Package 'prolfqua'

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Type Package

Title Proteomics Label Free Quantification

Version 0.99.4

Description The prolfqua package integrates essential steps
of the mass spectrometry based label free quantification data
analysis workflow: quality control, data normalization, protein aggregation,
modeling, hypothesis testing and sample size estimation.
We use prolfqua to : develop highly customizable, visually appealing,
and interactive data analysis reports in pdf or HTML format;
to visualize and model simple experimental designs
with a single explanatory variable and complex experiments with multiple factors;
to benchmark data acquisition,
data preprocessing or data modeling methods.
We developed and improved the package by applying the ``Eating your own dog food" principle,
when analysing dozens of proteomics datasets.

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BugReports https://github.com/fgcz/prolfqua/issues

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UpSetR, withr

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`prolfqua-package` *prolfqua: Proteomics Label Free Quantification*

Description

The prolfqua package integrates essential steps of the mass spectrometry based label free quantification data analysis workflow: quality control, data normalization, protein aggregation, modeling, hypothesis testing and sample size estimation. We use prolfqua to : develop highly customizable, visually appealing, and interactive data analysis reports in pdf or HTML format; to visualize and model simple experimental designs with a single explanatory variable and complex experiments with multiple factors; to benchmark data acquisition, data preprocessing or data modeling methods. We developed and improved the package by applying the "Eating your own dog food" principle, when analysing dozens of proteomics datasets.

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See Also

Useful links:

- https://github.com/fgcz/prolfqua
- https://fgcz.github.io/prolfqua/
- Report bugs at https://github.com/fgcz/prolfqua/issues

.get_robscales *compute median and mad on matrix*

Description

compute median and mad on matrix

Usage

```
.get_robscales(data, dim = 2)
```

.lfqdata_to_elist *Convert LFQData to limma EList with design matrix and metadata*

Description

Shared preamble for all `build_model_limma*` and `build_model_limpa` functions. Pivots LFQData to wide format, builds the design matrix from the formula, resolves the subject_id / isotopeLabel, and creates a dummy lm for linfct extraction.

Usage

```
.lfqdata_to_elist(lfqdata, formula)
```

Arguments

`lfqdata`	an `LFQData` object
`formula`	a formula (with response and RHS)

Value

a list with components:

elist limma EList with `$E` = expression matrix

expr_matrix the expression matrix (same as `elist$E`)

design the design matrix

annotation sample-level annotation data.frame

subject_id character vector of hierarchy keys (possibly including isotopeLabel)

rowdata data.frame with one row per feature, columns = subject_id

rhs_formula the RHS-only formula

dummy_model a dummy `lm` fitted on one complete row

.make_progress *Build a progress reporter for the per-protein / per-contrast loops*

Description

Internal factory used by ‘model_analyse()‘ and the contrast loops. The returned object exposes ‘$tick(len = 1, tokens = list())‘, the same contract as ‘progress::progress_bar‘, so call sites are agnostic to which reporter they received.

Usage

```
.make_progress(
  total,
  label = NULL,
  reporter = getOption("prolfqua.progress", NULL)
)
```

Arguments

total	number of iterations; ‘<= 0‘ yields a no-op reporter.
label	short label naming the pass (e.g. "firth multi-peptide").
reporter	reporter selector; see Details. Defaults to ‘getOption("prolfqua.progress", NULL)‘.

Details

The ‘reporter‘ argument (defaulting to the ‘prolfqua.progress‘ option) selects the mode:

- ‘NULL‘ – the legacy ‘progress::progress_bar‘ (terminal, unchanged).
- a ‘function(i, total, label)‘ – a throttled user callback, e.g. one that calls ‘logger::log_info()‘.
- ‘"message"‘ – a throttled ‘message()‘ heartbeat with elapsed/ETA.

Value

an object with a ‘$tick()‘ method.

.resolve_weights *Resolve strategy weights to a matrix or vector for limma::lmFit*

Description

Shared weight resolution logic for `build_model_limma*` functions. Handles character (column name in annotation or LFQData), matrix, or NULL.

Usage

```
.resolve_weights(lfqdata, strategy, annotation)
```

Arguments

lfqdata	an LFQData object
strategy	a strategy object with a weights field
annotation	the sample-level annotation data.frame

Value

a weight matrix, vector, or NULL

---

adjust_p_values *adjust columns*

Description

adjust columns

Usage

```
adjust_p_values(
  contrast_df,
  column = "p.value",
  group_by_col = "contrast",
  newname = "FDR"
)
```

Arguments

contrast_df	data.frame with p-values to adjust
column	name of column containing p-values
group_by_col	column(s) to group by before adjusting (e.g. contrast), or NULL for no grouping
newname	name of the new column with adjusted p-values

Value

The computed result.

Examples

```
bb <- c(runif(1000), rexp(1500,rate=5))
length(bb)
bb <- bb[bb < 1]
length(bb)
bb <- bb[1:2000]
hist(bb)
data <- data.frame(contrast = rep(LETTERS[1:5],400), p.value = bb)

dataX <- adjust_p_values(data)
Adata <- dataX |> dplyr::filter(contrast == "A")
stopifnot(all.equal(Adata$FDR, p.adjust(Adata$p.value, method="BH")))
data2 <- adjust_p_values(data, group_by_col = NULL)
stopifnot(all.equal(data2$FDR, p.adjust(data2$p.value, method="BH")))
```

AggregateLimpa *AggregateLimpa*

Description

AggregateLimpa

AggregateLimpa

Details

Aggregates peptide/precursor intensities to protein level using limpa's probabilistic DPC-based quantification (`limpa::dpcQuant`). With `impute_only = TRUE`, performs same-level imputation without aggregation using `limpa::dpcQuantByRow`.

The output LFQData contains three value columns:

- intensity (`"limpa"`) — protein-level log-expression (complete, no NAs)
- standard error (in `config$opt_se`) — per-protein, per-sample posterior SEs
- observation count (in `config$nr_children`) — number of observed precursors

Value

An R6 class generator.

Super class

`prolfqua::AggregatorBase` -> `AggregateLimpa`

Public fields

`dpc_result` estimated DPC object from limpa::dpc

`dpc_slope` DPC slope parameter (default 0.8)

`impute_only` if TRUE use dpcQuantByRow (no aggregation)

Methods

Public methods:

- `AggregateLimpa$new()`
- `AggregateLimpa$aggregate()`
- `AggregateLimpa$plot()`
- `AggregateLimpa$write_plots()`
- `AggregateLimpa$clone()`

Method `new()`**:** initialize

Usage:

```
AggregateLimpa$new(
  lfq,
  prefix = "protein",
  dpc_slope = 0.8,
  impute_only = FALSE
)
```

Arguments:

`lfq` LFQData with log2-transformed intensities

`prefix` default "protein"

`dpc_slope` DPC slope parameter passed to limpa (default 0.8)

`impute_only` if TRUE, use dpcQuantByRow instead of dpcQuant

Method `aggregate()`**:** run limpa DPC-based aggregation (or imputation)

Usage:

```
AggregateLimpa$aggregate()
```

Returns: LFQData

Method `plot()`**:** creates aggregation plots (only for aggregation mode, not impute_only)

Usage:

```
AggregateLimpa$plot(subset = NULL, show.legend = FALSE)
```

Arguments:

`subset` create plots for a subset of the data only

`show.legend` default FALSE

Returns: data.frame

Method `write_plots()`**:** writes plots to folder

Usage:

```
AggregateLimpa$write_plots(
  qcpath,
  subset = NULL,
  show.legend = FALSE,
  width = 6,
  height = 6
)
```

Arguments:

`qcpath` qcpath

`subset` write plots only for some

`show.legend` legend

`width` figure width

`height` figure height

Returns: file path

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
AggregateLimpa$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other LFQData: `AggregateMedpolish`, `AggregateRlm`, `AggregateTopN`, `AggregatorBase`, `LFQData`, `LFQDataPlotter`, `LFQDataStats`, `LFQDataSummariser`, `LFQDataToSummarizedExperiment()`

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config()
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata <- lfqdata$get_Transformer()$log2()$lfq

agg <- AggregateLimpa$new(lfqdata, "protein")
agg$aggregate()
agg$lfq_agg$data_wide()
```

AggregateMedpolish *AggregateMedpolish*

Description

AggregateMedpolish

AggregateMedpolish

Details

Aggregates peptide intensities to protein level using median polish. Works best with variance-stabilized (log-transformed) intensities.

Value

An R6 class generator.

Super class

`prolfqua::AggregatorBase` -> `AggregateMedpolish`

Methods

Public methods:

- `AggregateMedpolish$aggregate()`
- `AggregateMedpolish$clone()`

Method `aggregate()`**:** run median polish aggregation

Usage:

```
AggregateMedpolish$aggregate()
```

Returns: LFQData

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
AggregateMedpolish$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

Other LFQData: `AggregateLimpa`, `AggregateRlm`, `AggregateTopN`, `AggregatorBase`, `LFQData`, `LFQDataPlotter`, `LFQDataStats`, `LFQDataSummariser`, `LFQDataToSummarizedExperiment()`

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config()
data <- istar$data |> dplyr::filter(protein_Id %in% sample(protein_Id, 100))
lfqdata <- LFQData$new(data, istar$config)
lfqTrans <- lfqdata$clone()$get_Transformer()$log2()$robscale()$lfq

agg <- AggregateMedpolish$new(lfqTrans, "protein")
agg$aggregate()
p <- agg$plot()
p$plots[[1]]
```

`AggregateRlm` *AggregateRlm*

Description

AggregateRlm

AggregateRlm

Details

Aggregates peptide intensities to protein level using robust regression (rlm). Works best with variance-stabilized (log-transformed) intensities.

Value

An R6 class generator.

Super class

`prolfqua::AggregatorBase` -> `AggregateRlm`

Methods

Public methods:

- `AggregateRlm$aggregate()`
- `AggregateRlm$clone()`

Method `aggregate()`**:** run robust regression aggregation

Usage:

```
AggregateRlm$aggregate()
```

Returns: LFQData

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
AggregateRlm$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

Other LFQData: AggregateLimpa, AggregateMedpolish, AggregateTopN, AggregatorBase, LFQData, LFQDataPlotter, LFQDataStats, LFQDataSummariser, LFQDataToSummarizedExperiment()

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config()
data <- istar$data |> dplyr::filter(protein_Id %in% sample(protein_Id, 100))
lfqdata <- LFQData$new(data, istar$config)
lfqTrans <- lfqdata$clone()$get_Transformer()$log2()$robscale()$lfq

agg <- AggregateRlm$new(lfqTrans, "protein")
agg$aggregate()
p <- agg$plot()
p$plots[[1]]
```

AggregateTopN *AggregateTopN*

Description

AggregateTopN

AggregateTopN

Details

Aggregates peptide intensities to protein level using top N peptides. Works with raw (untransformed) intensities.

Value

An R6 class generator.

Super class

prolfqua::AggregatorBase -> AggregateTopN

Public fields

`N` top N peptides by intensity

`func` aggregation function name: "sum" or "mean"

Methods

Public methods:

- AggregateTopN$new()
- AggregateTopN$aggregate()
- AggregateTopN$clone()

Method `new()`**:** initialize

Usage:

```
AggregateTopN$new(lfq, prefix = "protein", N = 3, func = "sum")
```

Arguments:

`lfq` LFQData

`prefix` default protein

`N` top N peptides (default 3)

`func` "sum" or "mean" (default "sum")

Method `aggregate()`**:** run top N aggregation

Usage:

```
AggregateTopN$aggregate()
```

Returns: LFQData

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
AggregateTopN$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other LFQData: `AggregateLimpa`, `AggregateMedpolish`, `AggregateRlm`, `AggregatorBase`, `LFQData`, `LFQDataPlotter`, `LFQDataStats`, `LFQDataSummariser`, `LFQDataToSummarizedExperiment()`

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config()
data <- istar$data |> dplyr::filter(protein_Id %in% sample(protein_Id, 100))
lfqdata <- LFQData$new(data, istar$config)

agg <- AggregateTopN$new(lfqdata, "protein", N = 3, func = "sum")
agg$aggregate()
p <- agg$plot()
p$plots[[1]]

agg_mean <- AggregateTopN$new(lfqdata, "protein", N = 3, func = "mean")
agg_mean$aggregate()
protPlotter <- agg_mean$lfq_agg$get_Plotter()
protPlotter$heatmap()
agg_mean$write_plots(tempdir())
```

---

aggregate_intensity_top_n

Aggregates top N intensities

Description

run `rank_peptide_by_intensity` first

Usage

```
aggregate_intensity_top_n(ranked_data, lfqdata, .func, N = 3)
```

Arguments

ranked_data	data.frame with ranked peptides
lfqdata	LFQData object
.func	function to use for aggregation
N	default 3 top intensities.

Value

list with data and new reduced configuration (config)

See Also

Other aggregation: INTERNAL_FUNCTIONS_BY_FAMILY, estimate_intensity(), plot_estimate(), plot_hierarchies_line()

Examples

```
dd <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(dd$data, dd$config)
ranked <- rank_peptide_by_intensity(lfq$data_long(), lfq$response(), lfq$hierarchy_keys())

mean_f <- function(x, name = FALSE) {
  if (name) return("mean")
  mean(x, na.rm = TRUE)
}

resTOPN <- aggregate_intensity_top_n(ranked, lfq, .func = mean_f, N = 3)
stopifnot(names(resTOPN) %in% c("data", "config"))
lfq_agg <- LFQData$new(resTOPN$data, resTOPN$config)
tmpRob <- plot_estimate(lfq, lfq_agg, show.legend = TRUE)
stopifnot("ggplot" %in% class(tmpRob$plots[[4]]))
```

AggregatorBase *Base class of the peptide to protein aggregators*

Description

Base class of the peptide to protein aggregators

Base class of the peptide to protein aggregators

Details

Holds the fields, construction, and plotting shared by AggregateMedpolish, AggregateRlm, AggregateTopN and AggregateLimpa. Subclasses implement aggregate().

Value

An R6 class generator.

Public fields

`lfq` LFQData

`lfq_agg` aggregation result

`prefix` to use for aggregation results e.g. protein

Methods

Public methods:

- `AggregatorBase$new()`
- `AggregatorBase$plot()`
- `AggregatorBase$write_plots()`
- `AggregatorBase$clone()`

Method `new()`**:** initialize

Usage:

```
AggregatorBase$new(lfq, prefix = "protein")
```

Arguments:

`lfq` LFQData

`prefix` default protein

Method `plot()`**:** creates aggregation plots

Usage:

```
AggregatorBase$plot(subset = NULL, show.legend = FALSE)
```

Arguments:

`subset` create plots for a subset of the data only

`show.legend` default FALSE

Returns: data.frame

Method `write_plots()`**:** writes plots to folder

Usage:

```
AggregatorBase$write_plots(
  qcpath,
  subset = NULL,
  show.legend = FALSE,
  width = 6,
  height = 6
)
```

Arguments:

`qcpath` qcpath

`subset` write plots only for some

`show.legend` legend

`width` figure width

`height` figure height

Returns: file path

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
AggregatorBase$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other LFQData: `AggregateLimpa`, `AggregateMedpolish`, `AggregateRlm`, `AggregateTopN`, `LFQData`, `LFQDataPlotter`, `LFQDataStats`, `LFQDataSummariser`, `LFQDataToSummarizedExperiment()`

`AnalysisConfiguration` *Analysis Configuration*

Description

Analysis Configuration — holds all table annotations, hierarchy definitions, factor definitions, and analysis parameters in a single flat object.

Value

An R6 class generator.

Public fields

`sep` separator to use when uniting columns is necessary

`file_name` column name of column containing raw file names

`sample_name` (will be generated from factors or file_name)

`norm_value` optional column with normalization values (e.g., Creatinine)

`isotope_label` which column contains the isotope label (e.g. heavy or light), or light only if LFQ.

`ident_q_value` column name with identification QValues (smaller better)

`ident_score` column with identification score (larger better)

`opt_rt` optional column with rt information

`opt_mz` optional column with mz information

`opt_se` optional column with standard errors (e.g. from limpa aggregation)

`nr_children` optional column containing for instance the number of peptides

`work_intensity` column which contains the intensities

`is_response_transformed` are the intensities transformed for constant variance

`bin_resp` column with encoded missing information

`pattern_decoys` optional regex identifying decoy / reverse-database ids, unioned with the built-in default prefixes (see `is_decoy`). `NULL` (default) leaves decoy handling off; set it (even to `""` for defaults only) to opt into flagging and the targets-only model fit.

`pattern_contaminants` optional regex identifying contaminant ids (keratin, trypsin, BSA, ...). `NULL` (default) means contaminants are not flagged; set it to enable contaminant flagging / removal.

`factors` Names of columns containing factors (annotations)

`factor_depth` number of relevant factors (used by plotting functions etc)

`hierarchy` list with columns describing the measurement hierarchy (i.e. protein peptide precursor fragment)

`hierarchy_depth` At which depth do you want to model i.e. protein than 1

`min_peptides_protein` minimum number of peptides per protein

Methods

Public methods:

- `AnalysisConfiguration$set_response()`
- `AnalysisConfiguration$get_response()`
- `AnalysisConfiguration$pop_response()`
- `AnalysisConfiguration$factor_keys()`
- `AnalysisConfiguration$factor_keys_depth()`
- `AnalysisConfiguration$hierarchy_keys()`
- `AnalysisConfiguration$hierarchy_keys_depth()`
- `AnalysisConfiguration$id_vars()`
- `AnalysisConfiguration$value_vars()`
- `AnalysisConfiguration$annotation_vars()`
- `AnalysisConfiguration$clone()`

Method `set_response()`**:** Add name of intensity column

Usage:

```
AnalysisConfiguration$set_response(col_name)
```

Arguments:

`col_name` name of intensity column

Method `get_response()`**:** Get name of working intensity column

Usage:

```
AnalysisConfiguration$get_response()
```

Method `pop_response()`**:** Remove last name in array of working intensity column names

Usage:

```
AnalysisConfiguration$pop_response()
```

Method `factor_keys()`**:** Get factor keys

Usage:

```
AnalysisConfiguration$factor_keys()
```

Returns: array with keys

Method `factor_keys_depth()`**:** Get factor keys till factorDepth

Usage:

```
AnalysisConfiguration$factor_keys_depth()
```

Method `hierarchy_keys()`**:** get hierarchy keys

Usage:

```
AnalysisConfiguration$hierarchy_keys()
```

Returns: array of column names

Method `hierarchy_keys_depth()`**:** get hierarchy keys up to depth

Usage:

```
AnalysisConfiguration$hierarchy_keys_depth(names = TRUE)
```

Arguments:

`names` if TRUE names only if FALSE key value pairs

Returns: array of column names

Method `id_vars()`**:** get names of columns annotating values (e.g. intensities)

Usage:

```
AnalysisConfiguration$id_vars()
```

Returns: character array

Method `value_vars()`**:** get names of columns containing observations e.g. (intensity, qValue, mz or rt)

Usage:

```
AnalysisConfiguration$value_vars()
```

Method `annotation_vars()`**:** get names of columns with sample annotations

Usage:

```
AnalysisConfiguration$annotation_vars()
```

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
AnalysisConfiguration$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other configuration: `ContrastConfiguration`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `R6_extract_values()`, `complete_cases()`, `list_to_ContrastConfiguration()`, `make_interaction_column()`, `make_reduced_hierarch`
`sample_subset()`, `separate_hierarchy()`, `setup_analysis()`, `table_factors()`, `table_factors_size()`

Examples

```
istar <- sim_lfq_data_peptide_config()
config <- istar$config
stopifnot("AnalysisConfiguration" %in% class(config))
stopifnot(length(config$hierarchy_keys()) > 0)
stopifnot(length(config$factor_keys()) > 0)
stopifnot(length(config$get_response()) == 1)
```

`annotation_add_contrasts` *DRY function: process and export annotated contrasts*

Description

DRY function: process and export annotated contrasts

Usage

```
annotation_add_contrasts(
  df,
  primary_col,
  secondary_col,
  prefix = "G_",
  dataset_id = "dataset",
  decreasing = FALSE,
  interactions = TRUE
)
```

Arguments

`df`	data.frame with annotation data
`primary_col`	character, name of the primary factor column
`secondary_col`	character, name of the secondary factor column
`prefix`	character, prefix for output naming (default "G_")
`dataset_id`	character, dataset identifier for output naming
`decreasing`	logical, if TRUE sort factor levels in decreasing order
`interactions`	logical, if TRUE include interaction contrasts

Value

Contrast definitions or contrast results.

See Also

Other contrasts: `generate_contrasts()`, `generate_contrasts_for_factor()`, `interaction_contrasts()`, `level_specific_contrasts()`, `main_effect_contrasts()`

Examples

```
data("x5463yzwer453bbb", package = "prolfqua")
annotation_add_contrasts(x5463yzwer453bbb, "factor_A", "factor_B", "primary")
annotation_add_contrasts(x5463yzwer453bbb, "factor_B", "factor_A", "secondary")
```

`AnovaExtractor` *R6 class for extracting ANOVA results as a data frame*

Description

R6 class for extracting ANOVA results as a data frame

R6 class for extracting ANOVA results as a data frame

Details

Wraps the ANOVA extraction logic and associated column names.

Value

An R6 class generator.

Public fields

`test` statistical test type ("F", "Chisq", etc.)

`col_pval` p-value column name in ANOVA output

Methods

Public methods:

- `AnovaExtractor$new()`
- `AnovaExtractor$fun()`
- `AnovaExtractor$clone()`

Method `new()`**:** Create a new AnovaExtractor

Usage:

```
AnovaExtractor$new(test = "F")
```

Arguments:

`test` statistical test type

Method `fun()`**:** Extract ANOVA table from a fitted model

Usage:

```
AnovaExtractor$fun(x)
```

Arguments:

`x` a fitted model

Returns: data.frame with factor column and ANOVA statistics

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
AnovaExtractor$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImputeFacade, ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
extractor <- AnovaExtractor$new(test = "F")
fit <- stats::lm(Sepal.Length ~ Species, data = iris)
res <- extractor$fun(fit)
stopifnot("factor" %in% colnames(res))
```

---

apply_to_response_matrix

Apply function requiring a matrix to tidy table

Description

Apply function requiring a matrix to tidy table

Usage

```
apply_to_response_matrix(lfqdata, .func, .funcname = NULL)
```

Arguments

lfqdata	LFQData object
.func	function taking and returning a matrix
.funcname	name of function (used for creating new column)

Value

list with ‘data‘ (data.frame) and ‘colname‘ (new column name)

See Also

Other preprocessing: INTERNAL_FUNCTIONS_BY_FAMILY, filter_proteins_by_peptide_count(), get_robscales(), nr_B_in_A(), robust_scale(), scale_with_subset()

Examples

```
bb <- sim_lfq_data_peptide_config(Nprot = 100)
lfqdata <- LFQData$new(bb$data, bb$config)
res <- apply_to_response_matrix(lfqdata, .func = base::scale)
stopifnot("abundance_base..scale" %in% colnames(res$data))

res <- apply_to_response_matrix(lfqdata, .func = robust_scale)

if (require("vsn")) {
  res <- apply_to_response_matrix(lfqdata, .func = vsn::justvsn)
}
```

---

build_contrast_analysis

Build a contrast analysis using one of several statistical methods

---

Description

A builder function that dispatches to the appropriate facade class based on the chosen method. Each facade encapsulates the full pipeline from strategy construction through modelling to contrast computation.

Usage

```
build_contrast_analysis(lfqdata, modelstr, contrasts, method = "lm", ...)
```

Arguments

lfqdata	an LFQData object
modelstr	model formula string without the response variable (e.g. "~ group_"). The response is taken automatically from lfqdata$get_config()$get_response().
contrasts	named character vector of contrasts (e.g. c("A_vs_B" = "group_A - group_B"))
method	a registered facade key. The built-in keys are "lm", "lm_impute", "limma", "limma_impute", "limma_voom", "limma_voom_impute", "limpa", "limpa_nested", "rlm", "rfit", "rfit_impute", "deqms", "deqms_voom", "firth", "firth_nested", "binomial_nested", "lmer_nested", "ropeca_nested"; downstream packages may add more via register_facade. The authoritative list is names(list_facades()). Defaults to "lm".
...	additional arguments forwarded to the underlying strategy function (e.g. trend, robust for strategy_limma)

Value

one of ContrastsLimmaFacade, ContrastsLMFacade, ContrastsRLMFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsLmerNestedFacade, ContrastsLMImputeFacade, ContrastsDEqMSFacade ContrastsROPECANestedFacade, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLimpaFacade ContrastsBinomialNestedFacade, or ContrastsLimpaNestedFacade

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 20)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")

fa_lm    <- build_contrast_analysis(lfqdata, "~ group_", contrasts, method = "lm")
head(fa_lm$get_contrasts())

fa_limma <- build_contrast_analysis(lfqdata, "~ group_", contrasts, method = "limma")
head(fa_limma$get_contrasts())

fa_deqms <- build_contrast_analysis(lfqdata, "~ group_", contrasts, method = "deqms")
head(fa_deqms$get_contrasts())

istar_pep <- sim_lfq_data_peptide_config()
lfqdata_pep <- LFQData$new(istar_pep$data, istar_pep$config)
lfqdata_pep <- lfqdata_pep$get_Transformer()$log2()$lfq

fa_lmer <- build_contrast_analysis(
  lfqdata_pep,
  "~ group_ + (1 | peptide_Id) + (1 | sampleName)",
  contrasts,
  method = "lmer_nested"
```

```
)
head(fa_lmer$get_contrasts())

fa_ropeca <- build_contrast_analysis(lfqdata_pep, "~ group_", contrasts, method = "ropeca_nested")
head(fa_ropeca$get_contrasts())

fa_firth <- build_contrast_analysis(lfqdata, "~ group_", contrasts, method = "firth")
head(fa_firth$get_contrasts())
```

`build_model` *Build protein models from data*

Description

Build protein models from data

Usage

```
build_model(
  data,
  model_strategy,
  subject_id = if ("LFQData" %in% class(data)) {
     data$subject_id()
 } else {

    "protein_Id"
 },
  model_name = model_strategy$model_name
)
```

Arguments

`data`	data - a data frame or LFQData object
`model_strategy`	model strategy object (e.g. from strategy_lmer or strategy_lm)
`subject_id`	grouping variable
`model_name`	model name

Value

a object of class `Model`

See Also

`model_analyse`, `strategy_lmer` `strategy_lm`

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu`
`ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste`
`ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`,

Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
D <- prolfqua::sim_lfq_data_peptide_config(Nprot = 20, weight_missing = 0.1)
D$data$abundance |> is.na() |> sum()
D <- prolfqua::sim_lfq_data_peptide_config(Nprot = 20, weight_missing = 0.1, seed =3)
D$data$abundance |> is.na() |> sum()
model_name <- "f_condtion_r_peptide"
formula_randomPeptide <-
  strategy_lmer("abundance  ~ group_ + (1 | peptide_Id) + (1 | sampleName)",
   model_name = model_name)


mod <- prolfqua::build_model(
 D$data,
 formula_randomPeptide,
 model_name = model_name,
 subject_id = D$config$hierarchy_keys_depth())
aovtable <- mod$get_anova()

mod <- prolfqua::build_model(
 LFQData$new(D$data, D$config),
 formula_randomPeptide,
 model_name = model_name)
model_summary(mod)
```

---

build_model_glm_peptide

Build Firth logistic model for nested LFQData

Description

Encodes missingness as a binary response and fits the peptide-aware Firth logistic backend. Proteins with multiple child features are fitted with the lowest hierarchy key appended to the formula.

Usage

```
build_model_glm_peptide(lfqdata, modelstr)
```

Arguments

lfqdata	nested LFQData object
modelstr	model formula string without the response variable (e.g. "~ group_")

Value

a ModelFirth object

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_peptide_config(
  Nprot = 10, with_missing = TRUE, weight_missing = 0.5, seed = 3)
lfqdata <- LFQData$new(istar$data, istar$config)
mod <- build_model_glm_peptide(lfqdata, "~ group_")
head(mod$get_coefficients())
```

---

build_model_glm_protein

Build Firth logistic model for aggregated LFQData

Description

Encodes missingness as a binary response and fits the Firth logistic backend used by the missingness model path in prolfquapp.

