Details**

Adds a small layer on list.files. Returning NULL rather than character(0) when no files. Making it better suited for programming.

---

log2counts	<i>Get/Set log2counts</i>
------------	---------------------------

---

**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 <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
object <- read_rnaseq_counts(file)
log2counts(object)[1:3, 1:3]
log2counts(object) <- values(object)
```

---

log2cpm	<i>Get/Set log2cpm</i>
---------	------------------------

---

**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 <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
object <- read_rnaseq_counts(file)
log2cpm(object)[1:3, 1:3]
log2cpm(object) <- values(object)
```

---

log2diffs

*Get/Set log2diffs*

---

**Description**

Get/Set log2diffs

**Usage**

```
log2diffs(object)

## S4 method for signature 'SummarizedExperiment'
log2diffs(object)

log2diffs(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
log2diffs(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
log2diffs(object) <- value
```

**Arguments**

object	SummarizedExperiment
value	occupancy matrix (features x samples)

**Value**

occupancy matrix (get) or updated object (set)

**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
log2diffs(object)[1:3, 1:3]
```

---

log2proteins	<i>Get/Set log2proteins</i>
--------------	-----------------------------

---

**Description**

Get/Set log2proteins

**Usage**

```
log2proteins(object)

## S4 method for signature 'SummarizedExperiment'
log2proteins(object)

log2proteins(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
log2proteins(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
log2proteins(object) <- value
```

**Arguments**

object	SummarizedExperiment
value	occupancy matrix (features x samples)

**Value**

occupancy matrix (get) or updated object (set)

**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
log2proteins(object)[1:3, 1:3]
```

---

log2sites	<i>Get/Set log2sites</i>
-----------	--------------------------

---

**Description**

Get/Set log2sites

**Usage**

```

log2sites(object)

## S4 method for signature 'SummarizedExperiment'
log2sites(object)

log2sites(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,matrix'
log2sites(object) <- value

## S4 replacement method for signature 'SummarizedExperiment,numeric'
log2sites(object) <- value

```

**Arguments**

```

object      SummarizedExperiment
value      occupancy matrix (features x samples)

```

**Value**

occupancy matrix (get) or updated object (set)

**Examples**

```

file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
log2sites(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 <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
object <- read_rnaseq_counts(file)
log2tpm(object) <- values(object)
log2tpm(object)[1:3, 1:3]
```

---

log2transform	<i>Transform values</i>
---------------	-------------------------

---

### Description

Transform values

### Usage

```
log2transform(
  object,
  assay = assayNames(object)[1],
  pseudo = 0,
  verbose = FALSE
)

exp2(object, verbose = FALSE)

zscore(object, verbose = FALSE)

quantnorm(object, verbose = FALSE)

invnorm(object, verbose = FALSE)

vsnorm(object, verbose = FALSE, delog = TRUE)
```

**Arguments**

object	SummarizedExperiment
assay	character vector : assays for which to perform transformation
pseudo	number : pseudo value to be added prior to transformation
verbose	TRUE or FALSE : whether to msg
deLog	TRUE or FALSE (vsN)

**Value**

Transformed sumexp

**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
```

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

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

object          %>% plot_sample_densities()
#vsN(object)    %>% plot_sample_densities() # dataset too small

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

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

---

logical2factor      *logical to factor*

---

**Description**

logical to factor

**Usage**

```
logical2factor(x, true = get_name_in_parent(x), false = paste0("not", true))

factor2logical(x)
```

**Arguments**

x	logical vector
true	string : truelevel
false	string : falselevel

**Value**

factor

**Examples**

```
t1up <- c( TRUE, FALSE, TRUE)
t1 <- c('flat', 'down', 'up' ) %>% factor(., .)
t1up
logical2factor(t1up)
factor2logical(t1)
```

---

make\_alpha\_palette      *Make alpha palette*

---

**Description**

Make alpha palette

**Usage**

```
make_alpha_palette(object, alpha)
```

**Arguments**

object	SummarizedExperiment
alpha	string

**Value**

character vector

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
make_alpha_palette(object, 'Time')
```

---

make_colors	<i>Make colors</i>
-------------	--------------------

---

**Description**

Make colors

**Usage**

```
make_colors(  
  varlevels,  
  sep = guess_sep(varlevels),  
  show = FALSE,  
  verbose = FALSE  
)
```

**Arguments**

varlevels	character vector
sep	string
show	TRUE or FALSE: whether to plot
verbose	TRUE or FALSE: whether to msg

**Examples**

```
make_colors(c('A', 'B', 'C', 'D' ), show = TRUE)  
make_colors(c('A.1', 'B.1', 'A.2', 'B.2'), show = TRUE)
```

---

make_volcano_dt	<i>Create volcano datatable</i>
-----------------	---------------------------------

---

**Description**

Create volcano datatable

**Usage**

```
make_volcano_dt(  
  object,  
  fit = fits(fdt(object))[1],  
  coefs = default_coefs(fdt(object), fit = fit)[1],  
  shape = "imputed",  
  size = NULL,  
  alpha = NULL,  
  label = "feature_id"  
)
```

**Arguments**

object	SummarizedExperiment
fit	'limma', 'lme', 'lm', 'wilcoxon'
coefs	character vector: coefs for which to plot volcanoes
shape	fvar or NULL
size	fvar or NULL
alpha	fvar or NULL
label	fvar or NULL

**Value**

data.table

**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file, impute = TRUE, fit = 'limma')
make_volcano_dt(object, fit = 'limma', coefs = 'Adult')
```

---

map\_fvalues

*Map fvalues*

---

**Description**

Map fvalues

**Usage**

```
map_fvalues(object, fvalues, from = "uniprot", to = "feature_id", sep = ";")
```

**Arguments**

object	SummarizedExperiment
fvalues	uncollapsed string vector
from	string (fvar)
to	string (svar)
sep	collapse separator

**Value**

string vector



**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
fdt(object)
map_fvalues(object, c('Q6DHL5', 'Q6PFS7'), from = 'uniprot', to = 'feature_id', sep = ';')
```

---

matrix2sumexp	<i>Convert matrix into SummarizedExperiment</i>
---------------	---

---

**Description**

Convert matrix into SummarizedExperiment

**Usage**

```
matrix2sumexp(x, verbose = TRUE)
```

**Arguments**

x	matrix
verbose	TRUE/FALSE

**Value**

SummarizedExperiment

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
x <- values(read_metabolon(file))
object <- matrix2sumexp(x)
object %<>% pca()
biplot(object, color = 'subgroup')
```

---

MAXQUANT_PATTERNS	<i>maxquant quantity patterns</i>
-------------------	-----------------------------------

---

**Description**

maxquant quantity patterns

**Usage**

```
MAXQUANT_PATTERNS
```

**Format**

An object of class character of length 7.

**Examples**

```
MAXQUANT_PATTERNS
```

---

```
merge_sample_excel      Merge sample excel
```

---

**Description**

Merge sample excel

**Usage**

```
merge_sample_excel(  
  object,  
  sfile,  
  range = NULL,  
  by.x = "sample_id",  
  by.y = "sample_id"  
)
```

**Arguments**

object	SummarizedExperiment
sfile	sample file
range	string
by.x	string
by.y	string

**Value**

SummarizedExperiment

---

merge_sample_file	<i>Merge sample / feature file</i>
-------------------	------------------------------------

---

**Description**

Merge sample / feature file

**Usage**

```
merge_sample_file(  
  object,  
  sfile = NULL,  
  by.x = "sample_id",  
  by.y = "sample_id",  
  all.x = TRUE,  
  select = NULL,  
  stringsAsFactors = FALSE,  
  verbose = TRUE  
)
```

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

**Arguments**

object	SummarizedExperiment
sfile	string : sample file path
by.x	string : object mergevar
by.y	string : file mergevvar
all.x	TRUE / FALSE : whether to keep samples / feature without annotation
select	character : [sf]file columns to select
stringsAsFactors	TRUE / FALSE
verbose	TRUE / FALSE
ffile	string : ffile path

**Value**

SummarizedExperiment

**Examples**

```

file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
subgroups <- c('E00', 'E01', 'E02', 'E05', 'E15', 'E30', 'M00')
subgroups %<>% paste0('_STD')
object <- read_maxquant_proteingroups(file, subgroups = subgroups)
sfile <- paste0(tempdir(), '/', basename(tools::file_path_sans_ext(file)))
sfile %<>% paste0('.samples.txt')
dt <- data.table(sample_id = object$sample_id,
                 day = split_extract_fixed(object$subgroup, '_', 1))
data.table::fwrite(dt, sfile)
sdt(object)
sdt(merge_sample_file(object, sfile))

```

merge\_sdata

*Merge sample/feature dt***Description**

Merge sample/feature dt

**Usage**

```

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

```

```

merge_sdt(
  object,
  dt,
  by.x = "sample_id",
  by.y = "sample_id",
  all.x = TRUE,
  verbose = TRUE
)

```

```

merge_fdata(
  object,
  dt,
  by.x = "feature_id",

```

```

    by.y = names(dt)[1],
    all.x = TRUE,
    verbose = TRUE
  )

merge_fdt(
  object,
  dt,
  by.x = "feature_id",
  by.y = "feature_id",
  all.x = TRUE,
  verbose = TRUE
)

```

### Arguments

object	SummarizedExperiment
dt	data.frame, data.table, DataFrame
by.x	string : object mergevar
by.y	string : df mergevar
all.x	TRUE / FALSE : whether to keep samples / features without annotation
verbose	TRUE / FALSE : whether to msg

### Value

SummarizedExperiment

### Examples