Usage

```
build_model_glm_protein(lfqdata, modelstr)
```

Arguments

lfqdata	aggregated LFQData object
modelstr	model formula string without the response variable (e.g. "~ group_")

Value

a ModelFirth object

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(
  Nprot = 10, with_missing = TRUE, weight_missing = 0.5, seed = 3)
lfqdata <- LFQData$new(istar$data, istar$config)
mod <- build_model_glm_protein(lfqdata, "~ group_")
head(mod$get_coefficients())
```

---

build_model_impute *Build protein models with LOD imputation for failed fits*

Description

Fits per-protein models, then re-fits failed/singular proteins after imputing missing values with the limit of detection (LOD) and clamping. Covariance is borrowed from successful fits so that variance is not underestimated by the constant imputation.

Usage

```
build_model_impute(
  lfqdata,
  model_strategy,
  model_name = paste0(model_strategy$model_name, "Imputed"),
  lod = NULL,
  borrow_method = c("sigma", "vcov"),
  df_method = c("observed", "borrowed"),
  on_misalign = c("fallback", "fail")
)
```

Arguments

lfqdata	LFQData object (aggregated to protein level)
model_strategy	model strategy object (e.g. from strategy_lm)
model_name	model name (default appends "Imputed")
lod	numeric limit of detection; if NULL, auto-computed from data
borrow_method	"sigma" borrows scalar sigma and uses per-protein (X'X)^-1; "vcov" borrows element-wise median of full vcov matrices
df_method	"observed" uses max(n_observed - p, 1); "borrowed" uses median df from successful fits
on_misalign	passed to compute_borrowed_variance via impute_refit_singular. "fallback" (default) preserves the lm behaviour; "fail" skips the rescue when a full covariance matrix cannot be borrowed (used by the rfit backend, which has no sigma-method fallback).

Value

a object of class Model

See Also

build_model, impute_refit_singular

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_limma(), build_model_limma_impute build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(),

sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median, vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 30, weight_missing = 0.5)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
strat <- strategy_lm(paste(lfqdata$response(), "~ group_"))
mod <- build_model_impute(lfqdata, strat)
```

---

build_model_limma *Build limma model from LFQData*

Description

Analogous to build_model but uses limma's matrix-based pipeline. Takes an LFQData object and a strategy from strategy_limma, pivots data to wide format, fits with lmFit, and returns a ModelLimma object.

Usage

```
build_model_limma(lfqdata, strategy, model_name = strategy$model_name)
```

Arguments

lfqdata	an LFQData object
strategy	output of strategy_limma
model_name	name of model (default from strategy)

Value

a ModelLimma object

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma_imput build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(),

linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res
model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma()
new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(),
sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(),
sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median
vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 50)
lProt <- LFQData$new(istar$data, istar$config)
lProt$rename_response("transformedIntensity")

strat <- strategy_limma("transformedIntensity ~ group_")
mod_limma <- build_model_limma(lProt, strat)
mod_limma$get_coefficients()
mod_limma$get_anova()
```

---

build_model_limma_impute

Build limma model with LOD imputation for failed proteins

Description

Analogous to build_model_impute but for limma's matrix-based pipeline. Fits all proteins with lmFit, identifies proteins with NA coefficients (typically from entire missing groups), imputes their missing values with the limit of detection (LOD), refits, and replaces the variance with a borrowed estimate from successful proteins.

Usage

```
build_model_limma_impute(
  lfqdata,
  strategy,
  model_name = paste0(strategy$model_name, "Imputed"),
  lod = NULL,
  df_method = c("observed", "borrowed")
)
```

Arguments

lfqdata	an LFQData object (aggregated to protein level)
strategy	output of strategy_limma
model_name	name of model (default: strategy name + "Imputed")
lod	numeric limit of detection; if NULL, auto-computed from data via MissingHelpers
df_method	how to set degrees of freedom for imputed proteins: "observed" (default) uses max(n_observed - p, 1) where n_observed counts only non-missing values; "borrowed" uses the median df from successful fits

Details

The LOD imputation gives plausible coefficients (fold change direction), while the borrowed sigma and corrected degrees of freedom ensure that inference is not artificially precise from the constant imputation.

Value

a ModelLimma object with a hybrid fit

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 50, weight_missing = 0.5)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")

strat <- strategy_limma("transformedIntensity ~ group_")
mod <- build_model_limma_impute(lfqdata, strat)
mod$get_coefficients()
```

---

build_model_limma_voom

Build limma model with vooma precision weights (proteomics)

Description

Estimates observation-level precision weights from a mean-variance trend (vooma) and fits a weighted least squares model via lmFit. For proteomics data that is already log2-transformed.

Usage

```
build_model_limma_voom(
  lfqdata,
  strategy,
  model_name = strategy$model_name,
  span = 0.5,
  plot = FALSE
)
```

Arguments

lfqdata	an LFQData object (aggregated to protein level)
strategy	output of strategy_limma
model_name	name of model (default from strategy)
span	lowess smoother span for mean-variance trend (default 0.5)
plot	logical; if TRUE, plot the mean-variance trend

Details

When strategy$weights is set (e.g. to nr_children), these external weights enter the preliminary fit (so the trend estimation accounts for measurement precision) and are multiplied element-wise with the vooma weights for the final fit. See the voom integration notes in ../TODO/prolfqua/Archive/TODO_limma_vo for the mathematical basis.

Value

a ModelLimma object

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 50)
lProt <- LFQData$new(istar$data, istar$config)
lProt$rename_response("transformedIntensity")

strat <- strategy_limma("transformedIntensity ~ group_")
mod <- build_model_limma_voom(lProt, strat)
mod$get_coefficients()
```

`build_model_limma_voom_impute` *Build limma-voom model with LOD imputation for failed proteins*

Description

Combines vooma precision weights with LOD imputation for proteins that have entire missing groups (NA coefficients). Mirrors `build_model_limma_impute` but uses vooma weights.

Usage

```
build_model_limma_voom_impute(
  lfqdata,
  strategy,
  model_name = paste0(strategy$model_name, "Imputed"),
  lod = NULL,
  df_method = c("observed", "borrowed"),
  span = 0.5,
  plot = FALSE
)
```

Arguments

`lfqdata`	an `LFQData` object (aggregated to protein level)
`strategy`	output of `strategy_limma`
`model_name`	name of model (default: strategy name + "Imputed")
`lod`	numeric limit of detection; if NULL, auto-computed from data
`df_method`	how to set degrees of freedom for imputed proteins: `"observed"` (default) uses `max(n_observed - p, 1)`; `"borrowed"` uses the median df from successful fits
`span`	lowess smoother span for vooma trend (default 0.5)
`plot`	logical; if TRUE, plot the mean-variance trend

Value

a `ModelLimma` object with a hybrid fit

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 50, weight_missing = 0.5)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")

strat <- strategy_limma("transformedIntensity ~ group_")
mod <- build_model_limma_voom_impute(lfqdata, strat)
mod$get_coefficients()
```

---

build_model_limpa *Build limpa vooma model from aggregated LFQData*

Description

Takes protein-level LFQData produced by AggregateLimpa (which contains standard error and observation count columns) and fits a limpa vooma model via `limpa::voomaLmFitWithImputation`. The standard errors from DPC quantification are used as a bivariate predictor for the vooma precision weights, and the observation counts identify imputed entries for degree-of-freedom correction.

Usage

```
build_model_limpa(lfqdata, strategy, model_name = strategy$model_name)
```

Arguments

lfqdata	LFQData object. Must have `config$nr_children` set (used to flag imputed observations via `nr_children == 0`). `config$opt_se` is optional: when set (e.g. from AggregateLimpa), the SE column is used as a vooma precision-weight predictor; otherwise vooma is fit without an external predictor.

strategy	StrategyLimpa object
model_name	model name (default from strategy)

Details

Returns a ModelLimma object (since the output is a standard MArrayLM), which can be passed directly to ContrastsLimma.

Value

ModelLimma object

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
if (requireNamespace("limpa", quietly = TRUE)) {
  istar <- sim_lfq_data_peptide_config(Nprot = 10)
  lfq <- LFQData$new(istar$data, istar$config)
  lfq <- lfq$get_Transformer()$log2()$lfq
  lfq <- AggregateLimpa$new(lfq, "protein")$aggregate()
  strat <- strategy_limpa("limpa ~ group_")
  mod <- build_model_limpa(lfq, strat)
  mod$model_name
}
```

build_model_logistf *build_model_logistf*

Description

build_model_logistf

Usage

```
build_model_logistf(data, formula)
```

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config(Nprot = 10, with_missing = TRUE,
  weight_missing = 0.5, seed = 3)
istar$data <- prolfqua::encode_bin_resp(LFQData$new(istar$data, istar$config))
istar$config$bin_resp <- "bin_resp"
tmp <- LFQData$new(istar$data, istar$config)
formula <- paste0(tmp$get_config()$bin_resp , "~ group_")
xx2 <- build_model_logistf(tmp, formula)

istar <- prolfqua::sim_lfq_data_protein_config(Nprot = 10, with_missing = TRUE,
  weight_missing = 0.5, seed = 3)
istar$data <- prolfqua::encode_bin_resp(LFQData$new(istar$data, istar$config))
istar$config$bin_resp <- "bin_resp"
tmp <- LFQData$new(istar$data, istar$config)
formula <- paste0(tmp$get_config()$bin_resp , "~ group_")
xx <- build_model_logistf(tmp, formula)
```

```
contrasts <- c(AvsB = "group_A - group_B")
m <- xx$models$models1$model_df$linear_model[[1]]
linfct_matrix_contrasts(linfct_from_model(m)$linfct_factors, contrasts)
m <- xx2$models$models2$model_df$linear_model[[1]]
linfct_matrix_contrasts(linfct_from_model(m)$linfct_factors, contrasts)
```

`center_to_reference_cfg` *center to reference*

Description

takes the median of the lfqdareference per sample and subtracts it from a copy of lfqdata

Usage

```
center_to_reference_cfg(lfqdata, lfqdareference)
```

Arguments

`lfqdata`	LFQData object containing the data to center
`lfqdareference`	LFQData object containing the reference subset

Value

The computed result.

Examples

```
# example code

bb <- sim_lfq_data_peptide_config(Nprot = 100)
x <- LFQData$new(bb$data, bb$config)
xc <- x$get_copy()
xc$set_data(xc$data_long() |> dplyr::filter(protein_Id == "0EfVhX~3967"))
xxd <- center_to_reference_cfg(x, xc)
xxd$response()
x$response()
```

`complete_cases` *Complete cases*

Description

The tidy table does not need to contain missing data. This function re-establishes the missing observations in a sample.

Usage

```
complete_cases(lfqdata)
```

Arguments

lfqdata	LFQData object

See Also

Other configuration: AnalysisConfiguration, ContrastConfiguration, INTERNAL_FUNCTIONS_BY_FAMILY, R6_extract_values(), list_to_ContrastConfiguration(), make_interaction_column(), make_reduced_hiera sample_subset(), separate_hierarchy(), setup_analysis(), table_factors(), table_factors_size()

Examples

```
bb <- sim_lfq_data_protein_config()
lfq <- LFQData$new(bb$data, bb$config)
xx <- complete_cases(lfq)
stopifnot(nrow(bb$data) <= nrow(xx))
```

---

compute_borrowed_variance

Compute borrowed variance from successful model fits

Description

Compute borrowed variance from successful model fits

Usage

```
compute_borrowed_variance(
  model_df,
  method = c("sigma", "vcov"),
  on_misalign = c("fallback", "fail")
)
```

Arguments

model_df	tibble from model_analyse
method	"sigma" borrows scalar sigma and uses per-protein (X'X)^-1, "vcov" borrows element-wise median of full vcov matrices
on_misalign	behaviour when donor vcov matrices cannot be aligned by coefficient name (method = "vcov" only). "fallback" (default) warns and falls back to the sigma method, preserving the lm behaviour. "fail" signals a prolfqua_borrow_failed condition so the caller can skip the rescue; backends without an lm-style summary(fit)$cov.unscal (e.g. rfit) must use this because the sigma fallback is not applicable to them.

Value

list with sigma, df, method, and optionally vcov

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median, vcov.rfit_prolfqua()

Examples

```
mod <- sim_build_models_lm(model = "parallel3", weight_missing = 1)

# Sigma method (default): returns median sigma and df from donors
borrowed_s <- prolfqua:::compute_borrowed_variance(
  mod$model_df, method = "sigma")
stopifnot(borrowed_s$method == "sigma")
stopifnot(is.numeric(borrowed_s$sigma) && borrowed_s$sigma > 0)
stopifnot(is.numeric(borrowed_s$df) && borrowed_s$df > 0)

# Vcov method: element-wise median vcov from donors.
# Falls back to sigma if donor models have misaligned coefficient names.
mod_no_missing <- sim_build_models_lm(model = "parallel3",
  Nprot = 10, with_missing = FALSE)
borrowed_v <- prolfqua:::compute_borrowed_variance(
  mod_no_missing$model_df, method = "vcov")
stopifnot(borrowed_v$method == "vcov")
stopifnot(is.matrix(borrowed_v$vcov))
```

`compute_borrowed_variance_limma` *Compute borrowed variance from successful limma fits*

Description

Extracts median sigma and df from proteins that fitted successfully (no NA coefficients). Used by build_model_limma_impute to replace the artificially low variance of LOD-imputed proteins.

Usage

```
compute_borrowed_variance_limma(fit)
```

Arguments

fit	MArrayLM object from lmFit

Value

list with sigma (median residual SD) and df (median residual df) from successful proteins

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

---

compute_contrast *handles incomplete models*

Description

only keeps non NA coefficients.

Usage

```
compute_contrast(m, linfct, confint = 0.95)
```

Arguments

m	linear model generated using lm
linfct	linear function
confint	confidence interval default 0.95

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
m <- sim_make_model_lm( "factors")
linfct <- linfct_from_model(m)$linfct_factors
compute_contrast(m, linfct, confint = 0.95)
compute_contrast(m, linfct, confint = 0.99)
```

---

compute_lmer_contrast *applies contrast computation using lmerTest::contest function*

Description

applies contrast computation using lmerTest::contest function

Usage

```
compute_lmer_contrast(model, linfct, ddf = c("Satterthwaite", "Kenward-Roger"))
```

Arguments

model	mixed effects model
linfct	linear function
ddf	method to determine denominator degrees of freedom

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median, vcov.rfit_prolfqua()

Examples

```
mb <- sim_make_model_lmer("interaction")
summary(mb)

linfct <- linfct_from_model(mb)
names(linfct)
compute_lmer_contrast(mb, linfct$linfct_factors)
compute_lmer_contrast(mb, linfct$linfct_interactions)
length(lme4::fixef(mb))
lmerTest::contest(mb, c( 0 ,1 , 0 , 0),joint = FALSE)
summary(mb)
```

---

compute_pooled *compute pooled variance*

Description

following the documentation here: https://online.stat.psu.edu/stat500/lesson/7/7.3/7.3.1/7.3.1.1

Usage

```
compute_pooled(x)

poolvar(res1, config)
```

Arguments

x	data.frame

Value

data.frame

See Also

Other stats: INTERNAL_FUNCTIONS_BY_FAMILY, lfq_power_t_test_proteins(), lfq_power_t_test_quantiles_V2(
plot_stat_density(), plot_stat_density_median(), plot_stat_violin(), plot_stat_violin_median(),
plot_stdv_vs_mean(), summarize_stats()

Other stats: INTERNAL_FUNCTIONS_BY_FAMILY, lfq_power_t_test_proteins(), lfq_power_t_test_quantiles_V2(
plot_stat_density(), plot_stat_density_median(), plot_stat_violin(), plot_stat_violin_median(),
plot_stdv_vs_mean(), summarize_stats()

Examples

```
x <- data.frame(nrMeasured =c(1,2,2), var = c(3,4,4), meanAbundance = c(3,3,3))
x <- data.frame(nrMeasured = c(1,2,1,1), var = c(NA, 0.0370, NA, NA),
  meanAbundance = c(-1.94,-1.46,-1.87,-1.45))
compute_pooled(x)
y <- data.frame(dilution.=c("a","b","c"),
     nrReplicates = c(4,4,4), nrMeasured = c(0,0,1), sd =c(NA,NA,NA),
     var = c(NA,NA,NA),meanAbundance = c(NaN,NaN,NaN))
compute_pooled(y)
yb <- y |> dplyr::filter(nrMeasured > 1)

bb <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(bb$data, bb$config)
res1 <- summarize_stats(lfq)
pv <- poolvar(res1, bb$config)
stopifnot(nrow(pv) == nrow(res1) / 3)
```

ContrastConfiguration *Contrast Configuration*

Description

Holds the column-role mapping and behaviour flags that describe how a specific contrast backend (lm, limma, SAINT, ...) lays out its result table. Mirrors AnalysisConfiguration for the modelling side: it carries names, not data.

Consumers that need to operate on a contrast table generically (filter, build ORA inputs, build rank lists, summarise per protein) should read column names through the accessors on this object rather than hard-coding them. This lets backends with different column conventions (e.g. SAINT's BFDR/log2_EFCs) plug into the same downstream code path as LM-style backends without renaming columns.

Defaults match the standard prolfqua contrast schema produced by Contrasts, ContrastsLimma, ContrastsModerated etc.

Value

An R6 class generator.

Public fields

`subject_id` columns identifying the contrast subject (e.g. protein id)

`model_name_col` column carrying the model name label

`contrast_col` column carrying the contrast label

`effect_col` column with the (signed) effect size; for LM this is `diff`, for SAINT `log2_EFCs`

`score_col` column with the per-contrast test statistic

`pvalue_col` column with the raw p-value, or `""` for backends that do not produce one (e.g. SAINTexpress). `NA_character_` is accepted by the constructor and stored as `""`.

`fdr_col` column with the FDR / BFDR / adjusted p-value

`avg_abundance_col` column with the per-feature mean abundance

`supports_dea_qc` whether the backend supports the legacy differential-expression QC HTML report

`needs_saint_annotation` whether the backend needs annotation reading in SAINT mode (bait / control columns)

`significance_directional` if `TRUE`, the backend only considers positive-effect features biologically meaningful (e.g. SAINTexpress, where negative `log2_EFCs` are not interpreted as "down" hits). Affects `filter_significant()`: when `TRUE` the filter is one-sided on the effect column; when `FALSE` it is symmetric (`|effect| > threshold`).

Methods

Public methods:

- `ContrastConfiguration$new()`
- `ContrastConfiguration$has_pvalue()`
- `ContrastConfiguration$clone()`

Method `new()`**:** Construct a ContrastConfiguration. All arguments map directly to fields of the same name.

Usage:

```
ContrastConfiguration$new(
  subject_id = character(),
  model_name_col = "modelName",
  contrast_col = "contrast",
  effect_col = "diff",
  score_col = "statistic",
  pvalue_col = "p.value",
  fdr_col = "FDR",
  avg_abundance_col = "avgAbd",
  supports_dea_qc = TRUE,
  needs_saint_annotation = FALSE,
  significance_directional = FALSE
)
```

Arguments:

`subject_id` columns identifying the contrast subject

`model_name_col` model-name column

`contrast_col` contrast-label column

`effect_col` signed effect column

`score_col` test-statistic column

`pvalue_col` raw p-value column, or `""` / `NA_character_` when the backend produces none

`fdr_col` FDR / adjusted-p column

`avg_abundance_col` mean-abundance column

`supports_dea_qc` supports DEA QC HTML

`needs_saint_annotation` needs SAINT-mode annotation

`significance_directional` one-sided filter on effect column

Method `has_pvalue()`**:** Does the backend produce a usable p-value column?

Usage:

```
ContrastConfiguration$has_pvalue()
```

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastConfiguration$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other configuration: `AnalysisConfiguration`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `R6_extract_values()`, `complete_cases()`, `list_to_ContrastConfiguration()`, `make_interaction_column()`, `make_reduced_hierarch` `sample_subset()`, `separate_hierarchy()`, `setup_analysis()`, `table_factors()`, `table_factors_size()`

Examples

```
cfg <- ContrastConfiguration$new(subject_id = "protein_Id")
cfg$effect_col
cfg$fdr_col
cfg$has_pvalue()
cfg$supports_dea_qc

# SAINT-flavoured config
saint <- ContrastConfiguration$new(
  subject_id = "protein_Id",
  contrast_col = "Bait",
  effect_col = "log2_EFCs",
  score_col = "SaintScore",
  pvalue_col = NA_character_,
  fdr_col = "BFDR",
  supports_dea_qc = FALSE,
  needs_saint_annotation = TRUE
)
saint$has_pvalue()
```

`Contrasts` *Estimate contrasts using Wald Test*

Description

Estimate contrasts using Wald Test

Estimate contrasts using Wald Test

Details

The per-protein contrast computation uses `compute_contrast` and `linfct_matrix_contrasts` internally.

Value

An R6 class generator.

Super class

`prolfqua::ContrastsInterface` -> `Contrast`

Public fields

`models` Model

`contrasts` character with contrasts

`contrastfun` function to compute contrasts

`model_name` model name

`subject_id` name of column containing e.g., protein Id's

`p.adjust` function to adjust p-values (default prolfqua::adjust_p_values)

`contrast_result` data frame containing results of contrast computation

`global` use a global linear function (determined by get_linfct)

Methods

Public methods:

- `Contrasts$new()`
- `Contrasts$get_contrast_sides()`
- `Contrasts$get_linfct()`
- `Contrasts$get_contrasts()`
- `Contrasts$clone()`

Method `new()`**:** initialize create Contrast

Usage:

```
Contrasts$new(
  model,
  contrasts,
  p.adjust = prolfqua::adjust_p_values,
  global = FALSE,
  model_name = "WaldTest"
)
```

Arguments:

`model` a dataframe with a structure similar to that generated by `build_model`

`contrasts` a character vector with contrast specification

`p.adjust` function to adjust the p-values

`global` development/internal argument (if FALSE determine linfct for each model.)

`model_name` name of contrast method, default WaldTest

Method `get_contrast_sides()`**:** get both sides of contrasts

Usage:

```
Contrasts$get_contrast_sides()
```

Method `get_linfct()`**:** get linear functions from contrasts

Usage:

```
Contrasts$get_linfct(global = TRUE, avg = TRUE)
```

Arguments:

`global` logical TRUE - get the a linear functions for all models, FALSE - linear function for each model

`avg` logical TRUE - get also linfct for averages

Method `get_contrasts()`**:** get table with contrast estimates

Usage:

```
Contrasts$get_contrasts(all = FALSE)
```

Arguments:

`all` should all columns be returned (default FALSE)

Returns: data.frame with contrasts

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
Contrasts$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: `AnovaExtractor`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImputeFacade`, `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste`
`ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf()`, `compute_borrowed_variance()`, `compute_borrowed_variance_`
`compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`,

impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
# Fitting mixed effects model to peptide data
istar <- prolfqua::sim_lfq_data_peptide_config()

modelFunction <-
  strategy_lmer("abundance  ~ group_ + (1 | peptide_Id) + (1 | sample)")

config <- istar$config
config$hierarchy_keys_depth()

mod <- build_model(
  istar$data,
  modelFunction,
  subject_id = config$hierarchy_keys_depth()
)

ref_lfc <- data.frame(
  `(Intercept)` = c(0, 0, 0),
  group_B = c(0, 1, 0),
  group_Ctrl = c(-1, -1, 1),
  row.names = c("groupA_vs_Ctrl", "dil.e_vs_b", "dil.ctrl_vs_b")
)
prolfqua::model_summary(mod)
Contr <- c(
  "groupA_vs_Ctrl" = "group_A - group_Ctrl",
  "dil.e_vs_b" = "group_B - group_Ctrl",
  "dil.ctrl_vs_b" = "group_Ctrl - group_A"
)
contrastX <- prolfqua::Contrasts$new(mod, Contr)
y <- contrastX$get_linfct(avg = FALSE)
stopifnot(all(ref_lfc == y))
t <- contrastX$get_linfct(global = FALSE)

x <- contrastX$get_contrasts()
stopifnot(all(x$p.value < 1 & x$p.value > 0))
stopifnot(all(x$avgAbd > 0))
stopifnot(all(x$FDR > 0 & x$FDR < 1))

x <- contrastX$get_contrast_sides()
xd <- contrastX$column_description()
modelFunction <-
  strategy_lm("abundance  ~ group_")
mod <- build_model(
  istar$data,
  modelFunction,
  subject_id = config$hierarchy_keys_depth()
)
contrastX <- prolfqua::Contrasts$new(mod, Contr)
y <- contrastX$get_linfct(avg = FALSE)
```

```
stopifnot(all(ref_lfc == y))
```

`ContrastsBinomialNestedFacade` *Quasibinomial detection-count facade for nested input*

Description

Quasibinomial detection-count facade for nested input

Quasibinomial detection-count facade for nested input

Details

Completes and encodes child-feature detection using the same preparation as `ContrastsFirthNestedFacade`, then collapses the binary rows into detected and undetected counts per parent and sample. The resulting quasibinomial model reports parent-level log odds ratios in `diff`; `avgAbd` is the average linear predictor on the log-odds scale.

Child features are treated as exchangeable binomial trials. The symmetric pseudo-count stabilizes complete separation but is not equivalent to Firth's bias-reducing penalty. Empirical-Bayes dispersion moderation uses `ContrastsModerated`; by default posterior dispersion is bounded below by one.

Value

An R6 class generator.

Super classes

`prolfqua::ContrastsInterface` -> `prolfqua::ContrastsFacadeBase` -> `ContrastsBinomialNestedFacade`

Methods

Public methods:

- `ContrastsBinomialNestedFacade$new()`
- `ContrastsBinomialNestedFacade$clone()`

Method `new()`**:** Fit the nested detection-count model and its contrasts.

Usage:

```
ContrastsBinomialNestedFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  prior_count = 0.1,
  binomial_bound = TRUE,
  ...
)
```

Arguments:

`lfqdata` nested `LFQData`

`modelstr` right-hand-side model formula

`contrasts` named contrast expressions

`prior_count` non-negative symmetric pseudo-count

`binomial_bound` bound posterior dispersion below by one

`...` passed to `strategy_binomial`

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsBinomialNestedFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
istar <- sim_lfq_data_peptide_config(Nprot = 20, weight_missing = 0.5, seed = 3)
lfqdata <- LFQData$new(istar$data, istar$config)
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
facade <- ContrastsBinomialNestedFacade$new(lfqdata, "~ group_", contrasts)
head(facade$get_contrasts())
```

`ContrastsDEqMSFacade` *DEqMS contrast analysis facade*

Description

DEqMS contrast analysis facade

DEqMS contrast analysis facade

Details

Encapsulates the pipeline: `strategy_lm` -> `build_model` -> `Contrasts` -> `ContrastsModeratedDEqMS`.

Value

An R6 class generator.

Super classes

`prolfqua::ContrastsInterface` -> `prolfqua::ContrastsFacadeBase` -> `ContrastsDEqMSFacade`

Methods

Public methods:

- `ContrastsDEqMSFacade$new()`
- `ContrastsDEqMSFacade$clone()`

Method `new()`**:** initialize

Usage:

```
ContrastsDEqMSFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  weights = lfqdata$nr_children_col(),
  ...
)
```

Arguments:

`lfqdata` LFQData object

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`weights` column name for per-observation weights (default: `lfqdata$nr_children_col()`). Pass `NULL` for unweighted.

`...` passed to `strategy_lm`

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsDEqMSFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImputeFacade`, `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste`
`ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf()`, `compute_borrowed_variance()`, `compute_borrowed_variance_`
`compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_results()`, `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()`, `new_imputed_model()`, `pivot_model_contrasts_to_wide()`
`register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median_p_scaled()`, `vcov.rfit_prolfqua()`

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 50)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsDEqMSFacade$new(lfqdata, "~ group_", contrasts)
```

```
head(fa$get_contrasts())
fa$to_wide()
```

`ContrastsDEqMSVoomFacade` *DEqMS contrast analysis with vooma weights facade*

Description

DEqMS contrast analysis with vooma weights facade

DEqMS contrast analysis with vooma weights facade

Details

Combines vooma precision weights (mean-variance trend) with DEqMS count-dependent variance moderation. Vooma runs **without** external weights so it captures only the mean-variance relationship; the peptide count enters solely through DEqMS moderation, avoiding double-counting.

Pipeline: `strategy_limma` (weights = NULL) -> `build_model_limma_voom` -> `ContrastsLimma` (eBayes = FALSE) -> `ContrastsModeratedDEqMS`.

Value

An R6 class generator.

Super classes

`prolfqua::ContrastsInterface` -> `prolfqua::ContrastsFacadeBase` -> `ContrastsDEqMSVoomFacade`

Methods

Public methods:

- `ContrastsDEqMSVoomFacade$new()`
- `ContrastsDEqMSVoomFacade$clone()`

Method `new()`**:** initialize

Usage:

```
ContrastsDEqMSVoomFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  span = 0.5,
  plot = FALSE,
  ...
)
```

Arguments:

`lfqdata` LFQData object

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`span` lowess smoother span for vooma trend (default 0.5)

`plot` logical; if TRUE, plot the mean-variance trend

`...` passed to `strategy_limma` (e.g. trend, robust)

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsDEqMSVoomFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImputeFacade`, `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste`
`ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf()`, `compute_borrowed_variance()`, `compute_borrowed_variance_`
`compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_results()`, `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()`, `new_imputed_model()`, `pivot_model_contrasts_to_wide()`
`register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median_p_scaled()`, `vcov.rfit_prolfqua()`

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 50)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsDEqMSVoomFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
```

ContrastsFacadeBase *Base class for contrast analysis facades*

Description

Base class for contrast analysis facades

Base class for contrast analysis facades

Details

Holds the fields and delegating methods shared by every facade in `ContrastsFacades.R` and `ContrastsChildToParentFacades.R`. Subclasses implement the unique pipeline wiring in `initialize()`: they call the private `.setup()` (input-shape check, `self$.lfqdata`, `self$.contrast_names`, `self$facade_name`), then build the model and the inner contrast object. `get_config()` defaults to the inner contrast object's configuration. The limma family additionally sets `self$.drop_na_diff <- TRUE` to drop rows whose fold change could not be estimated.

`get_contrasts()` delegates to the inner contrast object and then stamps the facade key into `modelName` via `.stamp_facade_identity()`; rescue/imputation state is carried in the `estimate_type` column set by the inner contrast classes.

Value

An R6 class generator.

Super class

`prolfqua::ContrastsInterface` -> `ContrastsFacadeBase`

Public fields

`model` fitted model object

`contrast` inner contrast object the facade delegates to

`.lfqdata` stored reference to the input LFQData (used by get_missing)

`.contrast_names` names of the requested contrasts

`facade_name` registry key stamped into the modelName column

`.drop_na_diff` drop rows with NA diff (limma family); default FALSE

Methods

Public methods:

- `ContrastsFacadeBase$get_config()`
- `ContrastsFacadeBase$get_contrasts()`
- `ContrastsFacadeBase$get_missing()`
- `ContrastsFacadeBase$get_Plotter()`
- `ContrastsFacadeBase$to_wide()`
- `ContrastsFacadeBase$clone()`

Method `get_config()`**:** get the `ContrastConfiguration`; defaults to the inner contrast object's configuration

Usage:

```
ContrastsFacadeBase$get_config()
```

Method `get_contrasts()`**:** get contrast results, stamped with the facade key

Usage:

```
ContrastsFacadeBase$get_contrasts(...)
```

Arguments:

`...` passed to the inner contrast object's get_contrasts

Method `get_missing()`: get subject x contrast pairs that could not be estimated

Usage:

```
ContrastsFacadeBase$get_missing()
```

Method `get_Plotter()`: get `ContrastsPlotter`

Usage:

```
ContrastsFacadeBase$get_Plotter(...)
```

Arguments:

`...` passed to the inner contrast object's get_Plotter

Method `to_wide()`: convert results to wide format

Usage:

```
ContrastsFacadeBase$to_wide(...)
```

Arguments:

`...` passed to the inner contrast object's to_wide

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
ContrastsFacadeBase$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImputeFacade`, `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste`
`ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf()`, `compute_borrowed_variance()`, `compute_borrowed_variance_`
`compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_results()`, `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()`, `new_imputed_model()`, `pivot_model_contrasts_to_wide()`
`register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median_p_scaled()`, `vcov.rfit_prolfqua()`

Examples

```
facade <- ContrastsFacadeBase$new()
inherits(facade, "ContrastsFacadeBase")
```

ContrastsFirth *Estimate contrasts using Wald Test*

Description

Estimate contrasts using Wald Test

Estimate contrasts using Wald Test

Value

An R6 class generator.

Super class

prolfqua::ContrastsInterface -> ContrastsFirth

Public fields

`models` Model

`contrasts` character with contrasts

`model_name` name of model

`subject_id` name of column containing e.g., protein Id's

`p.adjust` function to adjust p-values (default prolfqua::adjust_p_values)

`contrast_result` data frame containing results of contrast computation

Methods

Public methods:

- `ContrastsFirth$new()`
- `ContrastsFirth$get_contrast_sides()`
- `ContrastsFirth$get_linfct()`
- `ContrastsFirth$get_contrasts()`
- `ContrastsFirth$clone()`

Method `new()`**:** initialize create Contrast

Usage:

```
ContrastsFirth$new(
  model,
  contrasts,
  p.adjust = prolfqua::adjust_p_values,
  model_name = "firth"
)
```

Arguments:

`model` a dataframe with a structure similar to that generated by `build_model`

`contrasts` a character vector with contrast specification

`p.adjust` function to adjust the p-values

`model_name` name of contrast method, default firth

Method `get_contrast_sides()`: get both sides of contrasts

Usage:

```
ContrastsFirth$get_contrast_sides()
```

Method `get_linfct()`: get linear functions from contrasts

Usage:

```
ContrastsFirth$get_linfct(avg = TRUE)
```

Arguments:

`avg` logical TRUE - get also linfct for averages

Returns: a list with the linfct-annotated model containers (`models1` / `models2`); the shared input model is left untouched.

Method `get_contrasts()`: get table with contrast estimates

Usage:

```
ContrastsFirth$get_contrasts(all = FALSE)
```

Arguments:

`all` should all columns be returned (default FALSE)

Returns: data.frame with contrasts

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
ContrastsFirth$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImputeFacade`, `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste` `ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf()`, `compute_borrowed_variance()`, `compute_borrowed_variance_` `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_results()`, `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()`, `new_imputed_model()`, `pivot_model_contrasts_to_wide()` `register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median_p_scaled()`, `vcov.rfit_prolfqua()`

Examples

```
modi <- sim_build_models_logistf(model = "parallel3", weight_missing = 1)
contrasts <- c(Avs = "group_A - group_B", AvsCtrl = "group_A - group_Ctrl")

ctr <- ContrastsFirth$new(modi,contrasts)
ctr$get_contrast_sides()
ctr$get_linfct()
ctr$get_contrasts()

mod3 <- sim_build_models_logistf(model = "parallel3", weight_missing = 1, peptide=TRUE)

ctrpep <- ContrastsFirth$new(mod3,contrasts)
ctrpep$get_contrast_sides()

ctrpep$get_linfct()
ctrpep$get_contrasts()
pl <- ctrpep$get_Plotter()
```

ContrastsFirthFacade *Firth logistic missingness contrast analysis facade*

Description

Firth logistic missingness contrast analysis facade

Firth logistic missingness contrast analysis facade

Details

Encapsulates the pipeline: encode missingness -> `build_model_glm_protein` -> `ContrastsFirth`.

Requires aggregated (protein-level) LFQData. For nested peptide-level input use `ContrastsFirthNestedFacade`.

Value

An R6 class generator.

Super classes

`prolfqua::ContrastsInterface` -> `prolfqua::ContrastsFacadeBase` -> `ContrastsFirthFacade`

Methods

Public methods:

- `ContrastsFirthFacade$new()`
- `ContrastsFirthFacade$clone()`

Method `new()`**:** initialize

Usage:

```
ContrastsFirthFacade$new(lfqdata, modelstr, contrasts, ...)
```

Arguments:

`lfqdata` LFQData object

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`...` ignored; accepted for dispatch compatibility with other facades

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsFirthFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImputeFacade, ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 20, weight_missing = 0.5)
lfqdata <- LFQData$new(istar$data, istar$config)
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsFirthFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsFirthNestedFacade

Firth logistic missingness contrast analysis facade for nested input

---

Description

Firth logistic missingness contrast analysis facade for nested input

Firth logistic missingness contrast analysis facade for nested input

Details

Encapsulates the pipeline: encode missingness -> build_model_glm_peptide -> ContrastsFirth.

Takes nested (peptide-level) LFQData and returns protein-level fold-change estimates. For protein-level (aggregated) input use ContrastsFirthFacade instead.

Value

An R6 class generator.

Super classes

prolfqua::ContrastsInterface -> prolfqua::ContrastsFacadeBase -> ContrastsFirthNestedFacade

Methods

Public methods:

- ContrastsFirthNestedFacade$new()
- ContrastsFirthNestedFacade$clone()

Method `new()`**:** initialize

Usage:

```
ContrastsFirthNestedFacade$new(lfqdata, modelstr, contrasts, ...)
```

Arguments:

`lfqdata` nested LFQData (peptide-level)

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`...` ignored; accepted for dispatch compatibility with other facades

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsFirthNestedFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsLMFacade, ContrastsLMImputeFacad ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImputeFacade, ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNestedFacade, ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(),

impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_peptide_config(Nprot = 20, weight_missing = 0.5)
lfqdata <- LFQData$new(istar$data, istar$config)
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsFirthNestedFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsInterface *Base class for all Contrasts classes*

Description

Base class for all Contrasts classes

Base class for all Contrasts classes

Value

An R6 class generator.

Public fields

`config` ContrastConfiguration describing the backend's column-role mapping and behaviour flags. Subclasses should populate this in `initialize()` so generic consumers can resolve column names without hard-coding them.

Methods

Public methods:

- ContrastsInterface$get_config()
- ContrastsInterface$get_contrast_sides()
- ContrastsInterface$get_contrasts()
- ContrastsInterface$get_Plotter()
- ContrastsInterface$to_wide()
- ContrastsInterface$get_missing()
- ContrastsInterface$get_rank()
- ContrastsInterface$get_ora()
- ContrastsInterface$filter_significant()
- ContrastsInterface$contrast_summary_table()
- ContrastsInterface$extra_artifacts()
- ContrastsInterface$column_description()
- ContrastsInterface$clone()

Method `get_config()`: Return the `ContrastConfiguration`, constructing an LM-flavoured default on demand if a subclass has not set one.

Usage:

```
ContrastsInterface$get_config()
```

Method `get_contrast_sides()`: get table with sides of the contrast

Usage:

```
ContrastsInterface$get_contrast_sides()
```

Method `get_contrasts()`: get table with contrast results (similar to limma topTable function)

Usage:

```
ContrastsInterface$get_contrasts()
```

Method `get_Plotter()`: return `ContrastsPlotter` for the contrast results

Usage:

```
ContrastsInterface$get_Plotter(fc_threshold = 1, fdr_threshold = 0.1)
```

Arguments:

`fc_threshold` fold change threshold to show in plots

`fdr_threshold` FDR threshold to show in plots

Returns: `ContrastsPlotter`

Method `to_wide()`: convert contrast results to wide format

Usage:

```
ContrastsInterface$to_wide(columns = c("p.value", "FDR", "statistic"))
```

Arguments:

`columns` value columns to spread next to `diff`

Returns: data.frame

Method `get_missing()`: get protein × contrast pairs that could not be estimated. Returns a data.frame with hierarchy columns and contrast, or 0 rows.

Usage:

```
ContrastsInterface$get_missing()
```

Method `get_rank()`: get rank-list input table for enrichment tools.
If the backend's `ContrastConfiguration` has a p-value column the default rank score is signed `sign(effect) * -log10(p.value)`. Otherwise the default is the effect column itself.

Usage:

```
ContrastsInterface$get_rank(score = NULL)
```

Arguments:

`score` column name to use as rank score, or `NULL` to pick from the config

Returns: data.frame with subject id, contrast, and score columns.

Method `get_ora()`: get ORA input table — features passing the FDR and absolute effect-size threshold in the requested direction.

Usage:

```
ContrastsInterface$get_ora(up = TRUE, FDR_threshold = 0.05, diff_threshold = 1)
```

Arguments:

up if TRUE return positive effects, otherwise negative effects

FDR_threshold false discovery rate threshold

diff_threshold absolute effect-size threshold

Returns: filtered contrast data.frame for ORA input.

Method `filter_significant()`**:** Filter contrast rows that pass the FDR and effect-size threshold.

By default this is symmetric on the effect column (`|effect| > diff_threshold`). For backends whose `ContrastConfiguration` has `significance_directional = TRUE` (e.g. SAINTexpress, where only positive enrichment is biologically meaningful), the filter is one-sided (`effect > diff_threshold`).

Usage:

```
ContrastsInterface$filter_significant(FDR_threshold = 0.05, diff_threshold = 1)
```

Arguments:

FDR_threshold false discovery rate threshold

diff_threshold effect-size threshold

Returns: filtered contrast data.frame.

Method `contrast_summary_table()`**:** Per-subject summary table for downstream report grobs. Returns a small data.frame with canonical column names `contrast`, `effect`, `score`, `fdr` regardless of backend.

Usage:

```
ContrastsInterface$contrast_summary_table(rounded = TRUE)
```

Arguments:

rounded if TRUE round numeric columns to 3 significant digits (matches the prolfquapp report convention)

Method `extra_artifacts()`**:** Backend-specific extra artifacts that a report should carry along with the contrast results (e.g. SAINT input tables). Default returns an empty named list.

Usage:

```
ContrastsInterface$extra_artifacts()
```

Method `column_description()`**:** column description

Usage:

```
ContrastsInterface$column_description()
```

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsInterface$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

Examples

```
int <- ContrastsInterface$new()
testthat::expect_error(int$get_contrast_sides())
testthat::expect_error(int$get_contrasts())
testthat::expect_error(int$get_missing())
# get_Plotter / to_wide / get_rank / get_ora / filter_significant call get_contrasts()
# internally, which is not implemented on the bare interface, so they surface that error.
testthat::expect_error(int$get_Plotter())
testthat::expect_error(int$to_wide())
testthat::expect_error(int$get_rank())
testthat::expect_error(int$get_ora())
testthat::expect_error(int$filter_significant())
identical(int$extra_artifacts(), list())
int$column_description()
```

`ContrastsLimma` *Limma-based contrasts (direct limma pipeline)*

Description

Limma-based contrasts (direct limma pipeline)

Limma-based contrasts (direct limma pipeline)

Details

Uses limma's `contrasts.fit` + `eBayes` pipeline directly, rather than fitting per-protein lm models and then moderating. Inherits from `ContrastsInterface` with the same API as `Contrasts`.

Value

An R6 class generator.

Super class

`prolfqua::ContrastsInterface` -> `ContrastsLimma`

Public fields

`model` ModelLimma object

`contrasts` named character vector of contrasts

`model_name` model name

`subject_id` columns with subject_id (proteinID)

`p.adjust` function to adjust p-values

`contrast_result` cached contrast results

`eBayes` logical, apply limma eBayes moderation (default TRUE). Set to FALSE to return raw/unmoderated statistics, e.g. for downstream DEqMS moderation via `ContrastsModeratedDEqMS`.

Methods

Public methods:

- ContrastsLimma$new()
- ContrastsLimma$get_contrast_sides()
- ContrastsLimma$get_linfct()
- ContrastsLimma$get_contrasts()
- ContrastsLimma$clone()

Method `new()`: initialize ContrastsLimma

Usage:

```
ContrastsLimma$new(
  model,
  contrasts,
  p.adjust = prolfqua::adjust_p_values,
  model_name = NULL,
  eBayes = TRUE
)
```

Arguments:

`model` a ModelLimma object

`contrasts` named character vector of contrasts

`p.adjust` function to adjust p-values

`model_name` name of the contrast method

`eBayes` logical, apply limma eBayes moderation (default TRUE). Set to FALSE to return raw/unmoderated statistics suitable for wrapping with ContrastsModeratedDEqMS.

Method `get_contrast_sides()`: get both sides of contrasts

Usage:

```
ContrastsLimma$get_contrast_sides()
```

Method `get_linfct()`: get linear functions from contrasts

Usage:

```
ContrastsLimma$get_linfct(global = TRUE, avg = TRUE)
```

Arguments:

`global` ignored (for API compatibility)

`avg` logical, also compute avgAbd linfct

Method `get_contrasts()`: get table with contrast estimates via limma pipeline

Usage:

```
ContrastsLimma$get_contrasts(all = FALSE)
```

Arguments:

`all` should all columns be returned (default FALSE)

Returns: data.frame with contrasts

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
ContrastsLimma$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimmaFacade, ContrastsLimmaImputeFacade, ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 50)
lProt <- LFQData$new(istar$data, istar$config)
lProt$rename_response("transformedIntensity")

strat <- strategy_limma("transformedIntensity ~ group_")
mod_limma <- build_model_limma(lProt, strat)

Contr <- c("dil.b_vs_a" = "group_A - group_Ctrl")
contr_limma <- ContrastsLimma$new(mod_limma, Contr)
res <- contr_limma$get_contrasts()
head(res)
stopifnot(all(c("diff", "FDR", "p.value", "statistic") %in% colnames(res)))

# Compare with prolfqua's own pipeline
modelFunction <- strategy_lm("transformedIntensity ~ group_")
mod <- build_model(lProt, modelFunction)
contr_prolfqua <- Contrasts$new(mod, Contr)
res_prolfqua <- contr_prolfqua$get_contrasts()

# fold changes should be very similar
merged <- dplyr::inner_join(
  dplyr::select(res, protein_Id, diff_limma = diff),
  dplyr::select(res_prolfqua, protein_Id, diff_prolfqua = diff),
  by = "protein_Id")
stopifnot(cor(merged$diff_limma, merged$diff_prolfqua, use = "complete.obs") > 0.99)

# Plotter works
pl <- contr_limma$get_Plotter()

# to_wide works
wide <- contr_limma$to_wide()
```

```
head(wide)

# merge_contrasts_results works
Contr2 <- c("dil.b_vs_a" = "group_A - group_Ctrl")
imp <- ContrastsLMImputeFacade$new(lProt, "~ group_", Contr2)$contrast
merged_res <- merge_contrasts_results(contr_limma, imp)
```

`ContrastsLimmaFacade` *Limma contrast analysis facade*

Description

Limma contrast analysis facade

Limma contrast analysis facade

Details

Encapsulates the pipeline: `strategy_limma` -> `build_model_limma` -> `ContrastsLimma`.

Value

An R6 class generator.

Super classes

`prolfqua::ContrastsInterface` -> `prolfqua::ContrastsFacadeBase` -> `ContrastsLimmaFacade`

Methods

Public methods:

- `ContrastsLimmaFacade$new()`
- `ContrastsLimmaFacade$clone()`

Method `new()`**:** initialize

Usage:

```
ContrastsLimmaFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  weights = lfqdata$nr_children_col(),
  ...
)
```

Arguments:

`lfqdata` LFQData object

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`weights` column name for per-observation weights (default: `lfqdata$nr_children_col()`). Pass `NULL` for unweighted.

`...` passed to `strategy_limma` (e.g. trend, robust)

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsLimmaFacade$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaImputeFacade, ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config()
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsLimmaFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsLimmaImputeFacade

Limma contrast analysis with LOD imputation facade

Description

Limma contrast analysis with LOD imputation facade

Limma contrast analysis with LOD imputation facade

Details

Encapsulates the pipeline: strategy_limma -> build_model_limma_impute -> ContrastsLimma.

Proteins whose limma fit produces NA coefficients (typically from entire missing groups) are recovered by imputing missing values with the limit of detection (LOD) and refitting. The variance is borrowed from successful fits and degrees of freedom are corrected so that inference is not artificially precise from the constant imputation.

Value

An R6 class generator.

Super classes

prolfqua::ContrastsInterface -> prolfqua::ContrastsFacadeBase -> ContrastsLimmaImputeFacade

Methods

Public methods:

- ContrastsLimmaImputeFacade$new()
- ContrastsLimmaImputeFacade$clone()

Method `new()`**:** initialize

Usage:

```
ContrastsLimmaImputeFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  lod = NULL,
  df_method = c("observed", "borrowed"),
  weights = lfqdata$nr_children_col(),
  ...
)
```

Arguments:

`lfqdata` LFQData object (aggregated to protein level)

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`lod` numeric limit of detection; if NULL, auto-computed from data

`df_method` "observed" uses max(n_observed - p, 1); "borrowed" uses median df from successful fits

`weights` column name for per-observation weights (default: `lfqdata$nr_children_col()`). Pass `NULL` for unweighted.

`...` passed to strategy_limma (e.g. trend, robust)

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsLimmaImputeFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaVoom ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNestedFacade, ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 30, weight_missing = 0.5)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsLimmaImputeFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsLimmaVoomFacade

Limma-voom contrast analysis facade

Description

Limma-voom contrast analysis facade

Limma-voom contrast analysis facade

Details

Encapsulates the pipeline: strategy_limma -> build_model_limma_voom -> ContrastsLimma.

Uses vooma-style precision weights derived from a mean-variance trend, optionally combined with external weights (e.g. peptide/precursor counts).

Value

An R6 class generator.

Super classes

prolfqua::ContrastsInterface -> prolfqua::ContrastsFacadeBase -> ContrastsLimmaVoomFacade

Methods

Public methods:

- ContrastsLimmaVoomFacade$new()
- ContrastsLimmaVoomFacade$clone()

Method `new()`**:** initialize

Usage:

```
ContrastsLimmaVoomFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  weights = lfqdata$nr_children_col(),
  span = 0.5,
  plot = FALSE,
  ...
)
```

Arguments:

`lfqdata` LFQData object

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`weights` column name for per-observation weights (default: `lfqdata$nr_children_col()`). Pass `NULL` for unweighted.

`span` lowess smoother span for vooma trend (default 0.5)

`plot` logical; if TRUE, plot the mean-variance trend

`...` passed to `strategy_limma` (e.g. trend, robust)

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsLimmaVoomFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNestedFacade, ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(),

build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_
compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(),
get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(),
impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(),
lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(),
moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide()
register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(),
sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(),
strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config()
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsLimmaVoomFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsLimmaVoomImputeFacade

Limma-voom contrast analysis with LOD imputation facade

Description

Limma-voom contrast analysis with LOD imputation facade

Limma-voom contrast analysis with LOD imputation facade

Details

Encapsulates the pipeline: strategy_limma -> build_model_limma_voom_impute -> ContrastsLimma.

Combines vooma precision weights with LOD imputation for proteins whose fit produces NA coefficients (typically from entire missing groups).

Value

An R6 class generator.

Super classes

prolfqua::ContrastsInterface -> prolfqua::ContrastsFacadeBase -> ContrastsLimmaVoomImputeFacade

Methods

Public methods:

- ContrastsLimmaVoomImputeFacade$new()
- ContrastsLimmaVoomImputeFacade$clone()

Method new(): initialize

Usage:

```
ContrastsLimmaVoomImputeFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  lod = NULL,
  df_method = c("observed", "borrowed"),
  weights = lfqdata$nr_children_col(),
  span = 0.5,
  plot = FALSE,
  ...
)
```

Arguments:

`lfqdata` LFQData object (aggregated to protein level)

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`lod` numeric limit of detection; if NULL, auto-computed from data

`df_method` "observed" uses max(n_observed - p, 1); "borrowed" uses median df from successful fits

`weights` column name for per-observation weights (default: `lfqdata$nr_children_col()`). Pass `NULL` for unweighted.

`span` lowess smoother span for vooma trend (default 0.5)

`plot` logical; if TRUE, plot the mean-variance trend

`...` passed to `strategy_limma` (e.g. trend, robust)

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsLimmaVoomImputeFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu` `ContrastsLimmaVoomFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNestedFacade`, `ContrastsLmerNestedFaca` `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf` `compute_borrowed_variance()`, `compute_borrowed_variance_limma()`, `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_res` `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()` `new_imputed_model()`, `pivot_model_contrasts_to_wide()`, `register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median` `vcov.rfit_prolfqua()`

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 30, weight_missing = 0.5)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsLimmaVoomImputeFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsLimpaFacade *Limpa contrast analysis facade*

Description

Limpa contrast analysis facade

Limpa contrast analysis facade

Details

Encapsulates the pipeline: `strategy_limpa` -> `build_model_limpa` -> `ContrastsLimma`.