```

file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
sdt(object)
sdt(merge_sdt(object, data.table(sample_id = object$sample_id,
                                number = seq_along(object$sample_id))))

```

---

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))
```

---

 modelvar

*Get model variable*


---

**Description**

Get model variable

**Usage**

```
modelvar(
  featuredt,
  quantity,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)
```

```
effectvar(
  featuredt,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)
```

```
tvar(
  featuredt,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)
```

```
pvar(
  featuredt,
  fit = fits(featuredt),
```

```
    coef = default_coefs(featuredt, fit = fit)
  )

fdrvar(
  featuredt,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)

abstractvar(
  featuredt,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)

modelvec(
  featuredt,
  quantity,
  fit = fits(featuredt)[1],
  coef = default_coefs(featuredt, fit = fit)[1],
  fvar = "feature_id"
)

effectvec(
  featuredt,
  fit = fits(featuredt)[1],
  coef = default_coefs(featuredt, fit = fit)[1],
  fvar = "feature_id"
)

tvec(
  featuredt,
  fit = fits(featuredt)[1],
  coef = default_coefs(featuredt, fit = fit)[1],
  fvar = "feature_id"
)

pvec(
  featuredt,
  fit = fits(featuredt)[1],
  coef = default_coefs(featuredt, fit = fit)[1],
  fvar = "feature_id"
)

fdrvec(
  featuredt,
  fit = fits(featuredt)[1],
  coef = default_coefs(featuredt, fit = fit)[1],
```

```
fvar = "feature_id"
)

modeldt(
  featuredt,
  quantity,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)

effectdt(
  featuredt,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)

tdt(
  featuredt,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)

pdt(
  featuredt,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)

modelmat(
  featuredt,
  quantity,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)

effectmat(
  featuredt,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)

effectsize(
  featuredt,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)

tmat(
```



```
    featuredt,
    fit = fits(featuredt),
    coef = default_coefs(featuredt, fit = fit)
)

pmat(
  featuredt,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)

fdrmat(
  featuredt,
  fit = fits(featuredt),
  coef = default_coefs(featuredt, fit = fit)
)

modelfeatures(
  featuredt,
  fit = fits(featuredt)[1],
  coef = default_coefs(featuredt, fit = fit)[1],
  fvar = "feature_id",
  significancevar = "p",
  significance = 0.05,
  effectdirection = "<>",
  effectsize = 0
)

upfeatures(
  featuredt,
  fit = fits(featuredt)[1],
  coef = default_coefs(featuredt, fit = fit)[1],
  fvar = "feature_id",
  significancevar = "p",
  significance = 0.05,
  effectsize = 0
)

downfeatures(
  featuredt,
  fit = fits(featuredt)[1],
  coef = default_coefs(featuredt, fit = fit)[1],
  fvar = "feature_id",
  significancevar = "p",
  significance = 0.05,
  effectsize = 0
)
```

**Arguments**

featuredt	data.table
quantity	'p', 'effect', 'fdr', 't', or 'se'
fit	string (vector)
coef	string (vector)
fvar	'feature_id' or other fvar for values (pvec) or names (upfeatures)
significancevar	'p' or 'fdr'
significance	p or fdr cutoff (fractional number)
effectdirection	'<>', '<' or '>'
effectsize	effectsize cutoff (positive number)

**Value**

string (tvar), matrix (tmat), numeric vector (tvec), character vector (tfeatures)

**Examples**

```
# Read
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% fit_limma()
object %<>% fit_lm()
featuredt <- fdt(object)
featuredt %<>% add_adjusted_pvalues('fdr')

# modelvar
modelvar(featuredt, 'p');                pvar(featuredt)
modelvar(featuredt, 'effect');           effectvar(featuredt)
modelvar(featuredt, 'fdr');              fdrvar(featuredt)

# modelvec
modelvec(featuredt, 'p'   )[1:3];        pvec(featuredt)[1:3]
modelvec(featuredt, 'effect')[1:3];      effectvec(featuredt)[1:3]
modelvec(featuredt, 'fdr' )[1:3];        fdrvec(featuredt)[1:3]

# modelmatrix
modelmat(featuredt, 'p'   )[1:3, 1:3];   pmat(featuredt)[1:3, 1:3]
modelmat(featuredt, 'effect')[1:3, 1:3]; effectmat(featuredt)[1:3, 1:3]
modelmat(featuredt, 'fdr' )[1:3, 1:3];   fdrmat(featuredt)[1:3, 1:3]

# modelfeatures
modelfeatures(featuredt      )[1:3]
modelfeatures(featuredt, effectdirection = '<')[1:3];  downfeatures(featuredt)[1:3]
modelfeatures(featuredt, effectdirection = '>')[1:3];  upfeatures(featuredt)[1:3]
```

---

MSIGCOLLECTIONSHUMAN    *Human/Mouse Msigdb Collections*

---

**Description**

Human/Mouse Msigdb Collections

**Usage**

MSIGCOLLECTIONSHUMAN

MSIGCOLLECTIONSMOUSE

**Format**

An object of class character of length 25.

An object of class character of length 13.

---

MSIGDIR                    *local msigdb dir*

---

**Description**

local msigdb dir

**Usage**

MSIGDIR

**Format**

An object of class character of length 1.

---

nfactors	<i>stri_split and extract</i>
----------	-------------------------------

---

## Description

stri\_split and extract

## Usage

```
nfactors(x, sep = guess_sep(x))  
split_extract_fixed(x, sep, i)  
split_extract_regex(x, sep, i)  
split_extract(x, i, sep = guess_sep(x))
```

## Arguments

x	character vector
sep	string
i	integer

## Value

character vector

## Examples

```
# Read  
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')  
object <- read_metabolon(file)  
x <- object$sample_id[1:5]  
nfactors(x)  
# Split  
split_extract_fixed(x, '.', 1:2)  
split_extract_fixed(x, '.', seq_len(nfactors(x)-1))  
split_extract_fixed(x, '.', nfactors(x))  
split_extract_fixed(fdt(object)$PUBCHEM, ';', 1) # with NA values
```

---

OPENTARGETSDIR	<i>opentargets dir</i>
----------------	------------------------

---

**Description**

opentargets dir

**Usage**

OPENTARGETSDIR

**Format**

An object of class character of length 1.

---

order_on_p	<i>Order on p</i>
------------	-------------------

---

**Description**

Order on p

**Usage**

```
order_on_p(
  object,
  fit = autonomics::fits(fdt(object)),
  coefs = autonomics::coefs(fdt(object), fit = fit),
  combiner = "|",
  verbose = TRUE
)
```

```
order_on_effect(
  object,
  fit = autonomics::fits(fdt(object)),
  coefs = autonomics::coefs(fdt(object), fit = fit),
  combiner = "|",
  verbose = TRUE
)
```

**Arguments**

object	SummarizedExperiment
fit	string vector: subset of 'fits(fdt(object))'
coefs	string vector: subset of 'coefs(fdt(object))'
combiner	' ' or '&'
verbose	TRUE or FALSE

**Value**

SummarizedExperiment

**Examples**

```
# Read
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
order_on_p(object)
order_on_p(fit_limma(object), coefs = c('t1', 't2', 't3'))
```

---

pca

*PCA, SMA, LDA, PLS, SPLS, OPLS*

---

**Description**

Perform a dimension reduction. Store sample scores, feature loadings, and dimension variances.

**Usage**

```
pca(
  object,
  by = "sample_id",
  assay = assayNames(object)[1],
  ndim = 2,
  sep = FITSEP,
  minvar = 0,
  center_samples = TRUE,
  verbose = TRUE,
  plot = FALSE,
  ...
)

pls(
  object,
  by = "subgroup",
  assay = assayNames(object)[1],
  ndim = 2,
  sep = FITSEP,
  minvar = 0,
  verbose = FALSE,
  plot = FALSE,
  ...
)

sma(
  object,
```

```
    by = "sample_id",
    assay = assayNames(object)[1],
    ndim = 2,
    sep = FITSEP,
    minvar = 0,
    verbose = TRUE,
    plot = FALSE,
    ...
)

lda(
  object,
  assay = assayNames(object)[1],
  by = "subgroup",
  ndim = 2,
  sep = FITSEP,
  minvar = 0,
  verbose = TRUE,
  plot = FALSE,
  ...
)

splS(
  object,
  assay = assayNames(object)[1],
  by = "subgroup",
  ndim = 2,
  sep = FITSEP,
  minvar = 0,
  plot = FALSE,
  ...
)

opls(
  object,
  by = "subgroup",
  assay = assayNames(object)[1],
  ndim = 2,
  sep = FITSEP,
  minvar = 0,
  verbose = FALSE,
  plot = FALSE,
  ...
)
```

### Arguments

object            SummarizedExperiment

by	svar or NULL
assay	string
ndim	number
sep	string
minvar	number
center_samples	TRUE/FALSE: center samples prior to pca ?
verbose	TRUE/FALSE: message ?
plot	TRUE/FALSE: plot ?
...	passed to biplot

**Value**

SummarizedExperiment

**Author(s)**

Aditya Bhagwat, Laure Cougnaud (LDA)