Operates as a `"same"`-level facade: it consumes whatever aggregated LFQData prolfqua's normal aggregation pipeline produced and fits limpa at that hierarchy level. If `config$opt_se` is set (e.g. when the input came from `AggregateLimpa`), the per-observation standard error is used as a vooma precision-weight predictor; otherwise plain vooma is fit. The `config$nr_children` column is required and is used to flag imputed observations (`nr_children == 0`) for vooma's imputation-aware DF correction.

For nested (peptide/precursor) input that should be rolled up to proteins via limpa's DPC quantification, use `ContrastsLimpaNestedFacade` instead — that facade owns the `AggregateLimpa` pre-step.

Value

An R6 class generator.

Super classes

`prolfqua::ContrastsInterface` -> `prolfqua::ContrastsFacadeBase` -> `ContrastsLimpaFacade`

Methods

Public methods:

- `ContrastsLimpaFacade$new()`
- `ContrastsLimpaFacade$clone()`

Method `new()`**:** initialize

Usage:

```
ContrastsLimpaFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  plot = FALSE,
  span = NULL,
  ...
)
```

Arguments:

`lfqdata` aggregated LFQData. If `config$opt_se` is set (e.g. from `AggregateLimpa`), the SE column is used as a vooma precision-weight predictor; otherwise vooma is fit without an external predictor.

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`plot` logical; if TRUE, plot the vooma mean-variance trend

`span` lowess smoother span (NULL = auto)

`...` passed to `strategy_limpa` (e.g. trend, robust)

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsLimpaFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu` `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaNestedFacade`, `ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf()`, `compute_borrowed_variance()`, `compute_borrowed_variance_` `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_results()`, `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()`, `new_imputed_model()`, `pivot_model_contrasts_to_wide()` `register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median_p_scaled()`, `vcov.rfit_prolfqua()`

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config()
lfqdata <- LFQData$new(istar$data, istar$config)
```

```
lfqdata <- lfqdata$get_Transformer()$log2()$lfq
agg <- AggregateLimpa$new(lfqdata, "protein")
lfq_agg <- agg$aggregate()
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsLimpaFacade$new(lfq_agg, "~ group_", contrasts)
head(fa$get_contrasts())
```

`ContrastsLimpaNestedFacade` *Limpa contrast analysis facade for nested input*

Description

Limpa contrast analysis facade for nested input

Limpa contrast analysis facade for nested input

Details

Encapsulates the full precursor -> protein pipeline: `AggregateLimpa` -> `strategy_limpa` -> `build_model_limpa` -> `ContrastsLimma`.

Takes nested (precursor/peptide-level) LFQData, runs limpa's DPC-based aggregation internally to produce protein-level expression with posterior standard errors, then fits a vooma model with imputation-aware precision weights.

For protein-level input that was already aggregated upstream via `AggregateLimpa`, use `ContrastsLimpaFacade` instead.

Value

An R6 class generator.

Super classes

`prolfqua::ContrastsInterface` -> `prolfqua::ContrastsFacadeBase` -> `ContrastsLimpaNestedFacade`

Methods

Public methods:

- `ContrastsLimpaNestedFacade$new()`
- `ContrastsLimpaNestedFacade$clone()`

Method `new()`**:** initialize

Usage:

```
ContrastsLimpaNestedFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  prefix = "protein",
  dpc_slope = 0.8,
  plot = FALSE,
  span = NULL,
  ...
)
```

Arguments:

`lfqdata` nested LFQData (precursor/peptide-level, log2-transformed)

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`prefix` prefix for the aggregated hierarchy level (default "protein")

`dpc_slope` DPC slope parameter passed to `AggregateLimpa` (default 0.8)

`plot` logical; if TRUE, plot the vooma mean-variance trend

`span` lowess smoother span (NULL = auto)

`...` passed to `strategy_limpa` (e.g. trend, robust)

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsLimpaNestedFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu` `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLmerNested` `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf` `compute_borrowed_variance()`, `compute_borrowed_variance_limma()`, `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_res` `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()` `new_imputed_model()`, `pivot_model_contrasts_to_wide()`, `register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median` `vcov.rfit_prolfqua()`

Examples

```
if (requireNamespace("limpa", quietly = TRUE)) {
  istar <- prolfqua::sim_lfq_data_peptide_config(Nprot = 10)
  lfqdata <- LFQData$new(istar$data, istar$config)
  lfqdata <- lfqdata$get_Transformer()$log2()$lfq
  contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
  fa <- ContrastsLimpaNestedFacade$new(lfqdata, "~ group_", contrasts)
  head(fa$get_contrasts())
}
```

`ContrastsLmerNestedFacade` *Lmer (mixed-model) contrast analysis facade for nested input*

Description

Lmer (mixed-model) contrast analysis facade for nested input

Lmer (mixed-model) contrast analysis facade for nested input

Details

Encapsulates the pipeline: `strategy_lmer` -> `build_model` -> `Contrasts` -> `ContrastsModerated`.

Takes child-hierarchy LFQData (e.g. peptide-level measurements nested within proteins) and returns protein-level fold-change estimates.

`modelstr` may be either a fixed-effects-only formula (e.g. `"~ group_"`) - in which case the facade appends `(1 | <deepest child hierarchy key>) + (1 | <sample name>)` derived from the LFQData - or a full mixed-model formula already containing random effects, which is passed through unchanged.

Value

An R6 class generator.

Super classes

`prolfqua::ContrastsInterface` -> `prolfqua::ContrastsFacadeBase` -> `ContrastsLmerNestedFacade`

Methods

Public methods:

- `ContrastsLmerNestedFacade$new()`
- `ContrastsLmerNestedFacade$clone()`

Method `new()`**:** initialize

Usage:

```
ContrastsLmerNestedFacade$new(lfqdata, modelstr, contrasts, ...)
```

Arguments:

`lfqdata` nested LFQData (subject_id strict subset of hierarchy_keys)

`modelstr` model formula RHS as string. Fixed effects only (e.g. "~ group_") - random effects are derived from `lfqdata` as `(1 | <deepest child key>) + (1 | <sample name>)`. A formula already containing random-effect bars is passed through unchanged.

`contrasts` named character vector of contrasts

`...` passed to `strategy_lmer`

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsLmerNestedFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata <- lfqdata$get_Transformer()$log2()$lfq
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
# Random effects derived from lfqdata; equivalent to passing the full
# mixed-model formula explicitly.
fa <- ContrastsLmerNestedFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsLMFacade *LM contrast analysis facade*

Description

LM contrast analysis facade

LM contrast analysis facade

Details

Encapsulates the pipeline: strategy_lm -> build_model -> Contrasts -> ContrastsModerated.

Value

An R6 class generator.

Super classes

prolfqua::ContrastsInterface -> prolfqua::ContrastsFacadeBase -> ContrastsLMFacade

Methods

Public methods:

- ContrastsLMFacade$new()
- ContrastsLMFacade$clone()

Method `new()`**:** initialize

Usage:

```
ContrastsLMFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  weights = lfqdata$nr_children_col(),
  ...
)
```

Arguments:

`lfqdata` LFQData object

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`weights` column name for per-observation weights (default: `lfqdata$nr_children_col()`). Pass `NULL` for unweighted.

`...` passed to strategy_lm

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsLMFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImputeFacade, ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(),

lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config()
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsLMFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsLMImputeFacade

LM contrast analysis with LOD imputation facade

Description

LM contrast analysis with LOD imputation facade

LM contrast analysis with LOD imputation facade

Details

Encapsulates the pipeline: strategy_lm -> build_model (with impute = TRUE) -> Contrasts -> ContrastsModerated.

Proteins whose initial lm fit fails or produces NA coefficients are re-fitted after imputing missing values with the limit of detection (LOD). The covariance matrix is borrowed from successful fits so that the variance is not underestimated by the constant imputation.

Value

An R6 class generator.

Super classes

prolfqua::ContrastsInterface -> prolfqua::ContrastsFacadeBase -> ContrastsLMImputeFacade

Methods

Public methods:

- ContrastsLMImputeFacade$new()
- ContrastsLMImputeFacade$clone()

Method new(): initialize

Usage:

```
ContrastsLMImputeFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  lod = NULL,
  borrow_method = c("sigma", "vcov"),
  df_method = c("observed", "borrowed"),
  weights = lfqdata$nr_children_col(),
  ...
)
```

Arguments:

`lfqdata` LFQData object (aggregated to protein level)

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`lod` numeric limit of detection; if NULL, auto-computed from data

`borrow_method` "sigma" borrows scalar sigma and uses per-protein (X'X)^-1; "vcov" borrows element-wise median of full vcov matrices

`df_method` "observed" uses max(n_observed - p, 1); "borrowed" uses median df from successful fits

`weights` column name for per-observation weights (default: `lfqdata$nr_children_col()`). Pass `NULL` for unweighted.

`...` passed to `strategy_lm`

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsLMImputeFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImputeFacade`, `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste` `ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf()`, `compute_borrowed_variance()`, `compute_borrowed_variance_` `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_results()`, `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()`, `new_imputed_model()`, `pivot_model_contrasts_to_wide()` `register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median_p_scaled()`, `vcov.rfit_prolfqua()`

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 30, weight_missing = 0.5)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsLMImputeFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsModerated *Limma moderated contrasts*

Description

Limma moderated contrasts

Limma moderated contrasts

Value

An R6 class generator.

Super class

`prolfqua::ContrastsInterface` -> `ContrastsModerated`

Public fields

`Contrast` Class implementing the Contrast interface

`model_name` name of model

`subject_id` columns with subject_id (proteinID)

`p.adjust` function to adjust p-values

`variance_floor` optional lower bound for posterior variances

Methods

Public methods:

- `ContrastsModerated$new()`
- `ContrastsModerated$get_contrast_sides()`
- `ContrastsModerated$get_linfct()`
- `ContrastsModerated$get_contrasts()`
- `ContrastsModerated$clone()`

Method `new()`**:** initialize

Usage:

```
ContrastsModerated$new(
  Contrast,
  model_name = paste0(Contrast$model_name, "_moderated"),
  p.adjust = prolfqua::adjust_p_values,
  variance_floor = NULL
)
```

Arguments:

`Contrast` class implementing the ContrastInterface

`model_name` name of the model

`p.adjust` function to adjust p-values - default BH

`variance_floor` optional positive lower bound for posterior variances

Method `get_contrast_sides()`**:** get both sides of contrasts

Usage:

```
ContrastsModerated$get_contrast_sides()
```

Method `get_linfct()`**:** get linear functions from contrasts

Usage:

```
ContrastsModerated$get_linfct(global = TRUE)
```

Arguments:

`global` logical TRUE - get the a linear functions for all models, FALSE - linear function for each model

Method `get_contrasts()`**:** applies limma moderation

Usage:

```
ContrastsModerated$get_contrasts(all = FALSE)
```

Arguments:

`all` should all columns be returned (default FALSE)

`global` use a global linear function (determined by get_linfct)

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsModerated$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

`moderated_p_limma`

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu`
`ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste`
`ContrastsLmerNestedFacade`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf`
`compute_borrowed_variance()`, `compute_borrowed_variance_limma()`, `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_res`
`model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()`

new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median, vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 50)
protIntensity <- istar$data
config <- istar$config


lProt <- LFQData$new(protIntensity, config)
lProt$rename_response("transformedIntensity")
modelFunction <-
  strategy_lm("transformedIntensity  ~ group_")
mod <- build_model(
 lProt,
 modelFunction)

Contr <- c("dil.b_vs_a" = "group_A - group_Ctrl")
contrast <- prolfqua::Contrasts$new(mod,
 Contr)
contrast <- ContrastsModerated$new(contrast)
bb <- contrast$get_contrasts()
# LOD-imputed refit for proteins the plain lm cannot estimate
imp <- ContrastsLMImputeFacade$new(lProt, "~ group_", Contr)$contrast

contrast$get_contrasts() |> dim()
(xx <- imp$get_contrasts())   |> dim()
merged <- merge_contrasts_results(contrast, imp)

merged$more$get_contrasts() |> dim()
stopifnot(all(dim(merged$merged$get_contrasts()) == c(50, 16)))
stopifnot(all(dim(merged$same$get_contrasts()) == c(49, 16)))

cs <- contrast$get_contrast_sides()
cslf <- contrast$get_linfct()
ctr <- contrast$get_contrasts()
ctrwide <- contrast$to_wide()
cp <- contrast$get_Plotter()

print(cp$histogram()$p.value, vp=NULL)
print(cp$histogram()$FDR, vp = NULL)

cp$volcano()
cp$ma_plot()
```

ContrastsModeratedDEqMS

DEqMS count-dependent moderated contrasts

Description

DEqMS count-dependent moderated contrasts

DEqMS count-dependent moderated contrasts

Details

Decorator that wraps any Contrasts object and applies count-dependent empirical Bayes variance shrinkage. Similar to `ContrastsModerated` but the prior variance depends on the number of quantified peptides/PSMs per protein: proteins with many peptides get less shrinkage, proteins with few peptides get more.

Value

An R6 class generator.

Super class

`prolfqua::ContrastsInterface` -> `ContrastsModeratedDEqMS`

Public fields

`Contrast` Class implementing the Contrast interface

`count_df` data.frame with subject_id + count column

`count_column` name of the count column in count_df

`loess_span` span parameter for LOESS fit

`model_name` name of model

`subject_id` columns with subject_id (proteinID)

`p.adjust` function to adjust p-values

Methods

Public methods:

- `ContrastsModeratedDEqMS$new()`
- `ContrastsModeratedDEqMS$get_contrast_sides()`
- `ContrastsModeratedDEqMS$get_linfct()`
- `ContrastsModeratedDEqMS$get_contrasts()`
- `ContrastsModeratedDEqMS$clone()`

Method `new()`: initialize

Usage:

```
ContrastsModeratedDEqMS$new(
  Contrast,
  count_df,
  count_column,
  loess_span = 0.75,
  model_name = paste0(Contrast$model_name, "_DEqMS"),
  p.adjust = prolfqua::adjust_p_values
)
```

Arguments:

`Contrast` class implementing the ContrastInterface
`count_df` data.frame with subject_id columns and a count column
`count_column` name of the count column in count_df
`loess_span` span for LOESS variance fit (default 0.75)
`model_name` name of the model
`p.adjust` function to adjust p-values - default BH

Method `get_contrast_sides()`: get both sides of contrasts

Usage:

```
ContrastsModeratedDEqMS$get_contrast_sides()
```

Method `get_linfct()`: get linear functions from contrasts

Usage:

```
ContrastsModeratedDEqMS$get_linfct(global = TRUE)
```

Arguments:

`global` logical TRUE - get linear functions for all models

Method `get_contrasts()`: applies DEqMS-style count-dependent moderation

Usage:

```
ContrastsModeratedDEqMS$get_contrasts(all = FALSE)
```

Arguments:

`all` should all columns be returned (default FALSE)

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
ContrastsModeratedDEqMS$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

`moderated_p_deqms_long`

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu` `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste` `ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf` `compute_borrowed_variance()`, `compute_borrowed_variance_limma()`, `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_res` `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()` `new_imputed_model()`, `pivot_model_contrasts_to_wide()`, `register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median` `vcov.rfit_prolfqua()`

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 50)
protIntensity <- istar$data
config <- istar$config

lProt <- LFQData$new(protIntensity, config)
lProt$rename_response("transformedIntensity")
modelFunction <-
  strategy_lm("transformedIntensity ~ group_")
mod <- build_model(
 lProt,
 modelFunction)

Contr <- c("dil.b_vs_a" = "group_A - group_Ctrl")
contrast <- prolfqua::Contrasts$new(mod, Contr)

# Build count_df from config
count_df <- dplyr::select(protIntensity,
  dplyr::all_of(c(config$hierarchy_keys_depth(), "nrPeptides"))) |>
  dplyr::distinct()

deqms <- ContrastsModeratedDEqMS$new(contrast,
  count_df = count_df,
  count_column = "nrPeptides")

bb <- deqms$get_contrasts()
stopifnot(all(c("diff", "p.value", "FDR", "sigma") %in% colnames(bb)))

# Merge with LOD-imputed refits for proteins the plain lm cannot estimate
imp <- ContrastsLMImputeFacade$new(lProt, "~ group_", Contr)$contrast
merged <- merge_contrasts_results(deqms, imp)

cs <- deqms$get_contrast_sides()
cslf <- deqms$get_linfct()
ctrwide <- deqms$to_wide()
cp <- deqms$get_Plotter()
cp$volcano()
```

`ContrastsPlotter` *plot contrasts*

Description

plot contrasts

plot contrasts

Value

An R6 class generator.

Public fields

`model_name` of column with model name

`subject_id` hierarchy key columns

`diff` column with fold change differences

`contrast` column with contrasts names, default "contrast"

`group` crosstalk group name for linked brushing, default "BB"

`volcano_spec` volcano plot specification

`score_spec` score plot specification

`histogram_spec` plot specification

`fcthresh` fold change threshold

`avg.abundance` name of column containing avg abundance values.

Methods

Public methods:

- `ContrastsPlotter$new()`
- `ContrastsPlotter$histogram()`
- `ContrastsPlotter$histogram_diff()`
- `ContrastsPlotter$volcano()`
- `ContrastsPlotter$volcano_plotly()`
- `ContrastsPlotter$ma_plot()`
- `ContrastsPlotter$ma_plotly()`
- `ContrastsPlotter$score_plot()`
- `ContrastsPlotter$barplot_threshold()`
- `ContrastsPlotter$clone()`

Method `new()`**:** create ContrastsPlotter

Usage:

```
ContrastsPlotter$new(
  contrast_df,
  subject_id,
  volcano = list(list(score = "FDR", thresh = 0.1)),
 histogram = list(list(score = "p.value", xlim = c(0, 1, 0.05)), list(score = "FDR",
    xlim = c(0, 1, 0.05))),
  score = list(list(score = "statistic", thresh = NULL)),
  fcthresh = 1,
  modelName = "modelName",
  diff = "diff",
  contrast = "contrast",
  avg.abundance = "avgAbd",
  group = "BB"
)
```

Arguments:

`contrast_df` frame with contrast data

`subject_id` columns containing subject Identifier

`volcano` which score to plot and which ablines to add.

`histogram` which scores to plot and which range (x) should be shown.

`score` score parameters

`fcthresh` default 1 (log2 FC threshold)

`modelName` name of the colour column. Defaults to `"modelName"`; when left at the default and the contrast carries an `estimate_type` column, that column is used for colouring instead (so observed vs imputed/fallback rows stay distinguishable).

`diff` fold change (difference) diff column

`contrast` contrast column

`avg.abundance` name of column with average abundance

`group` crosstalk group name for linked brushing, default "BB"

Method `histogram()`**:** plot histogram of selected scores (e.g. p-value, FDR, t-statistics)

Usage:

```
ContrastsPlotter$histogram()
```

Method `histogram_diff()`**:** plot histogram of differences (diff) fold change

Usage:

```
ContrastsPlotter$histogram_diff(binwidth = 0.05)
```

Arguments:

`binwidth` with of bin in histogram

Method `volcano()`**:** volcano plots (fold change vs FDR)

Usage:

```
ContrastsPlotter$volcano(
  colour = self$model_name,
  legend = TRUE,
  scales = c("fixed", "free", "free_x", "free_y"),
  min_score = NULL
)
```

Arguments:

`colour` column name with color information default modelName

`legend` default TRUE

`scales` default fixed `facet_wrap`, scales argument

`min_score` optional lower bound for p-values or FDR values. If NULL, only exact zero and negative values are replaced with the smallest positive observed value in the same score column.

Method `volcano_plotly()`**:** plotly volcano plots

Usage:

```
ContrastsPlotter$volcano_plotly(
  colour = self$model_name,
  legend = TRUE,
  scales = c("fixed", "free", "free_x", "free_y"),
  min_score = NULL
)
```

Arguments:

`colour` column in contrast matrix with colour coding

`legend` default TRUE

`scales` default fixed `facet_wrap`, scales argument

`min_score` optional lower bound for p-values or FDR values. If NULL, only exact zero and negative values are replaced with the smallest positive observed value in the same score column.

Returns: list of ggplots

Method `ma_plot()`**:** ma plot

MA plot displays the effect size estimate as a function of the mean protein intensity across groups. Each dot represents an observed protein. Red horizontal lines represent the fold-change threshold.

Sometimes measured effects sizes (differences between samples groups) are biased by the signal intensity (here protein abundance). Such systematic effects can be explored using MA-plots.

Usage:

```
ContrastsPlotter$ma_plot(
  fc = self$fcthresh,
  colour = self$model_name,
  legend = TRUE,
  rank = TRUE
)
```

Arguments:

`fc` fold change abline

`colour` column in contrast matrix with colour coding

`legend` enable legend default TRUE

`rank` default FALSE, if TRUE then rank of avgAbd is used.

Returns: ggplot

Method `ma_plotly()`**:** ma plotly

Usage:

```
ContrastsPlotter$ma_plotly(
  fc = self$fcthresh,
  colour = self$model_name,
  legend = TRUE,
  rank = FALSE
)
```

Arguments:

`fc` horizontal lines

`colour` column in contrast matrix with colour coding.

`legend` enable legend default TRUE

`rank` default FALSE, if TRUE then rank of avgAbd is used.

Returns: list of ggplots

Method `score_plot()`**:** plot a score against the log2 fc e.g. t-statistic

Usage:

```
ContrastsPlotter$score_plot(scorespec, colour = self$model_name, legend = TRUE)
```

Arguments:

`scorespec` list(score="statistics", fcthres = 2, thresh = 5)

`colour` column with colour coding

`legend` enable legend default TRUE

Returns: list of ggplots

Method `barplot_threshold()`**:** shows the number of significant proteins per contrasts

Usage:

```
ContrastsPlotter$barplot_threshold()
```

Returns: list which contains ggplots and summary tables

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsPlotter$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Other plotting: INTERNAL_FUNCTIONS_BY_FAMILY, missigness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), plot_estimate(), plot_heatmap(), plot_heatmap_cor(), plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_na_heatmap(), plot_pca(), plot_raster(), plot_sample_correlation(), upset_interaction_missing_s upset_missing_stats()

Examples

```
istar <- sim_lfq_data_peptide_config(Nprot = 20)
model_name <- "Model"
modelFunction <-
  strategy_lmer("abundance  ~ group_ + (1 | peptide_Id) + (1|sample)",
   model_name = model_name)
pepIntensity <- istar$data
config <- istar$config

mod <- build_model(
```

```
  pepIntensity,
  modelFunction,
  model_name = model_name,
  subject_id = config$hierarchy_keys_depth())

 Contr <- c("group_A_vs_Ctrl" = "group_A - group_Ctrl",
 "group_B_vs_Ctrl" = "group_B - group_Ctrl"
 )
contrast <- prolfqua::Contrasts$new(mod,
  Contr)
contr <- contrast$get_contrasts()
cp <- ContrastsPlotter$new(contr,
  contrast$subject_id,
  volcano = list(list(score = "FDR", thresh = 0.1)),
  histogram = list(list(score = "p.value", xlim = c(0,1,0.05)),
                list(score = "FDR", xlim = c(0,1,0.05))),
  score =list(list(score = "statistic",  thresh = 5))
  )

stopifnot("plotly" %in% class(cp$volcano_plotly()$FDR))
stopifnot("ggplot" %in% class(cp$score_plot(legend=FALSE)$statistic))
p <- cp$histogram()
stopifnot("ggplot" %in% class(p$FDR))
stopifnot("ggplot" %in% class(p$p.value))
res <- cp$volcano()
stopifnot("ggplot" %in% class(res$FDR))
res_plotly <- cp$volcano_plotly()
stopifnot("plotly" %in% class(res_plotly$FDR))
stopifnot("ggplot" %in% class(cp$ma_plot()))
stopifnot("plotly" %in%   class(cp$ma_plotly(rank=TRUE)))
res  <- cp$barplot_threshold()
stopifnot("ggplot" %in% class(res$FDR$plot))
stopifnot("ggplot" %in%  class(cp$histogram_diff()))
```

`ContrastsRfitFacade` *Rfit rank-based regression contrast analysis facade*

Description

Rfit rank-based regression contrast analysis facade

Rfit rank-based regression contrast analysis facade

Details

Encapsulates the pipeline: `strategy_rfit` -> `build_model` -> `Contrasts` -> `ContrastsModerated`, using `rfit` rank-based linear regression. Output is the standard Wald contrast schema; the empirical-Bayes moderation shrinks the rank-based scale across proteins.

Unlike `ContrastsLMFacade` this backend takes no observation weights (`rfit` has no `weights` argument), so `nr_children` weighting is not applied.

Value

An R6 class generator.

Super classes

prolfqua::ContrastsInterface -> prolfqua::ContrastsFacadeBase -> ContrastsRfitFacade

Methods

Public methods:

- ContrastsRfitFacade$new()
- ContrastsRfitFacade$clone()

Method `new()`**:** initialize

Usage:

```
ContrastsRfitFacade$new(lfqdata, modelstr, contrasts, ...)
```

Arguments:

`lfqdata` LFQData object

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`...` passed to strategy_rfit

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsRfitFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config()
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsRfitFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsRfitImputeFacade

Rfit rank-regression contrast analysis with LOD imputation facade

---

Description

Rfit rank-regression contrast analysis with LOD imputation facade

Rfit rank-regression contrast analysis with LOD imputation facade

Details

The rank-based analogue of ContrastsLMImputeFacade. Encapsulates the pipeline: strategy_rfit -> build_model_impute -> Contrasts -> ContrastsModerated, using rfit.

Proteins whose initial rfit fit fails, is singular, or has an incomplete design are re-fitted after imputing missing values with the limit of detection (LOD). Uncertainty is borrowed from successful donor fits so it is not underestimated by the constant imputation.

Differences from ContrastsLMImputeFacade:

- Covariance borrowing is **vcov-only** (element-wise median of the donors' full named covariance matrices). rfit exposes no lm-style cov.unscaled, so the scalar-sigma borrowing mode is not available and is not exposed.
- Borrowing is **fail-hard** (on_misalign = "fail"): if the donor covariance matrices cannot be aligned by coefficient name, the rescue is skipped and those proteins remain in get_missing() rather than carrying an lm-specific approximation.
- No observation weights (rfit has no weights argument), matching plain rfit.

modelName is the facade key "rfit_impute"; rescued rows are flagged in the estimate_type column as "lod_imputed", the same convention used by ContrastsLMImputeFacade.

Value

An R6 class generator.

Super classes

prolfqua::ContrastsInterface -> prolfqua::ContrastsFacadeBase -> ContrastsRfitImputeFacade

Methods

Public methods:

- ContrastsRfitImputeFacade$new()
- ContrastsRfitImputeFacade$clone()

Method `new()`**:** initialize

Usage:

```
ContrastsRfitImputeFacade$new(
  lfqdata,
  modelstr,
  contrasts,
  lod = NULL,
  df_method = c("observed", "borrowed"),
  ...
)
```

Arguments:

`lfqdata` LFQData object (aggregated to protein level)

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`lod` numeric limit of detection; if NULL, auto-computed from data

`df_method` "observed" uses max(n_observed - p, 1); "borrowed" uses median df from successful fits

`...` passed to `strategy_rfit`

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsRfitImputeFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

ContrastsLMImputeFacade, ContrastsRfitFacade, build_model_impute

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma()

new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median, vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 30, weight_missing = 0.5)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsRfitImputeFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsRLMFacade *RLM contrast analysis facade*

Description

RLM contrast analysis facade

RLM contrast analysis facade

Details

Encapsulates the pipeline: strategy_rlm -> build_model -> Contrasts -> ContrastsModerated.

Value

An R6 class generator.

Super classes

prolfqua::ContrastsInterface -> prolfqua::ContrastsFacadeBase -> ContrastsRLMFacade

Methods

Public methods:

- ContrastsRLMFacade$new()
- ContrastsRLMFacade$clone()

Method `new()`**:** initialize

Usage:

```
ContrastsRLMFacade$new(lfqdata, modelstr, contrasts, ...)
```

Arguments:

`lfqdata` LFQData object

`modelstr` model formula string (e.g. "~ group_")

`contrasts` named character vector of contrasts

`...` passed to strategy_rlm

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ContrastsRLMFacade$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config()
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsRLMFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

ContrastsROPECA *ROPECA reproducibility-optimization method*

Description

ROPECA reproducibility-optimization method

ROPECA reproducibility-optimization method

Details

ROPECA optimizes the reproducibility of statistical testing on peptide-level and aggregates the peptide-level changes to determine differential protein-level expression.

Value

An R6 class generator.

Super class

`prolfqua::ContrastsInterface` -> `ContrastsROPECA`

Public fields

`Contrast` Contrast

`contrast_result` contrast result

`model_name` model name

`subject_id` columns with protein ID's

`p.adjust` method to use for p.value adjustment

Methods

Public methods:

- `ContrastsROPECA$new()`
- `ContrastsROPECA$get_contrast_sides()`
- `ContrastsROPECA$get_linfct()`
- `ContrastsROPECA$get_contrasts()`
- `ContrastsROPECA$get_Plotter()`
- `ContrastsROPECA$to_wide()`
- `ContrastsROPECA$clone()`

Method `new()`**:** initialize

Usage:

```
ContrastsROPECA$new(
  Contrast,
  model_name = "ROPECA",
  p.adjust = prolfqua::adjust_p_values
)
```

Arguments:

`Contrast` e.g. instance of Contrasts class, or ContrastsModerated

`model_name` default ROPECA

`p.adjust` function to use for p.value adjustment

Method `get_contrast_sides()`**:** show names of contrasts

Usage:

```
ContrastsROPECA$get_contrast_sides()
```

Returns: data.frame

Method `get_linfct()`**:** get linear function used to determine contrasts

Usage:

```
ContrastsROPECA$get_linfct()
```

Returns: data.frame

Method `get_contrasts()`: get contrasts

Usage:

```
ContrastsROPECA$get_contrasts(all = FALSE)
```

Arguments:

`all` should all columns be returned (default FALSE)

`global` use a global linear function (determined by get_linfct)

Returns: data.frame

Method `get_Plotter()`: get `ContrastsPlotter`

Usage:

```
ContrastsROPECA$get_Plotter(fdr_threshold = 0.1, fc_threshold = 2)
```

Arguments:

`fdr_threshold` FDR threshold

`fc_threshold` FC threshold

Returns: `ContrastsPlotter`

Method `to_wide()`: convert to wide format

Usage:

```
ContrastsROPECA$to_wide(
  columns = c("beta.based.significance", "FDR.beta.based.significance")
)
```

Arguments:

`columns` value column default beta.based.significance

Returns: data.frame

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
ContrastsROPECA$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

`summary_ROPECA_median_p_scaled`

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu` `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste` `ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf` `compute_borrowed_variance()`, `compute_borrowed_variance_limma()`, `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`,

get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config(Nprot=20)
istar_data <- istar$data
modelFunction <-
  strategy_lm("abundance  ~ group_")
pepIntensity <- istar_data
config <- istar$config$clone(deep = TRUE)
config$hierarchy_depth <- 2
config$hierarchy_keys_depth()

mod <- build_model(
 pepIntensity,
 modelFunction,
 subject_id = config$hierarchy_keys_depth())

 Contr <- c("AvsCtrl" = "group_A - group_Ctrl")


 contr <- prolfqua::Contrasts$new(mod, Contr)
 dim(contr$get_contrasts())
 contrM <- prolfqua::ContrastsModerated$new(contr)
 dim(contrM$get_contrasts())
 contrast <- prolfqua::ContrastsROPECA$new(contrM)
 contrast$get_contrasts()
 contrast <- prolfqua::ContrastsROPECA$new(contr)
 tmp <- contrast$get_contrasts()
 dim(tmp)
 pl <- contrast$get_Plotter()
 contrast$to_wide()
 contrast$get_linfct()
 contrast$get_contrast_sides()
 pl$histogram()
 pl$ma_plot()
```

ContrastsROPECANestedFacade

ROPECA contrast analysis facade for nested input

Description

ROPECA contrast analysis facade for nested input

ROPECA contrast analysis facade for nested input

Details

Encapsulates the pipeline: strategy_lm -> build_model -> Contrasts -> ContrastsROPECA.

ROPECA fits per-peptide linear models and aggregates peptide-level p-values to the protein level. Input must be nested LFQData (peptide subject_id strictly below the protein hierarchy).

Value

An R6 class generator.

Super classes

prolfqua::ContrastsInterface -> prolfqua::ContrastsFacadeBase -> ContrastsROPECANestedFacade

Methods

Public methods:

- ContrastsROPECANestedFacade$new()
- ContrastsROPECANestedFacade$get_contrasts()
- ContrastsROPECANestedFacade$get_Plotter()
- ContrastsROPECANestedFacade$to_wide()
- ContrastsROPECANestedFacade$clone()

Method new(): initialize

Usage:

```
ContrastsROPECANestedFacade$new(lfqdata, modelstr, contrasts, ...)
```

Arguments:

lfqdata nested LFQData (peptide-level)

modelstr model formula string (e.g. "~ group_")

contrasts named character vector of contrasts

... passed to strategy_lm

Method get_contrasts(): Get contrast results with standardized column names.

ROPECA's beta.based.significance is mapped to p.value and FDR.beta.based.significance to FDR.

Columns not directly produced by ROPECA are derived heuristically:

- std.error = diff / statistic (algebraic: t = estimate / SE)
- sigma = mad.estimate (MAD of peptide fold changes)
- df = n_not_na (number of contributing peptides)
- conf.low/conf.high via diff +/- qt(0.975, df) * |std.error|

Usage:

```
ContrastsROPECANestedFacade$get_contrasts()
```

Method get_Plotter(): get ContrastsPlotter (uses standardized column names)

Usage:

```
ContrastsROPECANestedFacade$get_Plotter(fc_threshold = 2, fdr_threshold = 0.1)
```

Arguments:

fc_threshold fold change threshold

fdr_threshold FDR threshold

Method `to_wide()`: convert results to wide format

Usage:

```
ContrastsROPECANestedFacade$to_wide(columns = c("p.value", "FDR", "statistic"))
```

Arguments:

`columns` value columns to pivot, default `c("p.value", "FDR", "statistic")`

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
ContrastsROPECANestedFacade$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata <- lfqdata$get_Transformer()$log2()$lfq
contrasts <- c("A_vs_Ctrl" = "group_A - group_Ctrl")
fa <- ContrastsROPECANestedFacade$new(lfqdata, "~ group_", contrasts)
head(fa$get_contrasts())
fa$to_wide()
```

`ContrastsTable` *holds results when contrasts are added.*

Description

holds results when contrasts are added.

holds results when contrasts are added.

Value

An R6 class generator.

Super class

`prolfqua::ContrastsInterface` -> `ContrastsTable`

Public fields

`contrast_result` contrast results

`model_name` model name

`subject_id` default protein_Id

Methods

Public methods:

- `ContrastsTable$new()`
- `ContrastsTable$get_contrast_sides()`
- `ContrastsTable$get_linfct()`
- `ContrastsTable$get_contrasts()`
- `ContrastsTable$get_Plotter()`
- `ContrastsTable$clone()`

Method `new()`**:** initialize

Usage:

```
ContrastsTable$new(
  contrastsdf,
  subject_id = "protein_Id",
  model_name = "ContrastTable"
)
```

Arguments:

`contrastsdf` data.frame

`subject_id` default protein_Id

`model_name` default ContrastTable

Method `get_contrast_sides()`**:** return sides of contrast

Usage:

```
ContrastsTable$get_contrast_sides()
```

Returns: data.frame

Method `get_linfct()`: not implemented

Usage:

```
ContrastsTable$get_linfct()
```

Method `get_contrasts()`: get contrasts

Usage:

```
ContrastsTable$get_contrasts(all = FALSE)
```

Arguments:

`all` should all columns be returned (default FALSE)

`global` use a global linear function (determined by get_linfct)

Method `get_Plotter()`: get `ContrastsPlotter`

Usage:

```
ContrastsTable$get_Plotter(fc_threshold = 1, fdr_threshold = 0.1)
```

Arguments:

`fc_threshold` fold change threshold

`fdr_threshold` fdr threshold

Returns: `ContrastsPlotter`

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
ContrastsTable$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

`summary_ROPECA_median_p_scaled`

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu` `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste` `ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf` `compute_borrowed_variance()`, `compute_borrowed_variance_limma()`, `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_res` `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()` `new_imputed_model()`, `pivot_model_contrasts_to_wide()`, `register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median` `vcov.rfit_prolfqua()`

Examples

```
istar <- prolfqua::sim_lfq_data_protein_config(Nprot = 30)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$rename_response("transformedIntensity")
Contrasts <- c("aC" = "group_A - group_Ctrl",
"bC" = "group_B - group_Ctrl")
fa <- ContrastsLMFacade$new(lfqdata, "~ group_", Contrasts)
ctr <- fa$get_contrasts()
fa$contrast$subject_id
xcx <- ContrastsTable$new(ctr, subject_id = fa$contrast$subject_id, model_name = "TableTest")
xcx$get_contrasts()
xcx$get_Plotter()$volcano()
stopifnot(is.null(xcx$get_contrast_sides()))
stopifnot(is.null(xcx$get_linfct()))
stopifnot(ncol(xcx$to_wide()) == 9)
```

---

contrasts_linfct *compute group averages*

Description

used in p2621, p2109

Usage

```
contrasts_linfct(
  models,
  linfct,
  subject_id = "protein_Id",
  contrastfun = prolfqua::compute_lmer_contrast
)
```

Examples

```
modelSummary_A <- sim_build_models_lm()
m <- get_complete_model_fit(modelSummary_A$model_df)

linfct <- linfct_from_model(m$linear_model[[1]], as_list = FALSE)
factor_contrasts <- linfct_matrix_contrasts(linfct, c(A_vs_B = "TreatmentA - TreatmentB"))

factor_levelContrasts <- contrasts_linfct( m,
        factor_contrasts,
        subject_id = "protein_Id",
        contrastfun = prolfqua::compute_contrast)
```

`data_checksummarizationrobust87`
Reference input for the robust summarisation check (87 percent)

Description

log2 peptide areas of one protein, used by the tests of the robust (medpolish/rlm) protein summarisation. See 'inst/script/README.md'.

Usage

```
data_checksummarizationrobust87
```

Format

A data frame with 20 rows and the columns 'log2Area', 'peptide_Id', 'sampleName'.

See Also

Other data: `PACKAGE_DATA`, `data_checksummarizerobust69`, `data_ionstar`, `prolfqua_data()`, `x5463yzwer453bbb`

`data_checksummarizerobust69`
Reference input for the robust summarisation check (69 percent)

Description

log2 peptide areas of one protein, used by the tests of the robust (medpolish/rlm) protein summarisation. See 'inst/script/README.md'.

Usage

```
data_checksummarizerobust69
```

Format

A data frame with 20 rows and the columns 'log2Area', 'peptide_Id', 'sampleName'.

See Also

Other data: `PACKAGE_DATA`, `data_checksummarizationrobust87`, `data_ionstar`, `prolfqua_data()`, `x5463yzwer453bbb`

data_ionstar *IonStar peptide-level example data*

Description

Peptide intensities of 200 proteins from the IonStar human cell lysate with E. coli spike-in dilution series (dilutions a to e, 4 replicates each), processed with MaxQuant. An R6 object holding the data, its `AnalysisConfiguration`, and the methods `filtered()`, `normalized()` and `subset_normalized()`. See 'inst/script/README.md' for its origin.

Usage

```
data_ionstar
```

Format

An R6 object of class 'IonstarData'; '$data' is a data frame with 26520 rows.

Source

PRIDE PXD003881

See Also

Other data: `PACKAGE_DATA`, `data_checksummarizationrobust87`, `data_checksummarizerobust69`, `prolfqua_data()`, `x5463yzwer453bbb`

df.residual.rfit_prolfqua *Residual degrees of freedom for an augmented rfit fit*

Description

Residual degrees of freedom for an augmented rfit fit

Usage

```
## S3 method for class 'rfit_prolfqua'
df.residual(object, ...)
```

Arguments

`object`	an 'rfit_prolfqua' fit
`...`	ignored

Value

number of observations minus number of coefficients.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
fit <- strategy_rfit("Sepal.Length ~ Species")$model_fun(iris)
df.residual(fit)
```

`df.residual.rlm` *Residual degrees of freedom for rlm objects*

Description

`stats::df.residual` returns `NA` for `rlm` objects. This S3 method computes weighted residual df instead.

Usage

```
## S3 method for class 'rlm'
df.residual(object, ...)
```

Arguments

`object`	an `rlm` object
`...`	ignored

Value

numeric scalar

encode_bin_resp *convert to binary response*

Description

convert to binary response

Usage

```
encode_bin_resp(lfqdata, name = "bin_resp")
```

Arguments

lfqdata	LFQData object
name	column name for binary response

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
lfq$set_data(encode_bin_resp(lfq))
lfq$set_config_value("bin_resp", "bin_resp")
lfq$data_long()[["bin_resp"]]
```

estimate_intensity *Aggregates e.g. protein abundances from peptide abundances*

Description

Aggregates e.g. protein abundances from peptide abundances

Usage

```
estimate_intensity(lfqdata, method = c("medpolish", "rlm"))
```

Arguments

lfqdata	LFQData object
method	"medpolish" (Tukey's median polish, column 'medpolish') or "rlm" (robust regression with 'MASS::rlm', column 'lmrob')

Value

returns list with data (data.frame) and config (AnalysisConfiguration)

See Also

Other aggregation: INTERNAL_FUNCTIONS_BY_FAMILY, aggregate_intensity_top_n(), plot_estimate(), plot_hierarchies_line()

Examples

```
dd <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(dd$data, dd$config)
lfq <- lfq$get_Transformer()$log2()$lfq
bbMed <- estimate_intensity(lfq, method = "medpolish")
bbRob <- estimate_intensity(lfq, method = "rlm")
nrow(bbMed$data)
nrow(bbRob$data)
xt <- dplyr::inner_join(bbMed$data, bbRob$data)
plot(xt$medpolish, xt$lmrob, log = "xy", pch = "*")
abline(0, 1, col = 2)
```

FACADE_REGISTRY *Registry of available contrast facade classes*

Description

Read-only snapshot of the built-in prolfqua facade registry, taken at package load time. It is derived from the single source of truth (`.seed_facade_registry()`); use `register_facade` to add entries from downstream packages, `lookup_facade` to resolve a single entry, and `list_facades()` to enumerate the live registry (which reflects downstream registrations).

Usage

```
FACADE_REGISTRY
```

Format

An object of class `facade_registry` (inherits from `list`) of length 18.

Details

Each entry has fields `class`, `needs`, `package`, and `needs_saint_annotation`.

Value

A named list of built-in facade registry entries.

Examples

```
names(FACADE_REGISTRY)
FACADE_REGISTRY$limma$class
```

filter_proteins_by_peptide_count *Keep only the proteins with enough peptides*

Description

Keeps the rows of the proteins with at least ‘config$min_peptides_protein‘ children at the next hierarchy level, counted by [nr_B_in_A()], and adds that count. The package dataset ‘data_ionstar‘ calls it from its ‘filtered()‘ method.

Usage

```
filter_proteins_by_peptide_count(pdata, config)
```

Arguments

pdata	data.frame in the long format of ‘config‘
config	AnalysisConfiguration

Value

list with the filtered ‘data‘ and the ‘name‘ of the count column, ‘NULL‘ when the hierarchy has no child level

See Also

Other preprocessing: INTERNAL_FUNCTIONS_BY_FAMILY, apply_to_response_matrix(), get_robscales(), nr_B_in_A(), robust_scale(), scale_with_subset()

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config()
filtered <- prolfqua:::filter_proteins_by_peptide_count(istar$data, istar$config)
stopifnot(all(filtered$data[[filtered$name]] >= istar$config$min_peptides_protein))
```

find_d0_deqms *Find prior degrees of freedom for DEqMS*

Description

Uses limma::trigammaInverse to estimate d0 from the mean residual variance after removing the count-dependent trend.

Usage

```
find_d0_deqms(mean_myfct)
```

Arguments

mean_myfct	mean of squared residuals minus trigamma correction

Value

scalar prior degrees of freedom (d0)

`find_package_file` *find file stored in package*

Description

find file stored in package

Usage

```
find_package_file(packagename, file)
```

Arguments

`packagename`	name of the R package
`file`	relative path to the file within the package

Value

The computed result.

Examples

```
find_package_file("prolfqua", "CITATION")
```

`generate_contrasts` *Combined generate_contrasts*

Description

Combined generate_contrasts

Usage

```
generate_contrasts(primary_levels, secondary_levels, interactions = TRUE)
```

Arguments

`primary_levels`	character vector of primary factor levels
`secondary_levels`	character vector of secondary factor levels
`interactions`	logical, if TRUE include interaction contrasts

Value

Contrast definitions or contrast results.

See Also

Other contrasts: annotation_add_contrasts(), generate_contrasts_for_factor(), interaction_contrasts(), level_specific_contrasts(), main_effect_contrasts()

Examples

```
primary_levels <- c("MI", "MINOCAM")
secondary_levels <- c("T0", "T150", "T300")
generate_contrasts(primary_levels, secondary_levels)
generate_contrasts(secondary_levels, primary_levels)
```

---

generate_contrasts_for_factor

Single-factor contrasts (pairwise comparisons)

Description

Single-factor contrasts (pairwise comparisons)

Usage

```
generate_contrasts_for_factor(levels)
```

Arguments

levels	character vector of factor levels

Value

Contrast definitions or contrast results.

See Also

Other contrasts: annotation_add_contrasts(), generate_contrasts(), interaction_contrasts(), level_specific_contrasts(), main_effect_contrasts()

Examples

```
# example code
primary_levels <- c("MI", "MINOCAM")
secondary_levels <- c("T0", "T150", "T300")
x2 <- level_specific_contrasts(primary_levels, secondary_levels)
x3 <- level_specific_contrasts(secondary_levels, primary_levels)
generate_contrasts_for_factor(names(x2))
```

get_anova_df *anova returning dataframe*

Description

anova returning dataframe

Usage

```
get_anova_df(test = "F")
```

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median, vcov.rfit_prolfqua()

Examples

```
x <- get_anova_df(test = "F")
x <- get_anova_df(test = "Chisq")
```

get_complete_model_fit *retrieve complete models.*

Description

retrieve complete models.

Usage

```
get_complete_model_fit(complete_models)
```

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median, vcov.rfit_prolfqua()

Examples

```
x <- sim_build_models_lmer(model = "factors", Nprot = 10)
cfits <- get_complete_model_fit(x$model_df)
stopifnot(nrow(cfits) == 6)
```

---

get_contrast *Compute fold changes given Contrasts*

Description

Compute fold changes given Contrasts

Usage

```
get_contrast(data, hierarchy_keys, contrasts)
```

Arguments

data	hierarchy_keys of Analysis Configuration
contrasts	list of contrasts to compute

See Also

Other imputation: missingness_histogram(), missingness_per_condition(), missingness_per_condition_cums upset_interaction_missing_stats(), upset_missing_stats()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
lfq$complete_cases()

Contrasts <- c("dilution.b-a" = "group_A - group_B", "dilution.c-e" = "group_A - group_Ctrl")

var <- summarize_stats(lfq)
var <- prolfqua::make_interaction_column(var, columns = lfq$relevant_factor_keys())

imp <- var |> tidyr::pivot_wider(id_cols = lfq$hierarchy_keys(),
                         names_from = interaction,
                         values_from = !!rlang::sym("meanAbundance"))

imputed <- get_contrast(imp, lfq$hierarchy_keys(), Contrasts)
```

---

get_p_values_pbeta *p-value of protein from p.value of the median fold change peptide.*

Description

p-value of protein from p.value of the median fold change peptide.

Usage

```
get_p_values_pbeta(median.p.value, n.obs, max.n = 10)
```

Arguments

max.n	limit number of peptides per protein.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma()

new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median, vcov.rfit_prolfqua()

Examples

```
plot(get_p_values_pbeta(0.1,1:10,10), ylim=c(0,0.1))
plot(get_p_values_pbeta(0.1,1:10,3), ylim=c(0,0.1))
plot(get_p_values_pbeta(0.3,1:30, 3), ylim=c(0,0.1))
abline(h=.05,col = 2)
plot(seq(0.0,1.0,length=30),get_p_values_pbeta(seq(0.0,1.0,length=30),rep(10,30)))
abline(0,1)
plot(seq(0.0,1.0,length=30),get_p_values_pbeta(seq(0.0,1.0,length=30),rep(10,30),3))
abline(0,1)
testthat::expect_equal(get_p_values_pbeta(0.3,10, 3),0.216, tolerance = 1e-4)
testthat::expect_equal(get_p_values_pbeta(0,10, 3),0, tolerance = 1e-4)
testthat::expect_equal(get_p_values_pbeta(1,10, 3),1, tolerance = 1e-4)
testthat::expect_equal(get_p_values_pbeta(1,10, 3),get_p_values_pbeta(1,3, 10), tolerance = 1e-4)
```

---

get_robscales *compute median and standard deviation for each sample*

Description

compute median and standard deviation for each sample

Usage

```
get_robscales(lfqdata)
```

See Also

Other preprocessing: INTERNAL_FUNCTIONS_BY_FAMILY, apply_to_response_matrix(), filter_proteins_by_pept nr_B_in_A(), robust_scale(), scale_with_subset()

Examples

```
bb <- prolfqua::sim_lfq_data_peptide_config()
lfqdata <- prolfqua::LFQData$new(bb$data, bb$config)
lfqdata <- lfqdata$get_Transformer()$log2()$lfq
s1 <- get_robscales(lfqdata)

res <- scale_with_subset(lfqdata, lfqdata)
lfqres <- prolfqua::LFQData$new(res$data, lfqdata$get_config()$clone(deep = TRUE))
s2 <- get_robscales(lfqres)
abs(mean(s1$mads) - mean(s2$mads)) < 0.1
```

get_uniprot_id_from_fasta_header *Extracts uniprot ID*

Description

Extracts uniprot ID

Usage

```
get_uniprot_id_from_fasta_header(df, idcolumn = "protein_Id")
```

Arguments

df	data.frame
idcolumn	character, column name to extract uniprot IDs from

Value

data.frame

See Also

Other utilities: INTERNAL_FUNCTIONS_BY_FAMILY, is_contaminant(), is_decoy(), matrix_to_tibble(), multigroup_volcano(), pairs_smooth(), panel_cor(), table_facade()

Examples

```
df <- data.frame(
  protein_Id = c("sp|P12345|PROT1_HUMAN", "sp|Q67890|PROT2_HUMAN",
                 "tr|A0A0A0|PROT3_HUMAN", "NOFASTA_ID"),
  value = 1:4
)
result <- get_uniprot_id_from_fasta_header(df, idcolumn = "protein_Id")
stopifnot("UniprotID" %in% colnames(result))
stopifnot(sum(!is.na(result$UniprotID)) == 3)
```

group_label *group label function*

Description

group label function

Usage

```
group_label(primary, secondary)
```

Arguments

primary	character, primary factor level
secondary	character, secondary factor level

Value

A character vector with combined group labels.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median, vcov.rfit_prolfqua()

Examples

```
group_label("a", "b")
```

HierarchyCountsSample *Count distinct elements for each level of hierarchy per sample*

Description

Count distinct elements for each level of hierarchy per sample

Count distinct elements for each level of hierarchy per sample

Details

Provides wide, long, and plot views of hierarchy counts.

Value

An R6 class generator.

Public fields

`.summary` summarised data frame

`.configuration` AnalysisConfiguration object

Methods

Public methods:

- `HierarchyCountsSample$new()`
- `HierarchyCountsSample$wide()`
- `HierarchyCountsSample$long()`
- `HierarchyCountsSample$plot()`
- `HierarchyCountsSample$clone()`

Method `new()`**:** Create a new HierarchyCountsSample

Usage:

```
HierarchyCountsSample$new(pdata, configuration, nr_children = 1)
```

Arguments:

`pdata` data frame

`configuration` AnalysisConfiguration

`nr_children` minimum number of children to include

Method `wide()`**:** Return wide-format summary

Usage:

```
HierarchyCountsSample$wide()
```

Method `long()`**:** Return long-format summary

Usage:

```
HierarchyCountsSample$long()
```

Method `plot()`**:** Return barplot of hierarchy counts

Usage:

```
HierarchyCountsSample$plot()
```

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
HierarchyCountsSample$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other summary: `INTERNAL_FUNCTIONS_BY_FAMILY`, `hierarchy_counts()`, `summarize_hierarchy()`

Examples

```
bb <- sim_lfq_data_protein_config()
counts <- HierarchyCountsSample$new(bb$data, bb$config)
head(counts$wide())
```

hierarchy_counts *Count distinct elements for each level of hierarchy and isotope*

Description

E.g. number of proteins, peptides, precursors in the dataset

Usage

```
hierarchy_counts(pdata, hierarchy_keys, isotope_label = "isotopeLabel")
```

Arguments

pdata	data.frame
hierarchy_keys	character vector — all hierarchy column names
isotope_label	character — isotope label column name

See Also

Other summary: HierarchyCountsSample, INTERNAL_FUNCTIONS_BY_FAMILY, summarize_hierarchy()

Examples

```
bb <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(bb$data, bb$config)

x <- hierarchy_counts(lfq$data_long(), lfq$hierarchy_keys(), lfq$isotope_label())
x$protein_Id
stopifnot(ncol(x) == length(lfq$hierarchy_keys()) + 1)
# select non existing protein
data0 <- lfq$data_long() |> dplyr::filter(protein_Id == "XYZ")
tmp <- hierarchy_counts(data0, lfq$hierarchy_keys(), lfq$isotope_label())
stopifnot(nrow(tmp) == 0)
```

impute_from_model *Fill missing responses with predictions from per-subject linear models*

Description

Completes the data to every subject x every sample and fills each missing response cell with `predict()` of that subject's fitted `lm`, on the response scale. Observed values are left unchanged. The imputed values carry no noise.

Usage

```
impute_from_model(model, lfqdata)
```

Arguments

model	a Model with lm fits, as returned by build_model or build_model_impute
lfqdata	the LFQData the model was fitted on (same response and subject_id)

Details

Each subject gets one route, checked in this order:

complete no missing cell.

lod_refit the subject was refitted at the LOD by `build_model_impute` (`model_df$imputed`); that fit's predictions fill the missing cells.

fitted the observed-data fit has no NA coefficient and knows every factor level of the missing cells; its predictions fill them.

none no usable fit; the missing cells stay NA.

Value

list with `lfqdata`, a new `LFQData` holding every subject x sample row with missing responses filled, and `summary`, a tibble with the subject_id columns and `n_observed`, `n_imputed` and `route` per subject

See Also

`build_model_impute`

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu`
`ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste`
`ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf()`, `compute_borrowed_variance()`, `compute_borrowed_variance_`
`compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_res`
`model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()`
`new_imputed_model()`, `pivot_model_contrasts_to_wide()`, `register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median`
`vcov.rfit_prolfqua()`

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 30, weight_missing = 0.5)
lfqdata <- LFQData$new(istar$data, istar$config)
strat <- strategy_lm(paste(lfqdata$response(), "~ group_"))
mod <- build_model_impute(lfqdata, strat)
res <- impute_from_model(mod, lfqdata)
table(res$summary$route)
n_missing <- function(x) sum(is.na(x$data_long()$abundance))
stopifnot(n_missing(res$lfqdata) <= n_missing(lfqdata))
```

`impute_refit_singular` *Impute and refit singular/failed models*

Description

For proteins where the initial lm fit failed or produced NA coefficients, impute missing values with LOD, clamp, refit, and attach borrowed covariance.