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
pca(object, plot = TRUE) # Principal Component Analysis
pls(object, plot = TRUE) # Partial Least Squares
lda(object, plot = TRUE) # Linear Discriminant Analysis
sma(object, plot = TRUE) # Spectral Map Analysis
spls(object, plot = TRUE) # Sparse PLS
# opl(s(object, plot = TRUE) # OPLS # outcommented because it produces a file named FALSE
```

percentiles

*survival percentiles***Description**

survival percentiles

**Usage**

percentiles(object)

**Arguments**

object SummarizedExperiment

**Value**

numeric vector



---

pg\_to\_canonical      *proteingroup to isoforms*

---

**Description**

proteingroup to isoforms

**Usage**

```
pg_to_canonical(x, unique = TRUE)
```

```
pg_to_isoforms(x, unique = TRUE)
```

**Arguments**

x                    proteingroups string vector  
unique                whether to remove duplicates

**Value**

string vector

**Examples**

```
(x <- c('Q96JP5;Q96JP5-2', 'Q96JP5', 'Q96JP5-2;P86791'))
pg_to_isoforms(x)
pg_to_canonical(x)
pg_to_isoforms(x, unique = FALSE)
pg_to_canonical(x, unique = FALSE)
# .pg_to_isoforms(x[1]) # unexported dot functions
# .pg_to_canonical(x[1]) # operate on scalars
```

---

plot\_contrastogram      *Plot contrastogram*

---

**Description**

Plot contrastogram

**Usage**

```
plot_contrastogram(
  object,
  subgroupvar,
  formula = as.formula(paste0("~ 0 +", subgroupvar)),
  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)
  plot_contrastogram(object, subgroupvar = 'subgroup')
}
```

---

plot\_contrast\_venn      *Plot contrast venn*

---

**Description**

Plot contrast venn

**Usage**

```
plot_contrast_venn(issig, colors = NULL)
```

**Arguments**

issig	matrix(nrow, ncontrast): -1 (down), +1 (up)
colors	NULL or colorvector

**Value**

nothing returned

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% fit_wilcoxon(~ subgroup, block = 'Subject')
object %<>% fit_limma( ~ subgroup, block = 'Subject', codingfun = contr.treatment.explicit)
isfdr <- is_sig(object, contrast = 't3-t0', quantity = 'p', fit = fits(fdt(object)))
plot_contrast_venn(isfdr)
```

---

`plot_data`*Plot data*

---

**Description**

Plot data

**Usage**

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

**Arguments**

<code>data</code>	<code>data.frame</code> '
<code>geom</code>	<code>geom_point</code> , etc.
<code>color</code>	variable mapped to color (symbol)
<code>fill</code>	variable mapped to fill (symbol)
<code>linetype</code>	variable mapped to linetype (symbol)
<code>...</code>	mapped aesthetics
<code>palette</code>	color palette (named character vector)
<code>fixed</code>	fixed aesthetics (list)
<code>theme</code>	list with ggplot theme specifications

**Value**

ggplot object

**Author(s)**

Aditya Bhagwat, Johannes Graumann

**Examples**

```

file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% pca()
data <- sdt(object)
plot_data(data, x = `effect~sample_id~pca1`, y = `effect~sample_id~pca2`)
plot_data(data, x = `effect~sample_id~pca1`, y = `effect~sample_id~pca2`, color = subgroup)
plot_data(data, x = `effect~sample_id~pca1`, y = `effect~sample_id~pca2`, color = NULL)
fixed <- list(shape = 15, size = 3)
plot_data(data, x = `effect~sample_id~pca1`, y = `effect~sample_id~pca2`, fixed = fixed)

```

---

plot\_densities

*Plot sample/feature distributions*


---

**Description**

Plot sample/feature distributions

**Usage**

```

plot_densities(
  object,
  assay = assayNames(object)[1],
  group,
  fill,
  color = NULL,
  linetype = NULL,
  facet = NULL,
  nrow = NULL,
  ncol = NULL,
  dir = "h",
  scales = "free_y",
  labeller = label_value,
  palette = NULL,
  fixed = list(alpha = 0.8, na.rm = TRUE)
)

plot_sample_densities(
  object,
  assay = assayNames(object)[1],
  group = "sample_id",
  fill = if ("subgroup" %in% svars(object)) "subgroup" else "sample_id",
  color = NULL,
  linetype = NULL,
  n = 100,
  facet = NULL,
  nrow = NULL,

```

```

    ncol = NULL,
    dir = "h",
    scales = "free_y",
    labeller = label_value,
    palette = NULL,
    fixed = list(alpha = 0.8, na.rm = TRUE)
  )

plot_feature_densities(
  object,
  assay = assayNames(object)[1],
  fill = "feature_id",
  group = fill,
  color = NULL,
  linetype = NULL,
  n = 9,
  facet = NULL,
  nrow = NULL,
  ncol = NULL,
  dir = "h",
  scales = "free",
  labeller = label_value,
  palette = NULL,
  fixed = list(alpha = 0.8, na.rm = TRUE)
)

```

### Arguments

object	SummarizedExperiment
assay	string
group	svar (string)
fill	svar (string)
color	svar (string)
linetype	svar (string)
facet	svar (character vector)
nrow	number of facet rows
ncol	number of facet cols
dir	'h' (horizontal) or 'v' (vertical)
scales	'free', 'fixed', 'free_y'
labeller	e.g. label_value
palette	named character vector
fixed	fixed aesthetics
n	number

**Value**

ggplot object

**See Also**

[plot\\_sample\\_violins](#), [plot\\_sample\\_boxplots](#)

**Examples**

```
# Data
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% extract(, order(.$subgroup))

# Sample distributions
plot_sample_densities(object)
plot_sample_violins( object, facet = 'Time')
plot_sample_boxplots(object)
plot_exprs(object)
plot_exprs(object, dim = 'samples', x = 'subgroup', facet = 'Time')

# Feature distributions
plot_feature_densities(object)
plot_feature_violins( object)
plot_feature_boxplots( object)
```

---

plot\_design

*Plot model*

---

**Description**

Plot model

**Usage**

```
plot_design(object, codingfun = contr.treatment)
```

**Arguments**

object	SummarizedExperiment
codingfun	factor coding function

- `contr.treatment`: intercept =  $y_0$ , coefi =  $y_i - y_0$
- `contr.treatment.explicit`: intercept =  $y_0$ , coefi =  $y_i - y_0$
- `code_control`: intercept =  $y_{\text{mean}}$ , coefi =  $y_i - y_0$
- `contr.diff`: intercept =  $y_0$ , coefi =  $y_i - y(i-1)$
- `code_diff`: intercept =  $y_{\text{mean}}$ , coefi =  $y_i - y(i-1)$
- `code_diff_forward`: intercept =  $y_{\text{mean}}$ , coefi =  $y_i - y(i+)$

- code\_deviation: intercept = ymean, coefi =  $y_i - \text{ymean}$  (drop last)
- code\_deviation\_first: intercept = ymean, coefi =  $y_i - \text{ymean}$  (drop first)
- code\_helmert: intercept = ymean, coefi =  $y_i - \text{mean}(y_0:(y_i-1))$
- code\_helmert\_forward: intercept = ymean, coefi =  $y_i - \text{mean}(y_{i+1}:y_p)$

## Value

ggplot

## Examples

```
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
subgroups <- paste0(c('E00', 'E01', 'E02', 'E05', 'E15', 'E30', 'M00'), '_STD')
object <- read_maxquant_proteingroups(file, subgroups = subgroups)
object$subgroup %<>% substr(1,3)
plot_design(object)
```

---

plot_detections	<i>Plot missingness per sample / subgroup</i>
-----------------	---

---

## Description

plot\_sample\_nas shows systematic and random missingness (white), and full detection (bright color) at sample resolution. Imputations are also shown (light color).

## Usage

```
plot_detections(...)

plot_summarized_detections(...)

plot_sample_nas(
  object,
  by = "subgroup",
  fill = by,
  palette = make_svar_palette(object, fill),
  axis.text.y = element_blank()
)

plot_subgroup_nas(
  object,
  by = "subgroup",
  fill = by,
  palette = NULL,
  na_imputes = TRUE
)
```

**Arguments**

...	used to maintain deprecated functions
object	SummarizedExperiment
by	svar (string)
fill	svar (string)
palette	color vector (names = levels, values = colors)
axis.text.y	passed to ggplot2::theme
na_imputes	TRUE or FALSE

**Details**

plot\_subgroup\_nas shows systematic missingness at subgroup resolution. Random missingness and full detection are shown together (bright color). Imputations are also shown (light color).

**Value**

ggplot object

**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
plot_sample_nas(object)
plot_sample_nas(impute(object))
plot_subgroup_nas(object)
plot_subgroup_nas(impute(object))

subgroups <- sprintf('%s_STD', c('E00', 'E01', 'E02', 'E05', 'E15', 'E30', 'M00'))
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file, subgroups = subgroups)
plot_subgroup_nas(object)
plot_subgroup_nas(object, 'subgroup')
plot_sample_nas(object)
plot_sample_nas(object, 'subgroup')
```

---

plot\_exprs

*Plot exprs for coef*

---

**Description**

Plot exprs for coef



**Usage**

```

plot_exprs(
  object,
  dim = "both",
  assay = assayNames(object)[1],
  fit = fits(fdt(object))[1],
  coefs = default_coefs(fdt(object), fit = fit),
  block = NULL,
  x = default_x(object, dim),
  geom = default_geom(object, x = x, block = block),
  color = x,
  fill = x,
  shape = NULL,
  size = NULL,
  alpha = NULL,
  linetype = NULL,
  highlight = NULL,
  combiner = "|",
  p = 1,
  fdr = 1,
  facet = if (dim == "both") "feature_id" else NULL,
  n = 4,
  ncol = NULL,
  nrow = NULL,
  scales = "free_y",
  labeller = "label_value",
  pointsize = if (is.null(block)) 0 else 0.5,
  jitter = if (is.null(block)) 0.1 else 0,
  fillpalette = make_var_palette(object, fill),
  colorpalette = make_var_palette(object, color),
  hlevels = NULL,
  title = switch(dim, both = x, features = "Feature Boxplots", samples =
    "Sample Boxplots"),
  subtitle = if (!is.null(fit)) coefs else "",
  xlab = NULL,
  ylab = "value",
  theme = ggplot2::theme(plot.title = element_text(hjust = 0.5)),
  file = NULL,
  width = 7,
  height = 7,
  verbose = TRUE
)

plot_sample_boxplots(
  object,
  fill = if ("subgroup" %in% svars(object)) "subgroup" else "sample_id",
  n = min(ncol(object), 16),
  ...

```

)

plot\_feature\_boxplots(object, ...)

**Arguments**

object	SummarizedExperiment
dim	'samples' (per-sample distribution across features), 'features' (per-feature distribution across samples ) or 'both' (subgroup distribution faceted per feature)
assay	string: value in assayNames(object)
fit	'limma', 'lm', 'lme', 'lmer', 'wilcoxon'
coefs	subset of coefs(fdt(object)) to consider in selecting top
block	group svar
x	x svar
geom	'boxplot' or 'point'
color	color svar: points, lines
fill	fill svar: boxplots
shape	shape svar
size	size svar
alpha	alpha svar
linetype	linetype svar
highlight	highlight svar
combiner	'&' or 'l'
p	fraction: p cutoff
fdr	fraction: fdr cutoff
facet	string: fvar mapped to facet
n	number of samples (dim = 'samples') or features (dim = 'features' or 'both') to plot
ncol	number of cols in faceted plot (if dim = 'both')
nrow	number of rows in faceted plot (if dim = 'both')
scales	'free_y', 'free_x', 'fixed'
labeller	string or function
pointsize	number
jitter	jitter width (number)
fillpalette	named character vector: fill palette
colorpalette	named character vector: color palette
hlevels	xlevels for which to plot hlines
title	string

subtitle	string
xlab	string
ylab	string
theme	ggplot2::theme(...) or NULL
file	NULL or filepath
width	inches
height	inches
verbose	TRUE or FALSE
...	used to maintain deprecated functions

**Value**

ggplot object

**See Also**

[plot\\_sample\\_densities](#), [plot\\_sample\\_violins](#)

**Examples**

```
# Without limma
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
plot_exprs(object, block = 'Subject', title = 'Subgroup Boxplots')
plot_exprs(object, dim = 'samples')
plot_exprs(object, dim = 'features', block = 'sample_id')
# With limma
object %<>% fit_limma(block = 'Subject')
plot_exprs(object, block = 'Subject')
plot_exprs(object, block = 'Subject', coefs = c('t1', 't2', 't3'))
plot_exprs_per_coef(object, x = 'Time', block = 'Subject')
# Points
plot_exprs(object, geom = 'point', block = 'Subject')
# Add highlights
controlfeatures <- c('biotin', 'phosphate')
fdt(object) %<>% cbind(control = .$feature_name %in% controlfeatures)
plot_exprs(object, dim = 'samples', highlight = 'control')
# Multiple pages
plot_exprs(object, block = 'Subject', n = 4, nrow = 1, ncol = 2)
```

---

plot\_exprs\_per\_coef *Plot exprs per coef*

---

### Description

Plot exprs per coef

### Usage

```
plot_exprs_per_coef(
  object,
  fit = fits(fdt(object))[1],
  coefs = default_coefs(fdt(object), fit = fit),
  x = default_x(object),
  geom = default_geom(object, x),
  block = NULL,
  orderbyp = FALSE,
  title = x,
  subtitle = default_subtitle(fit, x, coefs),
  n = 1,
  nrow = 1,
  ncol = NULL,
  theme = ggplot2::theme(legend.position = "bottom", legend.title = element_blank(),
    plot.title = element_text(hjust = 0.5), plot.subtitle = element_text(hjust = 0.5))
)
```

### Arguments

object	SummarizedExperiment
fit	'limma', 'lm', 'lme', 'lmer', 'wilcoxon'
coefs	subset of coefs(fdt(object)) to consider in selecting top
x	x svar
geom	'boxplot' or 'point'
block	group svar
orderbyp	TRUE or FALSE
title	string
subtitle	string
n	number
nrow	number of rows in faceted plot
ncol	number of cols in faceted plot
theme	ggplot2::theme(...) or NULL

**Value**

ggplot object

**See Also**

[plot\\_sample\\_densities](#), [plot\\_sample\\_violins](#)

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% fit_limma()
object %<>% pls(by = 'subgroup')
object %<>% pls(by = 'Diabetes')
object %<>% pls(by = 'Subject')
plot_exprs_per_coef(object)
plot_exprs_per_coef(object, orderbyp = TRUE)
plot_exprs_per_coef(object, fit = 'pls1', block = 'Subject')
```

---

plot_fit_summary	<i>Plot fit summary</i>
------------------	-------------------------

---

**Description**

Plot fit summary

**Usage**

```
plot_fit_summary(sumdt, nrow = NULL, ncol = NULL, order = FALSE)
```

**Arguments**

sumdt	data.table
nrow	number
ncol	number
order	TRUE or FALSE

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% fit_lm()
object %<>% fit_limma(block = 'Subject')
sumdt <- summarize_fit(fdt(object), coefs = c('t1', 't2', 't3'))
plot_fit_summary(sumdt)
```

---

plot_heatmap	<i>Plot heatmap</i>
--------------	---------------------

---

**Description**

Plot heatmap

**Usage**

```
plot_heatmap(
  object,
  fit = fits(fdt(object))[1],
  coef = default_coefs(fdt(object), fit = fit)[1],
  effectsize = 0,
  p = 1,
  fdr = 0.05,
  n = 100,
  assay = assayNames(object)[1],
  cluster_features = FALSE,
  cluster_samples = FALSE,
  flabel = intersect(c("gene", "feature_id"), fvars(object))[1],
  group = "subgroup",
  verbose = TRUE
)
```

**Arguments**

object	SummarizedExperiment
fit	'limma', 'lm', 'lme(r)', 'wilcoxon'
coef	string: one of coefs(fdt(object))
effectsize	number: effectsize filter
p	number: p filter
fdr	number: fdr filter
n	number: n filter
assay	string: one of assayNames(object)
cluster_features	TRUE or FALSE
cluster_samples	TRUE or FALSE
flabel	string: feature label
group	sample groupvar
verbose	TRUE or FALSE

**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file, fit = 'limma')
plot_heatmap(object)
```

---

plot_matrix	<i>Plot binary matrix</i>
-------------	---------------------------

---

**Description**

Plot binary matrix

**Usage**

```
plot_matrix(mat)
```

**Arguments**

mat                    matrix

**Value**

no return (base R plot)

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
mat <- sdt(object)[, .(replicate, subgroup)]
mat$present <- 1
mat %<>% data.table::dcast(replicate ~ subgroup, value.var = 'present', fill = 0)
mat %<>% dt2mat()
plot_matrix(mat)
```

---

plot_subgroup_points	<i>Plot features</i>
----------------------	----------------------

---

**Description**

Plot features

**Usage**

```
plot_subgroup_points(
  object,
  subgroup = "subgroup",
  block = NULL,
  x = subgroup,
  color = subgroup,
  group = block,
  facet = "feature_id",
  nrow = NULL,
  scales = "free_y",
  ...,
  palette = NULL,
  fixed = list(na.rm = TRUE),
  theme = list(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1))
)
```

**Arguments**

object	SummarizedExperiment
subgroup	subgroup svar
block	block svar
x	svar mapped to x
color	svar mapped to color
group	svar mapped to group
facet	svar mapped to facets
nrow	number of rows
scales	'free_y' etc.
...	mapped aesthetics
palette	color palette (named character vector)
fixed	fixed aesthetics
theme	ggplot theme specifications

**Value**

ggplot object

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file, fit = 'limma')
idx <- order(fdata(object)$`p~t1~limma`)[1:9]
object %<>% extract(idx, )
plot_sample_boxplots( object)
plot_feature_boxplots( object)
```



```

plot_sample_boxplots(object, x = 'Time')
plot_subgroup_points( object, subgroup = 'Time')
plot_subgroup_points( object, subgroup = 'Time', block = 'Subject')

```

---

plot\_summary

*Plot summary*


---

## Description

Plot summary

## Usage

```

plot_summary(
  object,
  fit = "limma",
  formula = default_formula(object),
  block = NULL,
  label = "feature_id",
  palette = make_svar_palette(object, svar = svar)
)

```

## Arguments

object	SummarizedExperiment
fit	linmod engine : 'limma', 'lm', 'lme', 'lmer' or 'wilcoxon'
formula	model formula
block	NULL or svar
label	fvar
palette	NULL or colorvector