Usage

```
impute_refit_singular(
  model_df,
  model_strategy,
  lod,
  response,
  sample_template,
  borrow_method = c("sigma", "vcov"),
  df_method = c("observed", "borrowed"),
  nr_children_col = NULL,
  on_misalign = c("fallback", "fail")
)
```

Arguments

`model_df`	tibble from model_analyse
`model_strategy`	strategy list from strategy_lm etc.
`lod`	numeric, limit of detection value
`response`	character, response column name in nested data
`sample_template`	data.frame with all sample/group combinations (columns matching the nested data minus the response). Used to complete proteins that are entirely missing in one or more groups.
`borrow_method`	"sigma" or "vcov"
`df_method`	"observed" uses max(n_observed - p, 1), "borrowed" uses median df from successful fits
`nr_children_col`	optional column name for nr_children (peptide counts); NA values in this column are filled with 1 for imputed rows so that weighted lm fits do not fail
`on_misalign`	passed to `compute_borrowed_variance`. With "fail", an unborrowable full covariance matrix skips the rescue (the model_df is returned unchanged) instead of crashing, so the affected proteins surface in `get_missing()`.

Value

modified model_df with imputed models replacing failed/singular ones

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

---

interaction_contrasts *Interaction contrasts (difference of differences)*

Description

Interaction contrasts (difference of differences)

Usage

```
interaction_contrasts(primary_levels, secondary_levels)
```

Arguments

primary_levels	character vector of primary factor levels
secondary_levels	character vector of secondary factor levels

Value

Contrast definitions or contrast results.

See Also

Other contrasts: annotation_add_contrasts(), generate_contrasts(), generate_contrasts_for_factor(), level_specific_contrasts(), main_effect_contrasts()

Examples

```
primary_levels <- c("MI", "MINOCAM")
secondary_levels <- c("T0", "T150", "T300")
interaction_contrasts(primary_levels, secondary_levels)
interaction_contrasts(secondary_levels, primary_levels)
```

INTERNAL_FUNCTIONS_BY_FAMILY

Internal Functions by category

Description

Internal Functions by category

Value

A documentation topic.

See Also

Other aggregation: aggregate_intensity_top_n(), estimate_intensity(), plot_estimate(), plot_hierarchies_line()

Other configuration: AnalysisConfiguration, ContrastConfiguration, R6_extract_values(), complete_cases(), list_to_ContrastConfiguration(), make_interaction_column(), make_reduced_hierarch sample_subset(), separate_hierarchy(), setup_analysis(), table_factors(), table_factors_size()

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Other plotting: ContrastsPlotter, missingness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), plot_estimate(), plot_heatmap(), plot_heatmap_cor(), plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_na_heatmap(), plot_pca(), plot_raster(), plot_sample_correlation(), upset_interaction_missing_s upset_missing_stats()

Other preprocessing: apply_to_response_matrix(), filter_proteins_by_peptide_count(), get_robscales(), nr_B_in_A(), robust_scale(), scale_with_subset()

Other stats: compute_pooled(), lfq_power_t_test_proteins(), lfq_power_t_test_quantiles_V2(), plot_stat_density(), plot_stat_density_median(), plot_stat_violin(), plot_stat_violin_median(), plot_stdv_vs_mean(), summarize_stats()

Other summary: HierarchyCountsSample, hierarchy_counts(), summarize_hierarchy()

Other utilities: get_uniprot_id_from_fasta_header(), is_contaminant(), is_decoy(), matrix_to_tibble(), multigroup_volcano(), pairs_smooth(), panel_cor(), table_facade()

`is_contaminant` *Detect contaminant identifiers*

Description

As is_decoy, but for contaminant entries (keratin, trypsin, BSA, ...). Built-in anchored default prefixes unioned with an optional configured `pattern`; empty / `NULL` uses the defaults only.

Usage

```
is_contaminant(ids, pattern = NULL)
```

Arguments

`ids`	character vector of (prefixed) identifiers
`pattern`	optional additional contaminant regex, unioned with defaults

Value

logical vector, `TRUE` where an id looks like a contaminant

See Also

Other utilities: INTERNAL_FUNCTIONS_BY_FAMILY, get_uniprot_id_from_fasta_header(), is_decoy(), matrix_to_tibble(), multigroup_volcano(), pairs_smooth(), panel_cor(), table_facade()

Examples

```
is_contaminant(c("zz|Cont00001|X", "sp|P2|X", "CON__ALBU"))
```

is_decoy *Detect decoy / reverse-database identifiers*

Description

Flags identifiers that look like decoy (reversed) database entries. Built-in anchored default prefixes are always considered, unioned with an optional configured `pattern`. An empty string or `NULL` pattern uses the defaults only.

Usage

```
is_decoy(ids, pattern = NULL)
```

Arguments

`ids`	character vector of (prefixed) identifiers
`pattern`	optional additional decoy regex, unioned with the defaults

Value

logical vector, `TRUE` where an id looks like a decoy

See Also

Other utilities: `INTERNAL_FUNCTIONS_BY_FAMILY`, `get_uniprot_id_from_fasta_header()`, `is_contaminant()`, `matrix_to_tibble()`, `multigroup_volcano()`, `pairs_smooth()`, `panel_cor()`, `table_facade()`

Examples

```
is_decoy(c("REV_sp|P1|X", "sp|P2|X", "decoy_3", "normalProtein"))
is_decoy(c("shuffled_1", "P2"), pattern = "^shuffled_")
```

level_specific_contrasts *Level-specific contrasts (per secondary level)*

Description

Level-specific contrasts (per secondary level)

Usage

```
level_specific_contrasts(primary_levels, secondary_levels)
```

Arguments

`primary_levels`	character vector of primary factor levels
`secondary_levels`	character vector of secondary factor levels

Value

Contrast definitions or contrast results.

See Also

Other contrasts: annotation_add_contrasts(), generate_contrasts(), generate_contrasts_for_factor(), interaction_contrasts(), main_effect_contrasts()

Examples

```
# example code

primary_levels <- c("MI", "MINOCAM")
secondary_levels <- c("T0", "T150", "T300")
x2 <- level_specific_contrasts(primary_levels, secondary_levels)
x3 <- level_specific_contrasts(secondary_levels, primary_levels)
```

LFQData *LFQData R6 class*

Description

LFQData R6 class

LFQData R6 class

Value

An R6 class generator.

Missing Data Assumptions

The filtering and imputation methods in this package assume that missing values are Missing Completely At Random (MCAR) or Missing At Random (MAR). Abundance-dependent missingness (MNAR), which is common in DDA proteomics, is not modelled. Users should be aware that MNAR can bias fold-change estimates and inflate false discovery rates.

Public fields

`prefix` e.g. "peptide_", "protein_", "compound_"

Methods

Public methods:

- LFQData$new()
- LFQData$set_data()
- LFQData$get_config()
- LFQData$set_config_value()
- LFQData$get_copy()
- LFQData$get_sample()
- LFQData$get_subset()

- LFQData$subject_id()
- LFQData$is_transformed()
- LFQData$remove_small_intensities()
- LFQData$filter_proteins_by_peptide_count()
- LFQData$remove_decoys()
- LFQData$decoy_proportion()
- LFQData$complete_cases()
- LFQData$data_wide()
- LFQData$factors()
- LFQData$hierarchy()
- LFQData$response()
- LFQData$hierarchy_keys()
- LFQData$relevant_hierarchy_keys()
- LFQData$factor_keys()
- LFQData$relevant_factor_keys()
- LFQData$sample_name()
- LFQData$file_name()
- LFQData$nr_children_col()
- LFQData$isotope_label()
- LFQData$data_long()
- LFQData$rename_response()
- LFQData$hierarchy_counts()
- LFQData$summarize_hierarchy()
- LFQData$get_Plotter()
- LFQData$get_Summariser()
- LFQData$get_Stats()
- LFQData$get_Transformer()
- LFQData$get_Aggregator()
- LFQData$clone()

Method `new()`**:** initialize

Usage:

```
LFQData$new(data, config, prefix = "ms_", setup = FALSE)
```

Arguments:

`data` data.frame

`config` configuration

`prefix` will be use as output prefix

`setup` is data setup needed, default = FALSE, if TRUE, calls `setup_analysis` on data first.

Method `set_data()`**:** set data (replaces the internal data frame)

Usage:

```
LFQData$set_data(new_data)
```

Arguments:

`new_data` data.frame

Returns: self (invisible)

Method `get_config()`: return the AnalysisConfiguration object

Usage:

```
LFQData$get_config()
```

Returns: AnalysisConfiguration

Method `set_config_value()`: set a config field value

Usage:

```
LFQData$set_config_value(field, value)
```

Arguments:

`field` character — field name

`value` the value to set

Method `get_copy()`: get deep copy

Usage:

```
LFQData$get_copy()
```

Method `get_sample()`: samples subset of data

Usage:

```
LFQData$get_sample(size = 100, seed = NULL)
```

Arguments:

`size` size of subset default 100

`seed` set seed

Method `get_subset()`: get subset of data

Usage:

```
LFQData$get_subset(x)
```

Arguments:

`x` data frame with columns containing subject_id

Method `subject_id()`: get subject ID columns

Usage:

```
LFQData$subject_id()
```

Method `is_transformed()`: is data transformed

Usage:

```
LFQData$is_transformed(is_transformed)
```

Arguments:

`is_transformed` logical

Returns: logical

Method `remove_small_intensities()`: some software is reporting NA's as 0, you must remove it from your data

Usage:

```
LFQData$remove_small_intensities(threshold = 4)
```

Arguments:

`threshold` default 4.

Returns: self

Method `filter_proteins_by_peptide_count()`: remove proteins with less than X peptides

Usage:

```
LFQData$filter_proteins_by_peptide_count()
```

Returns: self

Method `remove_decoys()`: remove decoy / reverse-database entries (rows whose top-level hierarchy id, e.g. protein_Id, is a decoy). Detection uses the configured 'pattern_decoys' unioned with the built-in defaults (see `is_decoy`); decoys are always detectable even when no pattern is configured. Returns a new decoy-free LFQData (self is not modified).

Usage:

```
LFQData$remove_decoys()
```

Returns: LFQData without decoys

Method `decoy_proportion()`: proportion of modelling-level keys (subject_id, e.g. protein or peptide by 'hierarchy_depth') that are decoys — an empirical-FDR / target-decoy QC signal. Decoy status derives from the top-level hierarchy id (protein_Id).

Usage:

```
LFQData$decoy_proportion()
```

Returns: numeric in [0, 1]

Method `complete_cases()`: some software is reporting NA's as 0, you must remove it from your data

Usage:

```
LFQData$complete_cases()
```

Arguments:

`threshold` default 4.

Returns: self

Method `data_wide()`: converts the data to wide

Usage:

```
LFQData$data_wide(as.matrix = FALSE, value = NULL)
```

Arguments:

`as.matrix` return as data.frame or matrix

`value` see possible lfqdata$get_config()$value_vars()

Returns: list with data, annotation, and configuration

Method `factors()`: Annotation table

Usage:

```
LFQData$factors()
```

Returns: data.frame

Method `hierarchy()`: Hierarchy table

Usage:

```
LFQData$hierarchy()
```

Method `response()`: name of response variable

Usage:

```
LFQData$response()
```

Returns: data.frame

Method `hierarchy_keys()`: return all hierarchy column names

Usage:

```
LFQData$hierarchy_keys()
```

Method `relevant_hierarchy_keys()`: return hierarchy column names at current depth (alias for subject_id)

Usage:

```
LFQData$relevant_hierarchy_keys()
```

Method `factor_keys()`: return all factor column names

Usage:

```
LFQData$factor_keys()
```

Method `relevant_factor_keys()`: return factor column names at current depth

Usage:

```
LFQData$relevant_factor_keys()
```

Method `sample_name()`: return sample name column

Usage:

```
LFQData$sample_name()
```

Method `file_name()`: return file name column

Usage:

```
LFQData$file_name()
```

Method `nr_children_col()`: return name of nr_children column

Usage:

```
LFQData$nr_children_col()
```

Method `isotope_label()`: return isotope label column name

Usage:

```
LFQData$isotope_label()
```

Method `data_long()`: return the tidy (long-format) data frame

Usage:

```
LFQData$data_long(na.omit = FALSE)
```

Arguments:

`na.omit` if TRUE, remove rows with NA in response column

Method `rename_response()`: new name of response variable

Usage:

```
LFQData$rename_response(newname = "Intensity")
```

Arguments:

newname default Intensity

Method `hierarchy_counts()`: number of elements at each level

Usage:

```
LFQData$hierarchy_counts()
```

Method `summarize_hierarchy()`: e.g. number of peptides per protein etc

Usage:

```
LFQData$summarize_hierarchy()
```

Returns: data.frame

Method `get_Plotter()`: get Plotter

Usage:

```
LFQData$get_Plotter()
```

Returns: LFQDataPlotter

Method `get_Summariser()`: get Summariser

Usage:

```
LFQData$get_Summariser()
```

Returns: LFQDataSummarizer

Method `get_Stats()`: Get `LFQDataStats`. For more details see `LFQDataStats`.

Usage:

```
LFQData$get_Stats(stats = c("everything", "interaction", "all"))
```

Arguments:

`stats` default interaction, computes statistics within interaction.

Returns: LFQDataStats

Method `get_Transformer()`: get Stats

Usage:

```
LFQData$get_Transformer()
```

Returns: LFQDataTransformer

Method `get_Aggregator()`: get Aggregator

Usage:

```
LFQData$get_Aggregator(method = "medpolish", ...)
```

Arguments:

`method` aggregation method: "medpolish", "rlm", or "topN"

`...` passed to aggregator constructor (e.g. prefix, N, func)

Returns: AggregateMedpolish, AggregateRlm, or AggregateTopN

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
LFQData$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other LFQData: AggregateLimpa, AggregateMedpolish, AggregateRlm, AggregateTopN, AggregatorBase, LFQDataPlotter, LFQDataStats, LFQDataSummariser, LFQDataToSummarizedExperiment()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata$filter_proteins_by_peptide_count()
tmp <- lfqdata$data_wide()
testthat::expect_equal(nrow(tmp$data) , nrow(tmp$rowdata))
testthat::expect_equal(ncol(tmp$data) , nrow(tmp$annotation) + ncol(tmp$rowdata))

stopifnot("data.frame" %in% class(tmp$data))
tmp <- lfqdata$data_wide(as.matrix = TRUE)
stopifnot("matrix" %in% class(tmp$data))
stopifnot(lfqdata$is_transformed()==FALSE)
lfqdata$summarize_hierarchy()

lfqdata$response()
lfqdata$rename_response("peptide.intensity")
lfqdata$response()
stopifnot("LFQData" %in% class(lfqdata$get_copy()))
stopifnot("LFQDataTransformer" %in% class(lfqdata$get_Transformer()))
stopifnot("LFQDataStats" %in% class(lfqdata$get_Stats()))
stopifnot("LFQDataSummariser" %in% class(lfqdata$get_Summariser()))
stopifnot("LFQDataPlotter" %in% class(lfqdata$get_Plotter()))
stopifnot("AggregateMedpolish" %in% class(lfqdata$get_Aggregator("medpolish")))

tmp <-lfqdata$get_sample(5, seed = 4)
stopifnot(nrow(tmp$hierarchy()) == 5)
```

`LFQDataPlotter` *LFQDataPlotter —- Create various visualization of the LFQdata*

Description

LFQDataPlotter —- Create various visualization of the LFQdata

LFQDataPlotter —- Create various visualization of the LFQdata

Value

An R6 class generator.

Public fields

`lfq` LFQData object

`prefix` prefix to figure names when writing, e.g. protein_

Methods

Public methods:

- LFQDataPlotter$new()
- LFQDataPlotter$raster()
- LFQDataPlotter$heatmap()
- LFQDataPlotter$heatmap_cor()
- LFQDataPlotter$pca()
- LFQDataPlotter$pca_plotly()
- LFQDataPlotter$boxplots()
- LFQDataPlotter$missigness_histogram()
- LFQDataPlotter$na_heatmap()
- LFQDataPlotter$intensity_distribution_density()
- LFQDataPlotter$intensity_distribution_violin()
- LFQDataPlotter$pairs_smooth()
- LFQDataPlotter$sample_correlation()
- LFQDataPlotter$upset_missing()
- LFQDataPlotter$write_boxplots()
- LFQDataPlotter$write_pdf()
- LFQDataPlotter$clone()

Method `new()`**:** create LFQDataPlotter

Usage:

```
LFQDataPlotter$new(lfqdata, prefix = "ms_")
```

Arguments:

`lfqdata` LFQData

`prefix` will be prepended to outputs written

Method `raster()`**:** plot intensities in raster

Usage:

```
LFQDataPlotter$raster(
  arrange = c("mean", "var"),
  not_na = FALSE,
  rownames = FALSE,
  max_rownames_chars = 60,
  max_sample_label_chars = 20
)
```

Arguments:

`arrange` arrange by either mean or var

`not_na` TRUE arrange by number of NA's, FALSE by arrange by intensity

`rownames` show rownames (default FALSE - do not show.)

`max_rownames_chars` maximum displayed row label length

`max_sample_label_chars` maximum displayed sample label length. Labels keep their suffix because sample prefixes are often shared.

Returns: ComplexHeatmap::Heatmap

Method `heatmap()`: heatmap of intensities - columns are samples, rows are proteins or peptides.

The abundances of each protein (row) are z-scored. Afterward, the mean abundance for each protein is zero, and the standard variation is one. z-scoring allows to compare (cluster) the proteins according to the difference in the expression in the samples. Without the z-scoring, the proteins would group according to their abundance, e.g., high abundant proteins would be one cluster.

Only the `top_n` most variable features are shown. Row clustering uses `stats::hclust`, which errors above 65536 features, so the rows are ranked by their variability statistic (CV for untransformed data, sd for transformed data; see `LFQDataStats`) and the most variable are kept. This keeps the heatmap feasible and legible for peptide-list / entrapment searches with tens of thousands of features.

Usage:

```
LFQDataPlotter$heatmap(
  na_fraction = 1,
  rownames = FALSE,
  max_rownames_chars = 60,
  max_sample_label_chars = 20,
  top_n = 1000
)
```

Arguments:

`na_fraction` maximum fraction of missing values per row. The default keeps every row that can be meaningfully z-scored.

`rownames` show rownames (default FALSE - do not show.)

`max_rownames_chars` maximum displayed row label length

`max_sample_label_chars` maximum displayed sample label length. Labels keep their suffix because sample prefixes are often shared.

`top_n` keep the `top_n` most variable features (default 1000); `NULL` or `Inf` keeps all features.

Returns: ComplexHeatmap::Heatmap

Method `heatmap_cor()`: heatmap of sample correlations.

The Spearman correlation among all samples is computed. Then the euclidean distance is used to compute the distances.

Usage:

```
LFQDataPlotter$heatmap_cor(max_sample_label_chars = 20)
```

Arguments:

`max_sample_label_chars` maximum displayed sample label length. Labels keep their suffix because sample prefixes are often shared.

Returns: ComplexHeatmap::Heatmap

Method `pca()`: PCA plot

A PCA is applied and the first and second principal component are shown. Features with missing values are removed. To keep all features, impute first, e.g. with `AggregateLimpa` in `impute_only` mode.

Usage:

```
LFQDataPlotter$pca(PC = c(1, 2), add_txt = TRUE, nudge = 0.1)
```

Arguments:

`PC` default c(1,2) - first and second principal component

`add_txt` show sample names

nudge default 0.1 nudge point labels

Returns: ggplot

Method `pca_plotly()`**:** pca plot

Usage:

```
LFQDataPlotter$pca_plotly(PC = c(1, 2), add_txt = FALSE)
```

Arguments:

`PC` default c(1,2) - first and second principal component

`add_txt` show sample names

Returns: plotly

Method `boxplots()`**:** boxplots for all proteins

Usage:

```
LFQDataPlotter$boxplots(facet = TRUE)
```

Arguments:

`facet` enable facet wrap if hierarchy_depth less then hierarchy length.

Returns: tibble with column boxplots containing ggplot objects

Method `missigness_histogram()`**:** histogram of intensities given number of missing in conditions

Usage:

```
LFQDataPlotter$missigness_histogram()
```

Returns: ggplot

Method `na_heatmap()`**:** heatmap of features with missing values

Usage:

```
LFQDataPlotter$na_heatmap()
```

Returns: ComplexHeatmap::Heatmap

Method `intensity_distribution_density()`**:** density distribution of intensities

Usage:

```
LFQDataPlotter$intensity_distribution_density(
  legend = NA,
  max_legend_samples = 16
)
```

Arguments:

`legend` show legend TRUE, FALSE do not show, NA selects automatically based on sample count.

`max_legend_samples` maximum number of samples for automatic legend display.

Returns: ggplot

Method `intensity_distribution_violin()`**:** Violinplot showing distribution of intensities in all samples

Usage:

```
LFQDataPlotter$intensity_distribution_violin()
```

Returns: ggplot

Method `pairs_smooth()`: pairsplot of intensities

Usage:

```
LFQDataPlotter$pairs_smooth(max = 10)
```

Arguments:

`max` maximal number of samples to show

Returns: NULL

Method `sample_correlation()`: plot of sample correlations

Usage:

```
LFQDataPlotter$sample_correlation()
```

Returns: NULL

Method `upset_missing()`: upset plot based on presence absence information

Usage:

```
LFQDataPlotter$upset_missing()
```

Returns: plot

Method `write_boxplots()`: write boxplots to file

Usage:

```
LFQDataPlotter$write_boxplots(path_qc, filename = NULL, width = 6, height = 6)
```

Arguments:

`path_qc` path to write to
`filename` file to write into
`width` fig width
`height` fig height

Method `write_pdf()`: write figure to pdf

Usage:

```
LFQDataPlotter$write_pdf(fig, path_qc, fig_name, width = 7, height = 7)
```

Arguments:

`fig` ggplot or ComplexHeatmap::Heatmap
`path_qc` path to write to
`fig_name` name of figure (no extension)
`width` figure width
`height` figure height

Returns: path the file was written to

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
LFQDataPlotter$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

plot_heatmap_cor

plot_pca

Other LFQData: AggregateLimpa, AggregateMedpolish, AggregateRlm, AggregateTopN, AggregatorBase, LFQData, LFQDataStats, LFQDataSummariser, LFQDataToSummarizedExperiment()

Examples

```
istar <- sim_lfq_data_peptide_config()

lfqdata <- LFQData$new(
 istar$data,
 istar$config)
lfqplotter <- lfqdata$get_Plotter()

stopifnot(methods::is(lfqplotter$heatmap(), "Heatmap"))
stopifnot(methods::is(lfqplotter$heatmap_cor(), "Heatmap"))
stopifnot("ggplot" %in% class(lfqplotter$pca()))
stopifnot("plotly" %in%  class(lfqplotter$pca_plotly()))
tmp <- lfqplotter$boxplots()
stopifnot("ggplot" %in%  class(tmp$boxplot[[1]]))
stopifnot("ggplot" %in% class(lfqplotter$missigness_histogram()))

stopifnot(methods::is(lfqplotter$na_heatmap(), "Heatmap"))
class(lfqplotter$intensity_distribution_density())
class(lfqplotter$intensity_distribution_violin())
stopifnot(is.null(lfqplotter$pairs_smooth()))
stopifnot(class(lfqplotter$sample_correlation()) == "list")
stopifnot(methods::is(lfqplotter$raster(), "Heatmap"))
stopifnot("upset" == class(lfqplotter$upset_missing()))
wide <- lfqdata$data_wide(as.matrix = TRUE)
stopifnot(class(prolfqua::plot_sample_correlation(wide$data)) == "list")
```

LFQDataStats *Decorates LFQData with methods to compute statistics of interactions*

Description

Decorates LFQData with methods to compute statistics of interactions

Decorates LFQData with methods to compute statistics of interactions

Details

compute stdv, mean and CV per peptide or protein and condition.

Value

An R6 class generator.

Public fields

`lfq` LFQData

`stat` either CV or sd (if is_transformed)

`statsdf` frame with statistics.

Methods

Public methods:

- `LFQDataStats$new()`
- `LFQDataStats$stats()`
- `LFQDataStats$stats_wide()`
- `LFQDataStats$stats_quantiles()`
- `LFQDataStats$density()`
- `LFQDataStats$density_median()`
- `LFQDataStats$violin()`
- `LFQDataStats$violin_median()`
- `LFQDataStats$stdv_vs_mean()`
- `LFQDataStats$power_t_test_quantiles()`
- `LFQDataStats$power_t_test()`
- `LFQDataStats$clone()`

Method `new()`**:** create analyse variances and CV

Usage:

```
LFQDataStats$new(lfqdata, stats = c("everything", "interaction", "all"))
```

Arguments:

`lfqdata` LFQData object

`stats` if 'interaction', compute within-group stats; if 'all', compute overall CV; if 'pooled', use pooled variance with grouping information

Method `stats()`**:** access data.frame with statistics

Usage:

```
LFQDataStats$stats()
```

Returns: data.frame with computed statistics

Method `stats_wide()`**:** access data.frame with statistics in wide format

Usage:

```
LFQDataStats$stats_wide()
```

Returns: data.frame with computed statistics in wide format

Method `stats_quantiles()`**:** Determine CV or sd for the quantiles

Usage:

```
LFQDataStats$stats_quantiles(probs = c(0.1, 0.25, 0.5, 0.75, 0.9))
```

Arguments:

`probs` for which quantile to determine CV or sd

Method `density()`**:** plots density or ecdf

Usage:

```
LFQDataStats$density(ggstat = c("density", "ecdf"))
```

Arguments:

`ggstat` either density or ecdf

Returns: ggplot

Method `density_median()`**:** plot density or ecdf of CV or sd for the 50

Usage:

```
LFQDataStats$density_median(ggstat = c("density", "ecdf"))
```

Arguments:

`ggstat` either density of ecdf

Returns: ggplot

Method `violin()`**:** plot violinplot of CV or sd

Usage:

```
LFQDataStats$violin()
```

Arguments:

`ggstat` either density of ecdf

Returns: ggplot

Method `violin_median()`**:** plot violinplot of CV or sd for the 50

Usage:

```
LFQDataStats$violin_median()
```

Returns: ggplot

Method `stdv_vs_mean()`**:** plot sd vs mean

Usage:

```
LFQDataStats$stdv_vs_mean(size = 200)
```

Arguments:

`size` number of points to sample (default 200)

Returns: ggplot

Method `power_t_test_quantiles()`**:** compute sample size for entire dataset

Usage:

```
LFQDataStats$power_t_test_quantiles(
  probs = c(0.1, 0.25, 0.5, 0.75, 0.9),
  delta = c(0.59, 1, 2),
  power = 0.8,
  sig.level = 0.05
)
```

Arguments:

`probs` quantiles of sd for which sample size should be computed

`delta` effect size

`power` power of test

`sig.level` significance level.

Method `power_t_test()`: compute sample for each protein

Usage:

```
LFQDataStats$power_t_test(delta = c(0.59, 1, 2), power = 0.8, sig.level = 0.05)
```

Arguments:

`delta` effect size

`power` power of test

`sig.level` significance level.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
LFQDataStats$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other LFQData: `AggregateLimpa`, `AggregateMedpolish`, `AggregateRlm`, `AggregateTopN`, `AggregatorBase`, `LFQData`, `LFQDataPlotter`, `LFQDataSummariser`, `LFQDataToSummarizedExperiment()`

Examples

```
# study variance of not normalized data
#source("c:/Users/wewol/prog/prolfqua/R/LFQData.R")
runallfuncs <- function(x){

  stopifnot("data.frame" %in% class(x$stats()))
  stopifnot("data.frame" %in% class(x$stats_wide()))
  stopifnot(c("long", "wide") %in% names(x$stats_quantiles()))
  stopifnot("ggplot" %in% class(x$density()))
  stopifnot("ggplot" %in% class(x$density_median()))
  stopifnot("ggplot" %in% class(x$density("ecdf")))
  stopifnot("ggplot" %in% class(x$density_median("ecdf")))
  stopifnot("ggplot" %in% class(x$violin()))
  stopifnot("ggplot" %in% class(x$violin_median()))
  stopifnot("ggplot" %in% class(x$stdv_vs_mean(size = 400)))
  if(!x$lfq$is_transformed()){
    stopifnot(is.null(x$power_t_test()))
    stopifnot(is.null(x$power_t_test_quantiles()))
  }
}
bb <- prolfqua::sim_lfq_data_peptide_config()



lfqdata <- LFQData$new(bb$data, bb$config)
lfqstats <- lfqdata$get_Stats()
stopifnot(ncol(lfqstats$stats_wide()) == 30)
lfqstats$violin()
runallfuncs(lfqstats)
x <- lfqstats

#study variance of normalized data
```

```
lfqdata <- LFQData$new(bb$data, bb$config)
lfqdata$is_transformed(TRUE)
lfqstats <- lfqdata$get_Stats()
stopifnot(ncol(lfqstats$stats_wide()) == 26)
runallfuncs(lfqstats)

#Slightly different dataset


# estimates statistics for all samples
lfqstats <- lfqdata$get_Stats(stats = "all")
stopifnot(ncol(lfqstats$stats_wide()) == 8)
runallfuncs(lfqstats)
lfqstats <- lfqdata$get_Stats(stats = "interaction")
stopifnot(ncol(lfqstats$stats_wide()) == 20)
runallfuncs(lfqstats)

# Group size 1
bb <- prolfqua::sim_lfq_data_peptide_config(N=1)
lfq1 <- LFQData$new(bb$data, bb$config)
table_factors_size(lfq1$data_long(), lfq1$file_name(),
  lfq1$sample_name(), lfq1$factor_keys(), lfq1$relevant_factor_keys())
lfqdata <- LFQData$new(bb$data, bb$config)
lfqstats <- lfqdata$get_Stats()

# stopifnot(ncol(lfqstats$stats_wide()) == 30)
lfqstats$violin()
runallfuncs(lfqstats)
```

`LFQDataSummariser` *Summarize LFQData*

Description

Summarize LFQData

Summarize LFQData

Value

An R6 class generator.

Public fields

`lfq` LFQData

Methods

Public methods:

- `LFQDataSummariser$new()`
- `LFQDataSummariser$hierarchy_counts()`
- `LFQDataSummariser$hierarchy_counts_sample()`
- `LFQDataSummariser$plot_hierarchy_counts_sample()`

- LFQDataSummariser$interaction_missing_stats()
- LFQDataSummariser$upset_interaction_missing_stats()
- LFQDataSummariser$missingness_per_group()
- LFQDataSummariser$missingness_per_group_cumsum()
- LFQDataSummariser$plot_missingness_per_group()
- LFQDataSummariser$plot_missingness_per_group_cumsum()
- LFQDataSummariser$percentage_abundance()
- LFQDataSummariser$clone()

Method `new()`: initialize

Usage:

```
LFQDataSummariser$new(lfqdata)
```

Arguments:

`lfqdata` LFQData

Method `hierarchy_counts()`: summarize hierarchy

Usage:

```
LFQDataSummariser$hierarchy_counts()
```

Method `hierarchy_counts_sample()`: number of elements at each level in every sample

Usage:

```
LFQDataSummariser$hierarchy_counts_sample(
  value = c("wide", "long"),
  nr_children = 1
)
```

Arguments:

`value` wide - wide format, long - long format, plot - ggplot

`nr_children` get summary for 1,2 or more number of children

Method `plot_hierarchy_counts_sample()`: barplot showing number of elements at each level in every sample

Usage:

```
LFQDataSummariser$plot_hierarchy_counts_sample(nr_children = 1)
```

Arguments:

`nr_children` get summary for 1,2 or more number of children

`value` wide - wide format, long - long format, plot - ggplot

Method `interaction_missing_stats()`: missing per condition and protein

Usage:

```
LFQDataSummariser$interaction_missing_stats()
```

Method `upset_interaction_missing_stats()`: upset plot with missing information per protein and condition

Usage:

```
LFQDataSummariser$upset_interaction_missing_stats(tr = 2)
```

Arguments:

`tr` if less than tr observations in condition then missing

Method `missingness_per_group()`: missing stats per condition

Usage:

```
LFQDataSummariser$missingness_per_group()
```

Method `missingness_per_group_cumsum()`: missing stats per condition as cumulative sum

Usage:

```
LFQDataSummariser$missingness_per_group_cumsum()
```

Method `plot_missingness_per_group()`: barplot with number of features with 1,2, etc missing in condition

Usage:

```
LFQDataSummariser$plot_missingness_per_group()
```

Returns: ggplot

Method `plot_missingness_per_group_cumsum()`: barplot with cumulative sum of features with 1,2, etc missing in condition

Usage:

```
LFQDataSummariser$plot_missingness_per_group_cumsum()
```

Returns: ggplot

Method `percentage_abundance()`: Does roll up to highest hierarchy and Computes the percent abundance of proteins overall and within each group

Usage:

```
LFQDataSummariser$percentage_abundance()
```

Returns: data frame

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
LFQDataSummariser$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other LFQData: `AggregateLimpa`, `AggregateMedpolish`, `AggregateRlm`, `AggregateTopN`, `AggregatorBase`, `LFQData`, `LFQDataPlotter`, `LFQDataStats`, `LFQDataToSummarizedExperiment()`

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config()

data <- istar$data
lfqdata <- LFQData$new(data, istar$config)
sum <- lfqdata$get_Summariser()
sum
sum$hierarchy_counts()
sum$hierarchy_counts_sample("wide")
sum$hierarchy_counts_sample("long")
sum$plot_hierarchy_counts_sample()
sum$plot_hierarchy_counts_sample()
```

```
tmp <- sum$interaction_missing_stats()

sum$missingness_per_group()
sum$missingness_per_group_cumsum()
sum$plot_missingness_per_group()
sum$plot_missingness_per_group_cumsum()
sum$upset_interaction_missing_stats()
sum$percentage_abundance()
```

`LFQDataToSummarizedExperiment` *converts LFQData object to SummarizedExperiment*

Description

For compatibility with Bioconductor

Usage

```
LFQDataToSummarizedExperiment(lfqdata)
```

Arguments

`lfqdata`	LFQData object

Value

SummarizedExperiment (bioconductor)

See Also

Other LFQData: `AggregateLimpa`, `AggregateMedpolish`, `AggregateRlm`, `AggregateTopN`, `AggregatorBase`, `LFQData`, `LFQDataPlotter`, `LFQDataStats`, `LFQDataSummariser`

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config()
data <- istar$data
lfqdata <- LFQData$new(data, istar$config)
lfqdata$data_wide()
if(require("SummarizedExperiment")){
   tmp <- LFQDataToSummarizedExperiment(lfqdata)
}
```

`LFQDataTransformer` *Decorate LFQData with Methods for transforming Intensities*

Description

Decorate LFQData with Methods for transforming Intensities

Decorate LFQData with Methods for transforming Intensities

Value

An R6 class generator.

Public fields

`lfq` LFQData object

Methods

Public methods:

- `LFQDataTransformer$new()`
- `LFQDataTransformer$log2()`
- `LFQDataTransformer$get_scales()`
- `LFQDataTransformer$robscale()`
- `LFQDataTransformer$robscale_subset()`
- `LFQDataTransformer$center_to_reference()`
- `LFQDataTransformer$intensity_array()`
- `LFQDataTransformer$intensity_matrix()`
- `LFQDataTransformer$clone()`

Method `new()`**:** initialize

Usage:

```
LFQDataTransformer$new(lfqdata)
```

Arguments:

`lfqdata` LFQData object to transform

Method `log2()`**:** log2 transform data

Usage:

```
LFQDataTransformer$log2(force = FALSE)
```

Arguments:

`force` if 'FALSE', data already log2 transformed will not be transformed a second time. 'TRUE' forces log transformation

Returns: LFQDataTransformer

Method `get_scales()`**:** get mean and variance and standard deviation in each sample

Usage:

```
LFQDataTransformer$get_scales()
```

Returns: list with means and mads

Method `robscale()`**:** robust scale data

Usage:

```
LFQDataTransformer$robscale(
  preserve_mean = TRUE,
  colname = "transformedIntensity"
)
```

Arguments:

`preserve_mean` should original mean value be preserved TRUE, if FALSE then center at zero

`colname` new name of transformed column

Returns: LFQDataTransformer (self)

Method `robscale_subset()`**:** log2 transform and robust scale data based on subset

Usage:

```
LFQDataTransformer$robscale_subset(
  lfqsubset,
  preserve_mean = TRUE,
  colname = "transformed_abundance"
)
```

Arguments:

`lfqsubset` LFQData subset to use for normalization

`preserve_mean` should original mean value be preserved TRUE, if FALSE then center at zero

`colname` - how to name the transformed intensities, default transformedIntensity

Returns: LFQDataTransformer (self)

Method `center_to_reference()`**:** center data to a reference subset

Usage:

```
LFQDataTransformer$center_to_reference(lfqsubset)
```

Arguments:

`lfqsubset` LFQData subset to use as reference

Returns: LFQDataTransformer (self)

Method `intensity_array()`**:** Transforms intensities

Usage:

```
LFQDataTransformer$intensity_array(.func = log2, force = FALSE)
```

Arguments:

`.func` transformation function working with arrays e.g. log2, log10, asinh etc.

`force` transformation on already transformed data.

Returns: LFQDataTransformer (self)

Method `intensity_matrix()`**:** pass a function which works with matrices, e.g., vsn::justvsn

Usage:

```
LFQDataTransformer$intensity_matrix(.func = robust_scale, force = FALSE)
```

Arguments:

`.func` any function taking a matrix and returning a matrix (columns sample, rows feature, e.g. 'base::scale()'), default 'robust_scale'

`force` transformation on data already transformed

Returns: LFQDataTransformer (self)

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
LFQDataTransformer$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
istar <- sim_lfq_data_peptide_config(Nprot = 50)
lfqdata <- LFQData$new(istar$data, istar$config)

lfqcopy <- lfqdata$get_copy()
lfqTrans <- lfqcopy$get_Transformer()

x <- lfqTrans$intensity_array(log2)

x$lfq$is_transformed()
x <- x$intensity_matrix(robust_scale)
plotter <- x$lfq$get_Plotter()
plotter$intensity_distribution_density()

# transform by asinh root and scale

lfqcopy <- lfqdata$get_copy()
lfqTrans <- lfqcopy$get_Transformer()
x <- lfqTrans$intensity_array(asinh)
mads1 <- mean(x$get_scales()$mads)
x <- lfqTrans$intensity_matrix(robust_scale, force = TRUE)
mads2 <- mean(x$get_scales()$mads)
stopifnot(abs(mads1 - mads2) < 1e-8)


stopifnot(abs(mean(x$get_scales()$medians)) < 1e-8)
lfqcopy <- lfqdata$get_copy()
lfqTrans <- lfqcopy$get_Transformer()
lfqTrans$log2()
before <- lfqTrans$get_scales()
lfqTrans$robscale()
after <- lfqTrans$get_scales()
stopifnot(abs(mean(before$medians) - mean(after$medians)) < 1e-8)
stopifnot(abs(mean(before$mads) - mean(after$mads)) < 1e-8)

# normalize data using vsn
lfqcopy <- lfqdata$get_copy()
lfqTrans <- lfqcopy$get_Transformer()
lfqTransCheck <- lfqcopy$get_Transformer()

lfqTransCheck$log2()
lfqTransCheck$get_scales()
lfqTransCheck$lfq$get_Plotter()$intensity_distribution_density()
```

```
if(require("vsn")){
 res <- lfqTrans$intensity_matrix( .func = vsn::justvsn)
 res$lfq$get_Plotter()$intensity_distribution_density()
 res$get_scales()
}
if(require("preprocessCore")){
quant <- function(y){
 ynorm <- preprocessCore::normalize.quantiles(y)
 rownames(ynorm) <- rownames(y)
 colnames(ynorm) <- colnames(y)
 return(ynorm)
}
 res <- lfqTrans$intensity_matrix( .func = quant)
 res$lfq$get_Plotter()$intensity_distribution_density()
}


#subset scaling

istar2 <- sim_lfq_data_peptide_config()
lfqdata2 <- LFQData$new(istar2$data, istar2$config)
lfqdata2 <- lfqdata2$get_Transformer()$intensity_array(log2)$lfq
head(lfqdata2$hierarchy())
internal <- lfqdata2$get_subset(head(lfqdata2$hierarchy()))
internal$hierarchy()
tr <- lfqdata2$get_Transformer()
tr$center_to_reference(internal)
pl <- tr$lfq$get_Plotter()
pl$intensity_distribution_density()
lfqdata2$get_Plotter()$intensity_distribution_density()
robscale <- lfqdata2$get_Transformer()$robscale_subset(internal)$lfq
robscale$get_Plotter()$intensity_distribution_density()
```

`lfq_power_t_test_proteins` *Compute theoretical sample sizes from factor level standard deviations*

Description

Compute theoretical sample sizes from factor level standard deviations

Usage

```
lfq_power_t_test_proteins(
  stats_res,
  delta = c(0.59, 1, 2),
  power = 0.8,
  sig.level = 0.05,
  min.n = 1.5
)
```

Arguments

stats_res	data.frame ‘summarize_stats‘ output
delta	effect size you are interested in
power	of test
sig.level	P-Value
min.n	smallest n to determine

See Also

Other stats: INTERNAL_FUNCTIONS_BY_FAMILY, compute_pooled(), lfq_power_t_test_quantiles_V2(), plot_stat_density(), plot_stat_density_median(), plot_stat_violin(), plot_stat_violin_median(), plot_stdv_vs_mean(), summarize_stats()

Examples

```
bb1 <- prolfqua::sim_lfq_data_peptide_config()
ldata <- LFQData$new(bb1$data, bb1$config)
stats_res <- summarize_stats(ldata)
bb <- lfq_power_t_test_proteins(stats_res)
```

---

lfq_power_t_test_quantiles_V2

estimate sample sizes

Description

estimate sample sizes

Usage

```
lfq_power_t_test_quantiles_V2(
  quantile_sd,
  delta = c(0.59, 1, 2),
  power = 0.8,
  sig.level = 0.05,
  min.n = 1.5
)
```

Arguments

quantile_sd	output of ‘summarize_stats_quantiles‘
delta	effect size you are interested in
power	of test
sig.level	P-Value
min.n	smallest n to determine

See Also

Other stats: INTERNAL_FUNCTIONS_BY_FAMILY, compute_pooled(), lfq_power_t_test_proteins(), plot_stat_density(), plot_stat_density_median(), plot_stat_violin(), plot_stat_violin_median(), plot_stdv_vs_mean(), summarize_stats()

Examples

```
bb1 <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(bb1$data, bb1$config)
stats_res <- summarize_stats(lfq)
xx <- summarize_stats_quantiles(stats_res, lfq$relevant_factor_keys(), probs = c(0.5, 0.8))
bbb <- lfq_power_t_test_quantiles_V2(xx$long)
bbb <- dplyr::bind_rows(bbb)
summary <- bbb |>
 dplyr::select( -N_exact, -quantiles, -sdtrimmed ) |>
 tidyr::pivot_wider(names_from = delta, values_from = N)
```

---

linfct_from_model *get linfct from model*

Description

get linfct from model

Usage

```
linfct_from_model(m, as_list = TRUE)
```

Arguments

m	linear model

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(),

impute_refit_singular(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_ moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
m <- sim_make_model_lm("factors")
linfct <- linfct_from_model(m, as_list = TRUE)

linfct$linfct_factors
linfct$linfct_interactions
lf <- matrix(
c(1, 1, 1, 1, 0.5, 0.5, 0, 1, 0, 1, 0.5, 0.5),
nrow = 4,
byrow = FALSE,
dimnames = list(c("BackgroundX", "BackgroundZ", "TreatmentA", "TreatmentB"),
                c("(Intercept)", "TreatmentB", "BackgroundZ"))
)
stopifnot(lf == linfct$linfct_factors)
m <- sim_make_model_lm("interaction")
linfct <- linfct_from_model(m)

m <- lm(Petal.Width ~ Species, data = iris)
linfct_from_model(m)
xx <- data.frame( Y = 1:10 , Condition = c(rep("a",5), rep("b",5)) )
m <- lm(Y ~ Condition, data = xx)
linfct_from_model(m)
xx <- data.frame( Y = 1:10 , Condition = c(rep("a",5), rep("b.b",5)) )
m <- lm(Y ~ Condition, data = xx)
linfct_from_model(m)
xx <- data.frame( Y = 1:10 , Condition = c(rep("a",5), rep("ab",5)) )
m <- lm(Y ~ Condition, data = xx)
linfct_from_model(m)
```

`linfct_matrix_contrasts` *linfct_matrix_contrasts*

Description

linfct_matrix_contrasts

Usage

```
linfct_matrix_contrasts(linfct, contrasts, p.message = FALSE)
```

Arguments

`linfct`	linear functions as created by linfct_from_model
`contrasts`	named character vector of contrasts to determine linear functions for
`p.message`	print messages default FALSE

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), list_facades(), lookup_facade(), merge_contrasts_resul model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median, vcov.rfit_prolfqua()

Examples

```
m <- sim_make_model_lm( "factors")
Contr <- c("TreatmentA_vs_B" = "TreatmentA - TreatmentB",
    "BackgroundX_vs_Z" = "BackgroundX - BackgroundZ",
    "IntoflintoA" = "`TreatmentA:BackgroundX` - `TreatmentA:BackgroundZ`",
    "IntoflintoB" = "`TreatmentB:BackgroundX` - `TreatmentB:BackgroundZ`",
    "IntoflintoX" = "`TreatmentA:BackgroundX` - `TreatmentB:BackgroundX`",
    "IntoflintoZ" = "`TreatmentA:BackgroundZ` - `TreatmentB:BackgroundZ`",
    "interactXZ" = "IntoflintoX - IntoflintoZ",
    "interactAB" = "IntoflintoA - IntoflintoB"
     )
linfct <- linfct_from_model(m, as_list = FALSE)
x <- linfct_matrix_contrasts(linfct, Contr )
stopifnot(sum(x["interactXZ",]) == 0 )
stopifnot(sum(x["interactAB",]) == 0 )

m <- sim_make_model_lm( "interaction")
linfct <- linfct_from_model(m, as_list = FALSE)
x <- linfct_matrix_contrasts(linfct, Contr )
stopifnot(sum(x["interactXZ",]) ==1 )
stopifnot(sum(x["interactAB",]) ==1 )
```

---

list_facades *List currently registered contrast facades*

Description

List currently registered contrast facades

Usage

```
list_facades()
```

Value

A list mirroring FACADE_REGISTRY but reflecting any entries added via register_facade from downstream packages.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_ moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
head(names(list_facades()))
```

---

list_to_AnalysisConfiguration

read minimal yaml to reconstruct configuration

Description

read minimal yaml to reconstruct configuration

Usage

```
list_to_AnalysisConfiguration(dd)
```

Arguments

dd	list with table and parameter elements as produced by R6_extract_values

Value

The computed result.

Examples

```
DEAconfig <- AnalysisConfiguration$new()
DEAconfig$file_name <- "Replicate.Name"
DEAconfig$hierarchy[["protein_Id"]] <- "Protein.Name"
DEAconfig$hierarchy[["peptide_Id"]] <- "Peptide.Sequence"
DEAconfig$hierarchy[["precursor_Id"]] <- c("Peptide.Sequence", "Precursor.Charge")
DEAconfig$hierarchy[["fragment_Id"]] <- c(
  "Peptide.Sequence", "Precursor.Charge",
  "Fragment.Ion", "Product.Charge"
)
DEAconfig$ident_q_value <- "annotation_QValue"
DEAconfig$set_response("Area")
DEAconfig$isotope_label <- "Isotope.Label"
configList <- prolfqua::R6_extract_values(DEAconfig)
stopifnot(class(configList) == "list")
config <- list_to_AnalysisConfiguration(configList)
all.equal(prolfqua::R6_extract_values(config), configList)
```

---

list_to_ContrastConfiguration

Rebuild a ContrastConfiguration from a list

Description

Round-trip partner of R6_extract_values, which keeps the fields but drops the methods. Use it to restore the column-role mapping from a serialized result artifact (e.g. 'SummarizedExperiment' metadata or an AnnData 'uns' entry) so consumers can call has_pvalue() and friends again.

Usage

```
list_to_ContrastConfiguration(dd)
```

Arguments

dd	named list of ContrastConfiguration fields

Value

A ContrastConfiguration.

See Also

Other configuration: AnalysisConfiguration, ContrastConfiguration, INTERNAL_FUNCTIONS_BY_FAMILY, R6_extract_values(), complete_cases(), make_interaction_column(), make_reduced_hierarchy_config(), sample_subset(), separate_hierarchy(), setup_analysis(), table_factors(), table_factors_size()

Examples

```
cfg <- ContrastConfiguration$new(
  subject_id = "protein_Id",
  contrast_col = "Bait",
  pvalue_col = NA_character_
)
values <- R6_extract_values(cfg)
restored <- list_to_ContrastConfiguration(values)
stopifnot(all.equal(R6_extract_values(restored), values))
restored$has_pvalue()
```

---

lookup_facade *Look up a contrast facade by short name*

Description

Look up a contrast facade by short name

Usage

```
lookup_facade(name)
```

Arguments

name	short method name (e.g. "lm", "saint").

Value

Registry entry list with at least class, needs, package, needs_saint_annotation; or NULL if no entry exists.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_ moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
lookup_facade("lm")$class
is.null(lookup_facade("does-not-exist"))
```

`LR_test` *Likelihood ratio test*

Description

Likelihood ratio test

Usage

```
LR_test(
  complete_models,
  model_name,
  complete_models_int,
  model_name_int,
  subject_id = "protein_Id",
  path = NULL
)
```

Arguments

`complete_models`	table with models (see build model)
`model_name`	name of model
`complete_models_int`	reduced model
`model_name_int`	name of reduced model
`subject_id`	subject id typically Accession or protein_Id
`path`	default NULL, set to a directory if you need to write diagnostic plots.

Value

The computed result.

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu` `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste` `ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf`

compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
data_2Factor <- prolfqua::sim_lfq_data_2factor_config(
 Nprot = 200,
 with_missing = TRUE,
 weight_missing = 2)

pMerged <- LFQData$new(data_2Factor$data, data_2Factor$config)

pMerged$response()
pMerged$factors()

formula_condition_and_Batches <-
  prolfqua::strategy_lm("abundance ~ Treatment + Background")
modCB <- prolfqua::build_model(
  pMerged,
  formula_condition_and_Batches)

formula_condition <-
  prolfqua::strategy_lm("abundance ~ Treatment")
modC <- prolfqua::build_model(
  pMerged,
  formula_condition)

tmp <- LR_test(modCB$model_df, "modCB", modC$model_df, "modB")
hist(tmp$likelihood_ratio_test.pValue)
```

---

main_effect_contrasts *main effects contrasts*

Description

main effects contrasts

Usage

```
main_effect_contrasts(primary_levels, secondary_levels)
```

Arguments

primary_levels	character vector of primary factor levels
secondary_levels	character vector of secondary factor levels

Value

Contrast definitions or contrast results.