## Examples

```

file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% pca()
object %<>% pls(by = 'subgroup')
object %<>% fit_limma()
plot_summary(object, block = 'Subject')

```

---

`plot_venn`*Plot venn*

---

**Description**

Plot venn

**Usage**`plot_venn(x)`**Arguments**`x`            `list`**Examples**

```
x <- list(roundfruit = c('apple', 'orange'), redfruit = c('apple', 'strawberry'))
plot_venn(x)
```

---

`plot_venn_heatmap`*Plot venn heatmap*

---

**Description**

Plot venn heatmap

**Usage**`plot_venn_heatmap(x)`**Arguments**`x`            `list`**Examples**

```
x <- list(roundfruit = c('apple', 'orange'), redfruit = c('apple', 'strawberry'))
plot_venn_heatmap(x)
```

---

plot_violins	<i>Plot sample/feature violins</i>
--------------	------------------------------------

---

**Description**

Plot sample/feature violins

**Usage**

```
plot_violins(  
  object,  
  assay = assayNames(object)[1],  
  x,  
  fill,  
  color = NULL,  
  group = NULL,  
  facet = NULL,  
  nrow = NULL,  
  ncol = NULL,  
  dir = "h",  
  scales = "free",  
  labeller = label_value,  
  highlight = NULL,  
  palette = NULL,  
  fixed = list(na.rm = TRUE)  
)
```

```
plot_feature_violins(  
  object,  
  assay = assayNames(object)[1],  
  x = "feature_id",  
  fill = "feature_id",  
  color = NULL,  
  n = 9,  
  facet = NULL,  
  nrow = NULL,  
  ncol = NULL,  
  dir = "h",  
  scales = "free",  
  labeller = label_value,  
  highlight = NULL,  
  fixed = list(na.rm = TRUE)  
)
```

```
plot_sample_violins(  
  object,  
  assay = assayNames(object)[1],
```

```

x = "sample_id",
fill = if ("subgroup" %in% svars(object)) "subgroup" else "sample_id",
color = NULL,
n = 100,
facet = NULL,
nrow = NULL,
ncol = NULL,
dir = "h",
scales = "free",
labeller = label_value,
highlight = NULL,
fixed = list(na.rm = TRUE)
)

plot_subgroup_violins(
  object,
  assay = assayNames(object)[1],
  subgroup,
  x = "subgroup",
  fill = "subgroup",
  color = NULL,
  highlight = NULL,
  facet = "feature_id",
  fixed = list(na.rm = TRUE)
)

```

### Arguments

object	SummarizedExperiment
assay	string
x	svar (string)
fill	svar (string)
color	svar (string)
group	svar (string)
facet	svar (character vector)
nrow	NULL or number
ncol	NULL or number
dir	'h' or 'v' : are facets filled horizontally or vertically ?
scales	'free', 'free_x', 'free_y', or 'fixed'
labeller	label_both or label_value
highlight	fvar expressing which feature should be highlighted (string)
palette	named color vector (character vector)
fixed	fixed aesthetics
n	number
subgroup	subgroup svar

**Value**

ggplot object

**See Also**

[plot\\_exprs](#), [plot\\_densities](#)

**Examples**

```
# data
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% extract(, order(.$subgroup))
control_features <- c('biotin', 'phosphate')
fdata(object) %<>% cbind(control = .$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 = 'subgroup')
```

---

plot\_volcano

*Plot volcano*

---

**Description**

Plot volcano

**Usage**

```
plot_volcano(
  object,
  fit = fits(fdt(object))[1],
  coefs = default_coefs(fdt(object), fit = fit)[1],
  facet = if (is_scalar(fit)) "coef" else c("fit", "coef"),
  shape = if ("imputed" %in% fvars(object)) "imputed" else NULL,
  size = NULL,
  alpha = NULL,
  label = "feature_id",
  max.overlaps = 10,
  features = NULL,
  nrow = length(fit),
  p = 0.05,
  fdr = 0.05,
  xndown = NULL,
  xnup = NULL,
  title = NULL
)
```

**Arguments**

object	SummarizedExperiment
fit	'limma', 'lme', 'lm', 'wilcoxon'
coefs	character vector
facet	character vector
shape	fvar (string)
size	fvar (string)
alpha	fvar (string)
label	fvar (string)
max.overlaps	number: passed to ggrepel
features	feature ids (character vector): features to encircle
nrow	number: no of rows in plot
p	number: p cutoff for labeling
fdr	number: fdr cutoff for labeling
xndown	x position of ndown labels
xnup	x position of nup labels
title	string or NULL

**Value**

ggplot object

**Examples**

```
# Regular Usage
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% fit_limma()
object %<>% fit_lm()
plot_volcano(object, coefs = 't3', fit = 'limma') # single contrast
plot_volcano(object, coefs = c('t2', 't3'), fit = 'limma') # multiple contrasts
plot_volcano(object, coefs = c('t2', 't3'), fit = c('limma', 'lm')) # multiple contrasts and methods

# When nothing passes FDR
fdr(object) %<>% add_adjusted_pvalues('fdr', fit = 'limma', coefs = 't3')
object %<>% extract( fdrvec(fdr(object), fit = 'limma', coef = 't3') > 0.05, )
plot_volcano(object, coefs = 't3', fit = 'limma')

# Additional mappings
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file, impute = TRUE)
object %<>% fit_limma()
plot_volcano(object)
plot_volcano(object, label = 'gene')
plot_volcano(object, label = 'gene', size = 'log2maxlfq')
plot_volcano(object, label = 'gene', size = 'log2maxlfq', alpha = 'pepcounts')
plot_volcano(object, label = 'gene', features = c('hmsb'))
```

---

```
PRECURSOR_QUANTITY    diann precursor quantity
```

---

**Description**

diann precursor quantity

**Usage**

```
PRECURSOR_QUANTITY
```

**Format**

An object of class character of length 1.

---

```
preprocess_rnaseq_counts
    Preprocess RNAseq counts
```

---

**Description**

Preprocess RNAseq counts

**Usage**

```
preprocess_rnaseq_counts(
  object,
  formula = ~subgroup,
  block = NULL,
  min_count = 10,
  pseudo = 0.5,
  tpm = FALSE,
  cpm = TRUE,
  voom = TRUE,
  log2 = TRUE,
  verbose = TRUE,
  plot = TRUE
)
```

**Arguments**

object	SummarizedExperiment
formula	designmat formula
block	block svar
min_count	min count required in some samples

pseudo	added pseudocount to avoid $\log(x)=-\text{Inf}$
tpm	TRUE or FALSE : tpm normalize?
cpm	TRUE or FALSE : cpm normalize? (counts per million (scaled) reads)
voom	TRUE or FALSE : voom weight?
log2	TRUE or FALSE : log2 transform?
verbose	TRUE or FALSE : msg?
plot	TRUE or FALSE : plot?

**Value**

SummarizedExperiment

**Examples**

```
file <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
object <- .read_rnaseq_counts(file)
object$subgroup
object %<>% preprocess_rnaseq_counts()
```

---

pull\_columns                      *Pull columns in a dataframe to the front*

---

**Description**

Pull columns in a dataframe to the front

**Usage**

```
pull_columns(df, first_cols, verbose = TRUE)
```

**Arguments**

df	data.frame
first_cols	character vector: columns to be pulled to the front
verbose	TRUE (default) or FALSE

**Value**

dataframe with re-ordered columns

**Examples**

```
df <- data.frame(
  symbol = c('A1BG', 'A2M'),
  id      = c('1', '2'),
  name    = c('alpha-1-B glycoprotein', 'alpha-2-macroglobulin'),
  type    = c('proteinencoding', 'proteinencoding'))
first_cols <- c('id', 'symbol', 'location', 'uniprot')
pull_columns(df, first_cols)
```



---

read_affymetrix	<i>Read affymetrix microarray</i>
-----------------	-----------------------------------

---

**Description**

Read affymetrix microarray

**Usage**

```
read_affymetrix(celfiles)
```

**Arguments**

celfiles            string vector: CEL file paths

**Value**

RangedSummarizedExperiment

**Examples**

```
# Downloading example dataset fails 600s limit - example outcommented.
# url <- paste0('http://www.bioconductor.org/help/publications/2003/Chiaretti/chiaretti2/T33.tgz')
# localdir <- file.path(tools::R_user_dir('autonomics', 'cache'), '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))
```

---

read_contaminants	<i>Read contaminants</i>
-------------------	--------------------------

---

**Description**

Read contaminants

**Usage**

```
read_contaminants(file = download_contaminants())
```

**Arguments**

file                contaminant file

**Value**

data.table

**Examples**

```
file <- download_contaminants()
dt <- read_contaminants(file)
```

---

read\_fragpipe

*Read\_fragpipe*

---

**Description**

Read fragpipe

**Usage**

```
read_fragpipe(
  dir = getwd(),
  file = if (is_file(dir)) dir else file.path(dir, "combined_protein.tsv"),
  contaminants = FALSE,
  verbose = TRUE
)
```

**Arguments**

dir	directory with 'combined_protein.tsv'
file	'combined_protein.tsv' (full path)
contaminants	whether to include contaminants
verbose	whether to msg

**Value**

SummarizedExperiment

**Examples**

```
file <- download_data('multiorganism.combined_protein.tsv')
object <- read_fragpipe(file = file)
object
fdt(object)
sdt(object)
```

---

read\_maxquant\_phosphosites  
*Read maxquant phosphosites*

---

## Description

Read maxquant phosphosites

## Usage

```
read_maxquant_phosphosites(  
  dir = getwd(),  
  fosfile = if (is_file(dir)) dir else file.path(dir, "phospho (STY)Sites.txt"),  
  profile = file.path(dirname(fosfile), "proteinGroups.txt"),  
  fastafilename = NULL,  
  restapi = FALSE,  
  quantity = NULL,  
  subgroups = NULL,  
  invert = character(0),  
  contaminants = FALSE,  
  reverse = FALSE,  
  rm_missing_in_all_samples = TRUE,  
  localization = 0.75,  
  impute = FALSE,  
  plot = FALSE,  
  label = "feature_id",  
  pca = plot,  
  pls = plot,  
  fit = if (plot) "limma" else NULL,  
  formula = ~subgroup,  
  block = NULL,  
  coefs = NULL,  
  contrasts = NULL,  
  palette = NULL,  
  verbose = TRUE  
)  
  
read_phosphosites(...)
```

## Arguments

dir	proteingroups directory
fosfile	phosphosites file
profile	proteingroups file
fastafilename	uniprot fastafilename
restapi	TRUE or FALSE : annotate non-fastadt uniprot using uniprot restapi

quantity	'normalizedratio', 'ratio', 'correctedreporterintensity', 'reporterintensity', 'maxlfq', 'labeledintensity', 'intensity' or NULL
subgroups	NULL or string vector : subgroups to retain
invert	string vector: subgroups which require inversion
contaminants	TRUE or FALSE: retain contaminants ?
reverse	TRUE or FALSE: include reverse hits
rm_missing_in_all_samples	TRUE or FALSE
localization	number: min localization probability (for phosphosites)
impute	TRUE or FALSE: impute group-specific NA values?
plot	TRUE or FALSE
label	fvar
pca	TRUE or FALSE: run pca ?
pls	TRUE or FALSE: run pls ?
fit	model engine: 'limma', 'lm', 'lme(r)', 'wilcoxon' or NULL
formula	model formula
block	model blockvar: string or NULL
coefs	model coefficients of interest: string vector or NULL
contrasts	model coefficient contrasts of interest: string vector or NULL
palette	color palette: named string vector
verbose	TRUE or FALSE: message ?
...	maintain deprecated functions

**Value**

SummarizedExperiment

**Examples**

```

profile <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
fosfile <- system.file('extdata/billing19.phosphosites.txt', package = 'autonomics')
fastafile <- system.file('extdata/uniprot_hsa_20140515.fasta', package = 'autonomics')
subgroups <- sprintf('%s_STD', c('E00', 'E01', 'E02', 'E05', 'E15', 'E30', 'M00'))
pro <- read_maxquant_proteingroups(file = profile, subgroups = subgroups)
fos <- read_maxquant_phosphosites( fosfile = fosfile, profile = profile, subgroups = subgroups)
fos <- read_maxquant_phosphosites( fosfile = fosfile, profile = profile, fastafile = fastafile, subgroups = subgroups)

```

---

read\_maxquant\_proteingroups  
*Read maxquant proteingroups*

---

## Description

Read maxquant proteingroups

## Usage

```
read_maxquant_proteingroups(  
  dir = getwd(),  
  file = if (is_file(dir)) dir else file.path(dir, "proteinGroups.txt"),  
  fastafilename = NULL,  
  restapi = FALSE,  
  quantity = NULL,  
  subgroups = NULL,  
  invert = character(0),  
  contaminants = FALSE,  
  reverse = FALSE,  
  rm_missing_in_all_samples = TRUE,  
  impute = FALSE,  
  plot = FALSE,  
  label = "feature_id",  
  pca = plot,  
  pls = plot,  
  fit = if (plot) "limma" else NULL,  
  formula = ~subgroup,  
  block = NULL,  
  coefs = NULL,  
  contrasts = NULL,  
  palette = NULL,  
  verbose = TRUE  
)  
  
read_proteingroups(...)
```

## Arguments

dir	proteingroups directory
file	proteingroups file
fastafilename	uniprot fastafilename
restapi	TRUE or FALSE : use uniprot restapi to annotate uniprot not in fastadt ?
quantity	'normalizedratio', 'ratio', 'correctedreporterintensity', 'reporterintensity', 'maxlfq', 'labeledintensity', 'intensity' or NULL

subgroups	NULL or string vector : subgroups to retain
invert	string vector : subgroups which require inversion
contaminants	TRUE or FALSE : retain contaminants ?
reverse	TRUE or FALSE : include reverse hits ?
rm_missing_in_all_samples	TRUE or FALSE
impute	TRUE or FALSE: impute group-specific NA values?
plot	TRUE or FALSE: plot ?
label	fvar
pca	TRUE or FALSE: run pca ?
pls	TRUE or FALSE: run pls ?
fit	model engine: 'limma', 'lm', 'lme(r)', 'wilcoxon' or NULL
formula	model formula
block	model blockvar: string or NULL
coefs	model coefficients of interest: character vector or NULL
contrasts	coefficient contrasts of interest: character vector or NULL
palette	color palette : named character vector
verbose	TRUE or FALSE : message ?
...	maintain deprecated functions

## Value

SummarizedExperiment

## Examples

```
# fukuda20 - LFQ
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
pro <- read_maxquant_proteingroups(file = file)

# billing19 - Normalized Ratios
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
fastafile <- system.file('extdata/uniprot_hsa_20140515.fasta', package = 'autonomics')
subgroups <- sprintf('%s_STD', c('E00', 'E01', 'E02', 'E05', 'E15', 'E30', 'M00'))
pro <- read_maxquant_proteingroups(file = file, subgroups = subgroups)
pro <- read_maxquant_proteingroups(file = file, fastafile = fastafile, subgroups = subgroups)
```

---

read_msigt	<i>Read msigdb datatable</i>
------------	------------------------------

---

**Description**

Read msigdb datatable

**Usage**

```
read_msigt(
  file = list_files(MSIGDIR, full.names = TRUE)[1],
  collections = if (is.null(file)) NULL else switch(basename(file) %>% substr(nchar(.)
    - 4, nchar(.) - 3), Hs = c("C2:CP:REACTOME", "C5:GO:BP", "C5:GO:MF", "C5:GO:CC"), Mm
    = c("M2:CP:REACTOME", "M5:GO:BP", "M5:GO:MF", "M5:GO:CC"))
)
```

**Arguments**

file	msigdb file: one of the files in dir(MSIGDB).
collections	subset of names(MSIGCOLLECTIONS)

**Examples**

```
read_msigt()
```

---

read_olink	<i>Read olink file</i>
------------	------------------------

---

**Description**

Read olink file

**Usage**

```
read_olink(file, sample_excel = NULL, sample_tsv = NULL, by.y = "SampleID")
```

**Arguments**

file	olinkfile
sample_excel	sample excel
sample_tsv	sample tsv
by.y	sample tsv mergeby column

**Value**

SummarizedExperiment

**Examples**

```
# Example data
npxdt <- data.table::data.table(OlinkAnalyze::npx_data1)[, c(1:11, 17)]
sampledt <- data.table::data.table(OlinkAnalyze::npx_data1)[, c(1, 12:15)]
sampledt %<>% extract(!grepl('CONTROL', SampleID))
sampledt %<>% unique()
# Write to file
file <- paste0(tempfile(), '.olink.csv')
samplefile <- paste0(tempfile(), '.samples.xlsx')
data.table::fwrite(npxdt, file)
writexl::write_xlsx(sampledt, samplefile)
# Read
object <- read_olink(file, sample_excel = samplefile)
biplot(pca(object), color = 'Time', group = 'Subject', shape = 'Treatment')
```

read\_salmon

*Read salmon***Description**

Read salmon

**Usage**

```
read_salmon(dir, sfile = NULL, by = NULL, ensdb = NULL)
```

**Arguments**

dir	salmon results rootdir
sfile	samplefile
by	samplefile column to merge by
ensdb	EnsDb object

**Value**

SummarizedExperiment

**Examples**

```
# dir <- '../bh/salmon_quants'
# sfile <- '../bh/samplesheet.csv'
# by <- 'salmonDir'
# ah <- AnnotationHub::AnnotationHub()
# ensdb <- ah[['AH98078']]
# read_salmon(dir, sfile = sfile, by = 'salmonDir', ensdb = ensdb)
```



---

read_uniprotDT	<i>Read fasta hdrs</i>
----------------	------------------------

---

**Description**

Read fasta hdrs

**Usage**

```
read_uniprotDT(fastafilename, fastafields = FASTAFIELDS, verbose = TRUE)
```

```
parse_maxquant_hdrs(fastahdrs)
```

```
read_contaminantDT(force = FALSE, verbose = TRUE)
```

**Arguments**

fastafilename	string (or character vector)
fastafields	character vector : which fastahdr fields to extract ?
verbose	bool
fastahdrs	character vector
force	whether to overwrite existing file

**Value**

data.table(uniprot, protein, gene, uniprot, reviewed, existence)

**Note**

existence values are always those of the canonical isoform (no isoform-level resolution for this field)

**Examples**

```
# uniprot hdrs
fastafilename <- system.file('extdata/uniprot_hsa_20140515.fasta', package = 'autonomics')
read_uniprotDT(fastafilename)

# maxquant hdrs
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
dt <- .read_maxquant_proteingroups(file)
parse_maxquant_hdrs(dt$`Fasta headers`)

profile <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
fosfile <- system.file('extdata/billing19.phosphosites.txt', package = 'autonomics')
prodt <- .read_maxquant_proteingroups(profile)
fosdt <- .read_maxquant_phosphosites(fosfile, profile)
parse_maxquant_hdrs(prodt$`Fasta headers`)
parse_maxquant_hdrs(fosdt$`Fasta headers`)
```

```
# contaminant hdrs
  read_contaminantdt()
```

---

reexports	<i>Objects exported from other packages</i>
-----------	---

---

### Description

These objects are imported from other packages. Follow the links below to see their documentation.

**data.table** [data.table](#)

**magrittr** [%<>%](#), [%>%](#), [extract](#)

---

reset_fit	<i>Reset fit</i>
-----------	------------------

---

### Description

Reset fit

### Usage

```
reset_fit(
  object,
  fit = fits(fdt(object)),
  coefs = autonomics::coefs(fdt(object), fit = fit),
  verbose = TRUE
)
```

### Arguments

object	SummarizedExperiment
fit	character vector
coefs	character vector
verbose	TRUE or FALSE

### Examples

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
(object <- read_metabolon(file))
object %<>% reset_fit()
object %<>% fit_limma() %>% reset_fit()
object %<>% fit_limma() %>% fit_lm() %>% reset_fit()
object %<>% fit_limma() %>% fit_lm() %>% reset_fit('limma')
```

---

rm\_diann\_contaminants *Rm contaminants*

---

### Description

Rm contaminants from DIA-NN SumExp

### Usage

```
rm_diann_contaminants(  
  object,  
  contaminants = read_contaminants(),  
  verbose = TRUE  
)
```

### Arguments

object	SummarizedExperiment
contaminants	uniprot (character vector)
verbose	TRUE or FALSE

### Value

SummarizedExperiment

### Examples

```
file <- download_data('dilution.report.tsv')  
object <- read_diann_proteingroups(file)  
object %<>% rm_diann_contaminants()
```

---

rm\_missing\_in\_all\_samples

*Rm features missing in some samples*

---

### Description

Rm features missing in some samples

### Usage

```
rm_missing_in_all_samples(object, verbose = TRUE)  
  
rm_missing_in_some_samples(object, verbose = TRUE)
```

**Arguments**

object	SummarizedExperiment
verbose	TRUE (default) or FALSE

**Value**

updated object

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
rm_missing_in_all_samples( object)
rm_missing_in_some_samples(object)
```

---

`rm_unmatched_samples` *rm unmatched singleton samples*

---

**Description**

rm unmatched singleton samples

**Usage**

```
rm_unmatched_samples(
  object,
  subgroupvar = "subgroup",
  subgroupctr = slevels(object, subgroupvar)[1],
  block,
  verbose = TRUE
)
```

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

**Arguments**

object	SummarizedExperiment
subgroupvar	subgroup variable (string)
subgroupctr	control subgroup (string)
block	block variable (string)
verbose	TRUE/FALSE

**Value**

SummarizedExperiment

**Examples**

```
file <- system.file('extdata/atkin.somascan.adat', package = 'autonomics')
object <- read_somascan(file)
object %<>% filter_samples(subgroup %in% c('t1', 't2'), verbose = TRUE)
rm_singleton_samples(object, subgroupvar = 'Subject')
rm_unmatched_samples(object, subgroupvar = 'subgroup', block = 'Subject')
```

---

scaledlibsizes	<i>Get tmm-scaled libsizes</i>
----------------	--------------------------------

---

**Description**

Get tmm-scaled libsizes

**Usage**

```
scaledlibsizes(counts)
```

**Arguments**

counts            counts matrix

**Value**

scaled libsize vector

**Examples**

```
file <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
object <- read_rnaseq_counts(file)
scaledlibsizes(counts(object))
```

---

scoremat	<i>Extract scores/loadings</i>
----------	--------------------------------

---

**Description**

Extract scores/loadings

**Usage**

```
scoremat(object, method = "pca", by = biplot_by(object, method), dim = 1:2)
```

```
scores(object, method = "pca", by = biplot_by(object, method), dim = 1)
```

```
loadingmat(object, method = "pca", by = biplot_by(object, method), dim = 1:2)
```

```
loadings(object, method = "pca", by = biplot_by(object, method), dim = 1)
```

**Arguments**

object	SummarizedExperiment
method	'pca', 'pls', etc.
by	svar (string)
dim	numeric vector

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% pca()
  scores(object)[1:2]
  loadings(object)[1:2]
  scoremat(object)[1:2, ]
  loadingmat(object)[1:2, ]
```

---

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 <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
slevels(object, 'subgroup')
subgroup_levels(object)
```

---

snames	<i>Get/Set snames</i>
--------	-----------------------

---

**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**

```
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
head(snames(object))
head(snames(object) %<>% paste0('SAMPLE_', .))
```

---

split_samples	<i>Split samples</i>
---------------	----------------------

---

**Description**

Split samples by svar

**Usage**

```
split_samples(object, by = "subgroup")

cbind_imputed(objlist)

split_features(object, by)
```

**Arguments**

object	SummarizedExperiment
by	svar to split by (string)
objlist	SummarizedExperiment list

**Value**

SummarizedExperiment list

**Examples**

```
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
objlist <- split_features(object, by = 'PLATFORM')
objlist <- split_samples(object, 'Diabetes')
objlist %<>% Map(impute, .)
object <- cbind_imputed(objlist)
```

---

stri_any_regex	<i>Does any string have a regex</i>
----------------	-------------------------------------

---

**Description**

Does any string have a regex

**Usage**

```
stri_any_regex(str, pattern)
```

**Arguments**

str	string vector
pattern	string

**Value**

TRUE or FALSE



## Examples

```
str <- c('s1 Spectral Count', 's1 Unique Spectral Count')
patterns <- c('Spectral Count', '(?!Unique) Spectral Count', 'Intensity')
stringi::stri_detect_regex(str, pattern = patterns[1])
stringi::stri_detect_regex(str, pattern = patterns[2])
stringi::stri_detect_regex(str, pattern = patterns[3])
stri_any_regex(str, pattern = patterns)
```

---

stri\_detect\_fixed\_in\_collapsed

*Detect fixed patterns in collapsed strings*

---

## Description

Detect fixed patterns in collapsed strings

## Usage

```
stri_detect_fixed_in_collapsed(x, patterns, sep)
```

## Arguments

x	vector with collapsed strings
patterns	vector with fixed patterns (strings)
sep	collapse separator (string) or NULL (if uncollapsed)

## Value

boolean vector

## Examples

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
x <- fdt(object)$uniprot
patterns <- c('A0A0R4IKT8', 'Q7T3G6')
table(stri_detect_fixed_in_collapsed(x = x, patterns = patterns, sep = ';'))
```

---

subgroup_array	<i>Get subgroup matrix</i>
----------------	----------------------------

---

**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 <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object$subgroup <- paste0(object$Diabetes, '.', object$subgroup)
subgroup_matrix(object, 'subgroup')
```

---

subtract_baseline	<i>Subtract baseline</i>
-------------------	--------------------------

---

**Description**

Subtract baseline level within block

**Usage**

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

```

subtract_pairs(
  object,
  subgroupvar = "subgroup",
  subgroupctr = slevels(object, subgroupvar)[1],
  block,
  assaynames = assayNames(object)[1],
  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
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object0 <- read_metabolon(file)
pca(object0, plot = TRUE, color = 'Time')

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

# subtract_pairs: optimized for many blocks
object <- subtract_pairs(object0, block = 'Subject', subgroupvar = 'Time')

```

```

pca(object, plot = TRUE, color = 'Time')

# subtract_differences
object <- subtract_differences(object0, block = 'Subject', subgroupvar = 'Time')
values(object) %<>% na_to_zero()
pca(object, plot = TRUE, color = 'Time')

```

---

sumexplist\_to\_longdt *SummarizedExperiment list to long data.table*

---

## Description

SummarizedExperiment list to long data.table

## Usage

```

sumexplist_to_longdt(
  sumexplist,
  svars = intersect("subgroup", autonomics::svars(sumexplist[[1]])),
  fvars = intersect("gene", autonomics::fvars(sumexplist[[1]])),
  setvarname = "set"
)

```

## Arguments

sumexplist	list of SummarizedExperiments
svars	character vector
fvars	character vector
setvarname	string

## Value

data.table

## Examples

```

subgroups <- paste0(c('E00', 'E01', 'E02', 'E05', 'E15', 'E30', 'M00'), '_STD')
rnafile <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
profile <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
fosfile <- system.file('extdata/billing19.phosphosites.txt', package = 'autonomics')
rna <- read_rnaseq_counts(rnafile)
pro <- read_maxquant_proteingroups(file = profile, subgroups = subgroups)
fos <- read_maxquant_phosphosites(fosfile = fosfile, profile = profile, subgroups = subgroups)
pro$subgroup %<>% stringi::stri_replace_first_fixed('_STD', '')
fos$subgroup %<>% stringi::stri_replace_first_fixed('_STD', '')

sumexplist <- list(rna = rna, pro = pro, fos = fos)
dt <- sumexplist_to_longdt(sumexplist, setvarname = 'platform')
dt %<>% extract(gene %in% c('TNMD', 'TSPAN6'))

```

---

sumexp_to_tsv	<i>Write sumexp to tsv</i>
---------------	----------------------------

---

**Description**

Write sumexp to tsv

**Usage**

```
sumexp_to_tsv(object, assay = assayNames(object)[1], file)
```

**Arguments**

object	SummarizedExperiment
assay	string
file	filename

**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file, fit = 'limma')
tsv <- file.path(tempdir(), 'fukuda20.proteingroups.tsv')
sumexp_to_tsv(object, file = tsv)
```

---

sumexp_to_widedt	<i>SummarizedExperiment to data.table</i>
------------------	---

---

**Description**

SummarizedExperiment to data.table

**Usage**

```
sumexp_to_widedt(
  object,
  fvars = autonomics::fvars(object),
  assay = assayNames(object)[1]
)

sumexp_to_longdt(
  object,
  fvars = intersect("feature_name", autonomics::fvars(object)),
  svars = intersect("subgroup", autonomics::svars(object)),
  assay = assayNames(object) %>% intersect(c(.[1], "is_imputed"))
)

sumexp_to_subrep_dt(object, subgroup = subgroup)
```

**Arguments**

object	sumexp
fvars	additional fvars to include in table
assay	matrix in assays(object) to be used
svars	additional svars to include in table
subgroup	subgroup (sym)

**Details**

- sumexp\_to\_widedt: feature x sample
- sumexp\_to\_subrep\_dt: feature.subgroup x replicate
- sumexp\_to\_longdt: feature.sample

**Value**

data.table

**Examples**

```
# Atkin Hypoglycemia
file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
sumexp_to_widedt(object)
sumexp_to_longdt(object)
sumexp_to_subrep_dt(object)

# Fukuda
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
values(object)
fdt(object)
object %<>% impute()
table(fdt(object)$imputed)
sumexp_to_longdt(object)
sumexp_to_widedt(object)
sumexp_to_longdt(object)
```

---

summarize\_fit

*Summarize fit*

---

**Description**

Summarize fit

**Usage**

```

summarize_fit(
  featuredt,
  fit = fits(featuredt),
  coefs = autonomics::coefs(featuredt, fit = fit)
)

```

**Arguments**

```

featuredt      fdt(object)
fit             'limma', 'lme', 'lm', 'lme', 'wilcoxon' or NULL
coefs          string vector

```

**Value**

```

data.table(contrast, nup, ndown)

```

**Examples**

```

file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file)
object %<>% fit_limma()
object %<>% fit_lm()
summarize_fit(fdt(object), coefs = c('t1', 't2', 't3'))

```

---

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 <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
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 factor with variable names



**Value**

sample variable names (get) or updated SummarizedExperiment

**Examples**

```
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
svars(object)[1]
(svars(object)[1] %<>% paste0('1'))
```

---

systematic_nas	<i>Is systematic/random/full NA</i>
----------------	-------------------------------------

---

**Description**

Is systematic/random/full NA

**Usage**

```
systematic_nas(object, by = "subgroup", frac = 0.5)
random_nas(object, by = "subgroup")
no_nas(object)
```

**Arguments**

object	SummarizedExperiment
by	svar (string)
frac	fraction

**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
table(systematic_nas(object)) # missing in some subgroups, present in others
table(random_nas(object))   # missing in some samples, independent of subgroup
table(no_nas(object))       # missing in no samples
```

---

tag_features	<i>Tag features</i>
--------------	---------------------

---

## Description

Tag features

## Usage

```
tag_features(
  object,
  keyvar,
  sep,
  features,
  tagvar = get_name_in_parent(features),
  verbose = TRUE
)
```

## Arguments

object	SummarizedExperiment
keyvar	string : intersection fvar
sep	string : keyvar collapse separator
features	character vector : intersection set
tagvar	string :
verbose	TRUE or FALSE

## Value

SummarizedExperiment

## Examples

```
file <- system.file('extdata/atkin.somascan.adat', package = 'autonomics')
object <- read_somascan(file)
features <- AnnotationDbi::keys(org.Hs.eg.db::org.Hs.eg.db, keytype = 'SYMBOL')
object %<>% tag_features(keyvar = 'EntrezGeneSymbol', sep = ' ', features)
table(fdt(object)$features)
```

---

tag_hdlproteins	<i>Tag hdlproteins</i>
-----------------	------------------------

---

**Description**

Tag hdlproteins

**Usage**

```
tag_hdlproteins(object, verbose = TRUE)
```

**Arguments**

object	SummarizedExperiment
verbose	TRUE or FALSE

**Value**

SummarizedExperiment

**Examples**

```
file <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
object %<>% tag_hdlproteins()
fdt(object)
```

---

TAXON_TO_ORGNAME	<i>Annotation Maps</i>
------------------	------------------------

---

**Description**

Annotation Maps

**Usage**

```
TAXON_TO_ORGNAME
ABBREV_TO_ORGNAME
REVIEWED_TO_NUMBER
EXISTENCE_TO_NUMBER
```

**Format**

An object of class character of length 7.

An object of class character of length 4.

An object of class character of length 2.

An object of class numeric of length 4.

**Examples**

```
TAXON_TO_ORGNAME['9606']
ABBREV_TO_ORGNAME['HSA']
REVIEWED_TO_NUMBER['reviewed']
EXISTENCE_TO_NUMBER['Evidence at protein level']
```

---

TESTS

*Statistical models supported in autonomies*

---

**Description**

Statistical models supported in autonomies

**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 <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
object <- read_rnaseq_counts(file, plot=FALSE)
tpm(object) <- values(object)
tpm(object)[1:3, 1:3]

```

---

uncollapse

*Uncollapse/Recollapse*


---

**Description**

Uncollapse data.table cols

**Usage**

```

uncollapse(dt, ..., sep = ";")

recollapse(dt, by, sep = ";")

```

**Arguments**

dt	data.table
...	cols
sep	string
by	string

**Examples**

```
(dt <- data.table::data.table(
  uniprot = 'Q9BQL6;Q96AC1;Q96AC1-3',
  protein = 'FERM1_HUMAN;FERM2_HUMAN',
  gene    = 'FERMT1;FERMT2'))
(dt %<>% uncollapse(protein, gene, sep = ';'))
(dt %>% recollapse(by = 'uniprot'))
```

---

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 <- system.file('extdata/billing19.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
values(object)[1:3, 1:3]
values(object) <- 0
values(object)[1:3, 1:3]
```

---

varlevels\_dont\_clash *Are varlevels unique*

---

**Description**

Are varlevels unique

**Usage**

```
varlevels_dont_clash(object, ...)
```

```
## S3 method for class 'data.table'
varlevels_dont_clash(object, vars = names(object), ...)
```

```
## S3 method for class 'SummarizedExperiment'
varlevels_dont_clash(object, vars = svars(object), ...)
```

**Arguments**

object	SummarizedExperiment or data.table
...	required for s3 dispatch
vars	character vector

**Value**

TRUE or FALSE

**Examples**

```
require(data.table)
object1 <- data.table(expand.grid(genome = c('WT', 'MUT'), treat = c('control', 'drug')))
object2 <- data.table(expand.grid(mutant = c('YES', 'NO'), treated = c('YES', 'NO')))
varlevels_dont_clash(object1)
varlevels_dont_clash(object2)
```

---

venn_detects	<i>Venn detects</i>
--------------	---------------------

---

**Description**

Venn diagram full/consistent/random detects

**Usage**

```
venn_detects(object, by = "subgroup")
```

**Arguments**

object	SummarizedExperiment
by	svar (string)

**Value**

NULL

**Examples**

```
file <- system.file('extdata/fukuda20.proteingroups.txt', package = 'autonomics')
object <- read_maxquant_proteingroups(file)
venn_detects(object, 'subgroup')
```

---

weights	<i>Get/Set weights</i>
---------	------------------------

---

**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
...	additional params
value	ratio matrix (features x samples)

**Value**

weight matrix (get) or updated object (set)

**Examples**

```
file <- system.file('extdata/billing19.rnacounts.txt', package = 'autonomics')
object <- read_rnaseq_counts(file)
weights(object)[1:3, 1:2]
weights(object) <- 1
weights(object)[1:3, 1:2]
```

---

write_xl	<i>Write xl/ods</i>
----------	---------------------

---

**Description**

Write xl/ods

**Usage**

```
write_xl(object, xlfile, fitcoefs = autonomics::fitcoefs(object))

write_ods(object, odsfile, fitcoefs = autonomics::fitcoefs(object))
```

**Arguments**

object	SummarizedExperiment
xlfile	file
fitcoefs	character vector
odsfile	file

**Value**

filepath

**Examples**

```

file <- system.file('extdata/atkin.metabolon.xlsx', package = 'autonomics')
object <- read_metabolon(file, fit = 'limma')
xlfile <- file.path(tempdir(), 'fukuda20.proteingroups.fdt.xlsx')
odsfile <- file.path(tempdir(), 'fukuda20.proteingroups.fdt.ods')
# write_xl(object, xlfile)
# write_ods(object, odsfile)

```

---

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)

na_to_string(x)

```

**Arguments**

x	matrix
verbose	logical(1)

**Value**

Updated matrix

**Examples**

```

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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