See Also

Other contrasts: annotation_add_contrasts(), generate_contrasts(), generate_contrasts_for_factor(), interaction_contrasts(), level_specific_contrasts()

Examples

```
primary_levels <- c("MI", "MINOCAM")
secondary_levels <- c("T150", "T0", "T300")
main_effect_contrasts(primary_levels, secondary_levels)
main_effect_contrasts(secondary_levels, primary_levels)
```

---

make_interaction_column

create interaction column from factors

Description

create interaction column from factors

Usage

```
make_interaction_column(data, columns, sep = ".")
```

See Also

Other configuration: AnalysisConfiguration, ContrastConfiguration, INTERNAL_FUNCTIONS_BY_FAMILY, R6_extract_values(), complete_cases(), list_to_ContrastConfiguration(), make_reduced_hierarchy_conf sample_subset(), separate_hierarchy(), setup_analysis(), table_factors(), table_factors_size()

Examples

```
xx <- data.frame(A = c("a","a","a"), B = c("d","d","e"))
x <- make_interaction_column(xx, c("B","A"))
x <- make_interaction_column(xx, c("A"))
bb <- prolfqua::sim_lfq_data_protein_config()
config <- bb$config
analysis <- bb$data

config$factor_depth <- 1
make_interaction_column(analysis,
   config$factor_keys_depth())
```

make_reduced_hierarchy_config *Make reduced hierarchy configuration*

Description

Make reduced hierarchy configuration

Usage

```
make_reduced_hierarchy_config(config, work_intensity, hierarchy)
```

Arguments

config	AnalysisConfiguration
work_intensity	work intensity column
hierarchy	new reduced hierarchy

Value

AnalysisConfiguration with reduced hierarchy

See Also

Other configuration: AnalysisConfiguration, ContrastConfiguration, INTERNAL_FUNCTIONS_BY_FAMILY, R6_extract_values(), complete_cases(), list_to_ContrastConfiguration(), make_interaction_column(), sample_subset(), separate_hierarchy(), setup_analysis(), table_factors(), table_factors_size()

Examples

```
bb <- prolfqua::sim_lfq_data_peptide_config()

red <- make_reduced_hierarchy_config(bb$config,
 "testintensity",
 bb$config$hierarchy[1])
stopifnot(red$get_response() == "testintensity")
stopifnot(length(red$hierarchy) == 1)
```

matrix_to_tibble *matrix or data.frame to tibble (taken from tidyquant)*

Description

matrix or data.frame to tibble (taken from tidyquant)

Usage

```
matrix_to_tibble(x, preserve_row_names = "row.names", ...)
```

Arguments

x	a matrix
preserve_row_names	give name to rownames column, if NULL discard rownames
...	further parameters passed to as_tibble

Value

The computed result.

See Also

Other utilities: INTERNAL_FUNCTIONS_BY_FAMILY, get_uniprot_id_from_fasta_header(), is_contaminant(), is_decoy(), multigroup_volcano(), pairs_smooth(), panel_cor(), table_facade()

Examples

```
x <- matrix(rnorm(20), ncol=4)
rownames(x) <- LETTERS[seq_len(nrow(x))]
matrix_to_tibble(x)
!(is.matrix(x) || is.data.frame(x))
```

---

merge_contrasts_results

Merge contrast results coming from two different model.

Description

Typically used to fill proteins missing from Contrasts with estimates from another model, e.g. the LOD-imputed refits of ContrastsLMImputeFacade

Usage

```
merge_contrasts_results(prefer, add, model_name = "mergedModel")
```

Arguments

prefer	contrasts to use preferentially
add	contrasts to add from if missing in prefer
model_name	name of the merged model default "mergedModel"

Value

Contrast definitions or contrast results.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
prefer_df <- data.frame(
  protein_Id = c("P1", "P2"),
  contrast = "A_vs_B",
  modelName = "prefer",
  diff = c(1, 2),
  p.value = c(0.01, 0.2),
  FDR = c(0.02, 0.2),
  statistic = c(3, NA)
)
add_df <- data.frame(
  protein_Id = c("P1", "P2"),
  contrast = "A_vs_B",
  modelName = "add",
  diff = c(1.1, 2.1),
  p.value = c(0.02, 0.03),
  FDR = c(0.03, 0.04),
  statistic = c(2.8, 2.5)
)
prefer <- ContrastsTable$new(prefer_df, subject_id = "protein_Id", model_name = "prefer")
add <- ContrastsTable$new(add_df, subject_id = "protein_Id", model_name = "add")
merged <- merge_contrasts_results(prefer, add)
merged$merged$get_contrasts()
```

---

missigness_histogram *Histogram summarizing missingness*

Description

Histogram summarizing missingness

Usage

```
missigness_histogram(
  lfqdata,
  showempty = FALSE,
  factors = lfqdata$relevant_factor_keys(),
  alpha = 0.1
)
```

Arguments

lfqdata	LFQData object
showempty	show empty values
factors	factor columns to use
alpha	transparency

See Also

Other plotting: ContrastsPlotter, INTERNAL_FUNCTIONS_BY_FAMILY, missingness_per_condition(), missingness_per_condition_cumsum(), plot_estimate(), plot_heatmap(), plot_heatmap_cor(), plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_na_heatmap(), plot_pca(), plot_raster(), plot_sample_correlation(), upset_interaction_missing_s upset_missing_stats()

Other imputation: get_contrast(), missingness_per_condition(), missingness_per_condition_cumsum(), upset_interaction_missing_stats(), upset_missing_stats()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
pl <- missigness_histogram(lfq, showempty = FALSE)
stopifnot("ggplot" %in% class(pl))
pl <- missigness_histogram(lfq, showempty = TRUE)
stopifnot("ggplot" %in% class(pl))
```

MissingHelpers *Group statistics and limit of detection*

Description

Group statistics and limit of detection

Group statistics and limit of detection

Details

Computes per-group statistics of the abundances and, from them, the limit of detection (LOD) used by build_model_impute to impute groups without observations.

Value

An R6 class generator.

Public fields

`data` data

`config` config

`prob` quantile of groups with one observed value to estimate LOD

`stats` data.frame with group statistics

Methods

Public methods:

- `MissingHelpers$new()`
- `MissingHelpers$get_stats()`
- `MissingHelpers$get_lod()`
- `MissingHelpers$clone()`

Method `new()`**:** initialize

Usage:

```
MissingHelpers$new(data, config, prob = 0.5)
```

Arguments:

`data` data

`config` config

`prob` default 0.5, median of groups with one observed value

Method `get_stats()`**:** get data.frame with statistics

Usage:

```
MissingHelpers$get_stats()
```

Returns: data.frame

Method `get_lod()`**:** determine limit of detection computes quantile of abundances in groups with a single observation; without such groups, of the partly observed groups with the fewest observations, and when every group is complete or empty, the lowest group mean

Usage:

```
MissingHelpers$get_lod()
```

Returns: numeric LOD

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
MissingHelpers$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
dd <- prolfqua::sim_lfq_data_protein_config(Nprot = 100,weight_missing = 2)
mh <- prolfqua::MissingHelpers$new(dd$data, dd$config, prob = 0.8)
xx <- mh$get_stats()
xx <- mh$get_lod()

dd <- prolfqua::sim_lfq_data_2factor_config(Nprot = 100,weight_missing = 0.1)
mh <- prolfqua::MissingHelpers$new(dd$data, dd$config, prob = 0.8)
mh$get_stats()$interaction |> table()
mh$get_lod()
```

missingness_per_condition

Summarize missing in condition as barplot

Description

Summarize missing in condition as barplot

Usage

```
missingness_per_condition(lfqdata, factors = lfqdata$relevant_factor_keys())
```

Arguments

lfqdata	LFQData object
factors	factor columns to use

See Also

Other plotting: ContrastsPlotter, INTERNAL_FUNCTIONS_BY_FAMILY, missigness_histogram(), missingness_per_condition_cumsum(), plot_estimate(), plot_heatmap(), plot_heatmap_cor(), plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_na_heatmap(), plot_pca(), plot_raster(), plot_sample_correlation(), upset_interaction_missing_s upset_missing_stats()

Other imputation: get_contrast(), missigness_histogram(), missingness_per_condition_cumsum(), upset_interaction_missing_stats(), upset_missing_stats()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
res <- missingness_per_condition(lfq)
stopifnot("ggplot" %in% class(res$figure))
stopifnot(ncol(res$data) >= 5)
```

missingness_per_condition_cumsum

cumulative sums of missing

Description

cumulative sums of missing

Usage

```
missingness_per_condition_cumsum(
  lfqdata,
  factors = lfqdata$relevant_factor_keys()
)
```

Arguments

lfqdata	LFQData object
factors	factor columns to use

See Also

Other plotting: ContrastsPlotter, INTERNAL_FUNCTIONS_BY_FAMILY, missigness_histogram(), missingness_per_condition(), plot_estimate(), plot_heatmap(), plot_heatmap_cor(), plot_hierarchies_b plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_na_heatmap(), plot_pca(), plot_raster(), plot_sample_correlation(), upset_interaction_missing_stats(), upset_missing_stats()

Other imputation: get_contrast(), missigness_histogram(), missingness_per_condition(), upset_interaction_missing_stats(), upset_missing_stats()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
res <- missingness_per_condition_cumsum(lfq)
stopifnot("ggplot" %in% class(res$figure))
stopifnot(ncol(res$data) >= 6)
```

Model *R6 class representing modelling result*

Description

R6 class representing modelling result

R6 class representing modelling result

Value

An R6 class generator.

Super class

prolfqua::ModelInterface -> Model

Public fields

model_df data.frame with modelling data and model.

model_name name of model

subject_id e.g. protein_Id

model_strategy function to create the models

p.adjust function to adjust p-values

Methods

Public methods:

- Model$new()
- Model$get_coefficients()
- Model$get_anova()
- Model$clone()

Method `new()`**:** initialize

Usage:

```
Model$new(
  model_df,
  model_strategy,
  model_name,
  subject_id = "protein_Id",
  p.adjust = prolfqua::adjust_p_values
)
```

Arguments:

`model_df` dataframe with modelling results

`model_strategy` model_strategy see strategy_lmer

`model_name` name of model

`subject_id` subject column name

`p.adjust` method to adjust p-values

Method `get_coefficients()`**:** return model coefficient table

Usage:

```
Model$get_coefficients()
```

Method `get_anova()`**:** return anova table

Usage:

```
Model$get_anova()
```

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
Model$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(),

build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_peptide_config(Nprot = 20)
lfqdata <- LFQData$new(istar$data, istar$config)
lfqdata <- lfqdata$get_Transformer()$log2()$lfq
model_name <- "f_condtion_r_peptide"
formula_randomPeptide <-
  strategy_lmer(paste0(lfqdata$response(), " ~ group_ + (1 | peptide_Id)"),
   model_name = model_name)
mod <- prolfqua::build_model(
 lfqdata,
 formula_randomPeptide,
 model_name = model_name)

mod$model_df
aovtable  <- mod$get_anova()
mod$get_coefficients()
mod$coef_histogram()
mod$coef_volcano()
mod$coef_pairs()
mod$anova_histogram()
```

`ModelFirth` *R6 class representing modelling result*

Description

R6 class representing modelling result

R6 class representing modelling result

Value

An R6 class generator.

Super class

prolfqua::ModelInterface -> ModelFirth

Public fields

`models` data.frame with modelling data and model.

`model_name` name of model

`subject_id` e.g. protein_Id

`p.adjust` function to adjust p-values

Methods

Public methods:

- `ModelFirth$new()`
- `ModelFirth$get_coefficients()`
- `ModelFirth$get_anova()`
- `ModelFirth$anova_histogram()`
- `ModelFirth$clone()`

Method `new()`**:** initialize

Usage:

```
ModelFirth$new(
  models,
  model_name = "modelFirth",
  subject_id = "protein_Id",
  p.adjust = prolfqua::adjust_p_values
)
```

Arguments:

`models` dataframe with modelling results

`model_name` name of model

`subject_id` subject column name

`p.adjust` method to adjust p-values

Method `get_coefficients()`**:** return model coefficient table

Usage:

```
ModelFirth$get_coefficients()
```

Method `get_anova()`**:** return anova table

Usage:

```
ModelFirth$get_anova()
```

Method `anova_histogram()`**:** histogram of ANOVA results

Usage:

```
ModelFirth$anova_histogram(what = c("p.value", "FDR"))
```

Arguments:

`what` show either "Pr..F." or "FDR.Pr..F."

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ModelFirth$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config(Nprot = 10, with_missing = TRUE,
  weight_missing = 0.5, seed = 3)
istar$data <- prolfqua::encode_bin_resp(LFQData$new(istar$data, istar$config))
istar$config$bin_resp <- "bin_resp"
tmp <- LFQData$new(istar$data, istar$config)
formula <- paste0(tmp$get_config()$bin_resp , "~ group_")
mod <- build_model_logistf(tmp, formula)
tmp <- mod$get_coefficients()
mod$coef_histogram()
mod$coef_pairs()
mod$get_anova()
mod$coef_volcano()
mod$anova_histogram()

istar <- prolfqua::sim_lfq_data_protein_config(Nprot = 10, with_missing = TRUE,
  weight_missing = 0.5, seed = 3)
istar$data <- prolfqua::encode_bin_resp(LFQData$new(istar$data, istar$config))
istar$config$bin_resp <- "bin_resp"
tmp <- LFQData$new(istar$data, istar$config)
formula <- paste0(tmp$get_config()$bin_resp , "~ group_")
mod <- build_model_logistf(tmp, formula)
tmp <- mod$get_coefficients()
stopifnot(nrow(tmp) == 30)
mod$coef_histogram()
mod$coef_pairs()
mod$get_anova()
mod$coef_volcano()
mod$anova_histogram()
```

`ModelInterface` *R6 interface class representing modelling result*

Description

R6 interface class representing modelling result

R6 interface class representing modelling result

Value

An R6 class generator.

Methods

Public methods:

- `ModelInterface$get_coefficients()`
- `ModelInterface$get_anova()`
- `ModelInterface$coef_histogram()`
- `ModelInterface$coef_volcano()`
- `ModelInterface$coef_pairs()`
- `ModelInterface$anova_histogram()`
- `ModelInterface$clone()`

Method `get_coefficients()`**:** return model coefficients

Usage:

```
ModelInterface$get_coefficients()
```

Returns: data.frame

Method `get_anova()`**:** perform ANOVA analysis

Usage:

```
ModelInterface$get_anova()
```

Returns: data.frame

Method `coef_histogram()`**:** histogram of coefficient p-values

Usage:

```
ModelInterface$coef_histogram()
```

Returns: list with `plot` (ggplot) and file `name`

Method `coef_volcano()`**:** volcano plot of non-intercept coefficients

Usage:

```
ModelInterface$coef_volcano()
```

Returns: list with `plot` (ggplot) and file `name`

Method `coef_pairs()`**:** coefficient estimates in wide format, one column per coefficient, for a pairs plot

Usage:

```
ModelInterface$coef_pairs()
```

Returns: list with `plot` (data.frame) and file `name`

Method `anova_histogram()`**:** histogram of ANOVA p-values or FDR

Usage:

```
ModelInterface$anova_histogram(what = c("p.value", "FDR"))
```

Arguments:

`what` show either "p.value" or "FDR"

Returns: list with `plot` (ggplot) and file `name`

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ModelInterface$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
mi <- ModelInterface$new()

testthat::expect_error(mi$get_coefficients())
testthat::expect_error(mi$get_anova())
testthat::expect_error(mi$coef_histogram())
testthat::expect_error(mi$coef_volcano())
testthat::expect_error(mi$coef_pairs())
testthat::expect_error(mi$anova_histogram())
```

`ModelLimma` *R6 class representing a limma modelling result*

Description

R6 class representing a limma modelling result

R6 class representing a limma modelling result

Details

Same API as `Model`: `get_anova()`, `get_coefficients()`, `coef_histogram()`, `coef_volcano()`, `anova_histogram()`.

Value

An R6 class generator.

Super class

`prolfqua::ModelInterface` -> `ModelLimma`

Public fields

`fit` limma MArrayLM object from lmFit

`subject_id` protein ID column name(s)

`model_name` model name

`rowdata` protein ID mapping from to_wide()$rowdata

`trend` passed to eBayes

`robust` passed to eBayes

`dummy_model` one fitted lm for linfct extraction

`p.adjust` function to adjust p-values

`imputed_proteins` character vector of protein ids (matching `rownames(fit$coefficients)`) that were rescued via LOD imputation. `ContrastsLimma$get_contrasts()` reads this to tag refit rows with a `"_imputed"` modelName suffix so the rescue is visible downstream. Empty for builders that do not impute.

Methods

Public methods:

- `ModelLimma$new()`
- `ModelLimma$get_coefficients()`
- `ModelLimma$get_anova()`
- `ModelLimma$clone()`

Method `new()`**:** initialize ModelLimma

Usage:

```
ModelLimma$new(
  fit,
  subject_id,
  model_name,
  rowdata,
  trend = FALSE,
  robust = FALSE,
  dummy_model = NULL,
  p.adjust = prolfqua::adjust_p_values,
  imputed_proteins = character(0)
)
```

Arguments:

`fit` limma MArrayLM from lmFit

`subject_id` protein ID column name(s)

`model_name` model name

`rowdata` protein ID mapping

`trend` passed to eBayes

`robust` passed to eBayes

`dummy_model` one fitted lm for linfct extraction

`p.adjust` function to adjust p-values

`imputed_proteins` character vector of LOD-rescued protein ids

Method `get_coefficients()`**:** return model coefficient table in long format

Usage:

```
ModelLimma$get_coefficients()
```

Returns: data.frame

Method `get_anova()`**:** return anova table (F-test per protein across all non-intercept coefficients)

Usage:

```
ModelLimma$get_anova()
```

Returns: data.frame

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ModelLimma$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median, vcov.rfit_prolfqua()

Examples

```
istar <- sim_lfq_data_protein_config(Nprot = 50)
lProt <- LFQData$new(istar$data, istar$config)
lProt$rename_response("transformedIntensity")
strat <- strategy_limma("transformedIntensity ~ group_")
mod <- build_model_limma(lProt, strat)

coeffs <- mod$get_coefficients()
head(coeffs)
anova_tbl <- mod$get_anova()
head(anova_tbl)
mod$coef_histogram()
mod$coef_volcano()
```

```
mod$anova_histogram()
```

`model_analyse` *analyses lmer4 and lm models created using help function 'strategy_lm' or 'strategy_lmer'*

Description

used in project p2901

Usage

```
model_analyse(
  pepIntensity,
  model_strategy,
  subject_id = "protein_Id",
  model_name = "Model",
  label = model_name,
  progress = getOption("prolfqua.progress", NULL)
)
```

Arguments

`label`	short label naming this fitting pass in progress output; defaults to 'model_name'.
`progress`	progress reporter selector passed to [.make_progress()]; 'NULL' (default) keeps the legacy terminal 'progress::progress_bar', a 'function(i, total, label)' or '"message"' emits batch-visible progress. Defaults to 'getOption("prolfqua.progress", NULL)'.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_summary(), moderated_p_deqms(), moderated_p_deqms_ moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
x <- sim_lfq_data_peptide_config()
formula_randomPeptide <-
  strategy_lmer("abundance  ~ group_ + (1 | peptide_Id)")
mr <- model_analyse( x$data,
 formula_randomPeptide,
 subject_id = x$config$hierarchy_keys_depth())
stopifnot(nrow(get_complete_model_fit(mr$model_df)) == 6)
```

`model_summary` *Summarize modelling and error reporting*

Description

Summarize modelling and error reporting

Usage

```
model_summary(mod)
```

Arguments

mod	model table see `build_model`

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu` `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste` `ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf()`, `compute_borrowed_variance()`, `compute_borrowed_variance_` `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_results()`, `model_analyse()`, `moderated_p_deqms()`, `moderated_p_deqms_` `moderated_p_limma()`, `new_imputed_model()`, `pivot_model_contrasts_to_wide()`, `register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median_p_scaled()`, `vcov.rfit_prolfqua()`

Examples

```
D <- prolfqua::sim_lfq_data_peptide_config(Nprot = 20, weight_missing = 0.1)
formula_rp <- strategy_lmer("abundance ~ group_ + (1 | peptide_Id) + (1 | sampleName)")
mod <- prolfqua::build_model(
  LFQData$new(D$data, D$config), formula_rp)
res <- model_summary(mod)
stopifnot(is.list(res))
stopifnot(all(c("exists", "isSingular") %in% names(res)))
```

`moderated_p_deqms` *DEqMS-style count-dependent variance moderation*

Description

Applies count-dependent empirical Bayes variance shrinkage to a contrast result table. Proteins quantified from many peptides get less shrinkage; proteins from few peptides get more.

Usage

```
moderated_p_deqms(
  mm,
  count_col,
  df = "df",
  estimate = "diff",
  loess_span = 0.75,
  confint = 0.95
)
```

Arguments

`mm`	data.frame from one contrast group with columns: sigma, df, statistic, std.error, and the estimate column
`count_col`	name of column with peptide/PSM count per protein
`df`	name of the degrees of freedom column
`estimate`	name of the fold change column
`loess_span`	span parameter for LOESS fit (default 0.75)
`confint`	confidence level for intervals (default 0.95)

Value

data.frame with added moderated.* columns

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu` `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste` `ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`,

ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms_long moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
mm <- data.frame(
  sigma = c(0.25, 0.32, 0.28, 0.40, 0.35),
  df = rep(6, 5),
  statistic = c(2.1, -1.8, 0.5, 3.0, -2.2),
  std.error = c(0.8 / 2.1, 0.6 / 1.8, 0.2 / 0.5, 1.2 / 3.0, 0.9 / 2.2),
  diff = c(0.8, -0.6, 0.2, 1.2, -0.9),
  count = c(2, 3, 4, 6, 8)
)
res <- moderated_p_deqms(mm, count_col = "count")
"moderated.p.value" %in% colnames(res)
```

---

moderated_p_deqms_long

DEqMS-style moderation for long contrast table

Description

Splits by contrast group and applies moderated_p_deqms to each group independently.

Usage

```
moderated_p_deqms_long(
  mm,
  count_col,
  group_by_col = "contrast",
  estimate = "diff",
  loess_span = 0.75
)
```

Arguments

mm	contrast result data.frame (long format)
count_col	name of column with peptide/PSM count per protein
group_by_col	column to group by (default "contrast")
estimate	name of the fold change column
loess_span	span parameter for LOESS fit (default 0.75)

Value

data.frame with moderated columns added

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
mm <- data.frame(
  contrast = rep(c("A_vs_B", "C_vs_D"), each = 5),
  sigma = rep(c(0.25, 0.32, 0.28, 0.40, 0.35), 2),
  df = rep(6, 10),
  statistic = rep(c(2.1, -1.8, 0.5, 3.0, -2.2), 2),
  std.error = rep(c(0.8 / 2.1, 0.6 / 1.8, 0.2 / 0.5, 1.2 / 3.0, 0.9 / 2.2), 2),
  diff = rep(c(0.8, -0.6, 0.2, 1.2, -0.9), 2),
  count = rep(c(2, 3, 4, 6, 8), 2)
)
res <- moderated_p_deqms_long(mm, count_col = "count")
table(res$contrast)
```

---

moderated_p_limma *Moderate p-values - limma approach*

Description

Moderate p-values - limma approach

Usage

```
moderated_p_limma(
  contrast_df,
  df = "df",
```

```
  estimate = "diff",
  robust = FALSE,
  confint = 0.95,
  variance_floor = NULL
)
```

Arguments

variance_floor optional positive lower bound for posterior variances

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
contrast_df <- data.frame(
  sigma = c(0.25, 0.32, 0.28, 0.40, 0.35),
  df = rep(6, 5),
  statistic = c(2.1, -1.8, 0.5, 3.0, -2.2),
  std.error = c(0.8 / 2.1, 0.6 / 1.8, 0.2 / 0.5, 1.2 / 3.0, 0.9 / 2.2),
  diff = c(0.8, -0.6, 0.2, 1.2, -0.9)
)
res <- moderated_p_limma(contrast_df)
"moderated.p.value" %in% colnames(res)
```

---

multigroup_volcano *plot volcano given multiple contrasts*

Description

plot volcano given multiple contrasts

Usage

```
multigroup_volcano(
  .data,
  effect = "fc",
  significance = "p.adjust",
  contrast = "condition",
  colour = "colour",
  xintercept = c(-2, 2),
  yintercept = 0.05,
  label = NULL,
  size = 1,
  segment.size = 0.3,
  segment.alpha = 0.3,
  scales = "fixed",
  max_nr_significant_text = 20
)
```

Arguments

.data	data in long format
effect	column containing effect sizes
significance	column containing p-values, q.values etc
contrast	column with contrast
colour	colouring of points
xintercept	fc thresholds
yintercept	significance threshold
label	column containing labels
size	controls size of text
segment.size	controls size of lines
segment.alpha	controls visibility of lines
scales	parameter to ggplot2::facet_wrap
max_nr_significant_text	maximum number of significant labels to display

See Also

Other utilities: INTERNAL_FUNCTIONS_BY_FAMILY, get_uniprot_id_from_fasta_header(), is_contaminant(), is_decoy(), matrix_to_tibble(), pairs_smooth(), panel_cor(), table_facade()

Examples

```
show <- data.frame(logFC = rnorm(100, 0, 1), adj.P.Val = runif(100, 0, 1),
  Condition = sample(c("a","b")), colour = "forward", Name = paste0("n", 1:100))
prolfqua::multigroup_volcano( show,
effect="logFC",
significance = "adj.P.Val",
contrast="Condition",
colour=NULL,
label="Name",
max_nr_significant_text = 300)
```

`new_imputed_model` *Create an imputed model wrapper*

Description

Wraps a refitted model (`lm`, `rfit`, ...) with borrowed covariance information. S3 generics vcov(), sigma(), and df.residual() dispatch to the borrowed values instead of the original model's, while coef()/terms() still fall through to the wrapped fit. The wrapper is backend-neutral: the class is prepended to whatever the refit already carries (e.g. `c("imputed_model", "lm")` or `c("imputed_model", "rfit_prolfqua", "rfit")`).

Usage

```
new_imputed_model(
  model,
  borrowed_vcov,
  borrowed_sigma,
  borrowed_df,
  n_observed
)
```

Arguments

`model`	model object fitted on imputed data
`borrowed_vcov`	matrix, borrowed variance-covariance matrix
`borrowed_sigma`	numeric, borrowed residual standard error / scale
`borrowed_df`	numeric, borrowed residual degrees of freedom
`n_observed`	integer, number of non-imputed observations

Value

imputed_model object

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(),

lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
# Fit a normal lm, then wrap it with borrowed covariance
dat <- data.frame(group_ = rep(c("A", "B"), each = 4),
                  y = c(20.1, 20.5, 19.8, 20.3, 22.1, 22.4, 21.9, 22.2))
fit <- lm(y ~ group_, data = dat)

# Wrap with borrowed variance (in practice these come from donor pool)
wrapped <- prolfqua:::new_imputed_model(fit,
  borrowed_vcov = vcov(fit),
  borrowed_sigma = 0.8,
  borrowed_df = 6,
  n_observed = 5)

# S3 dispatch returns borrowed values
stopifnot(inherits(wrapped, "imputed_model"))
stopifnot(sigma(wrapped) == 0.8)
stopifnot(df.residual(wrapped) == 6)
# coefficients() still dispatches to underlying lm
stopifnot(identical(coefficients(wrapped), coefficients(fit)))
```

---

nr_B_in_A *Count the children of each parent in the hierarchy*

Description

The number of distinct ‘level_b‘ entries, e.g. peptides, within each ‘level_a‘ entry, e.g. protein.

Usage

```
nr_B_in_A(
  pdata,
  level_a,
  level_b,
 name = paste0("nr_", paste(level_b, collapse = "_"), "_IN_", paste(level_a, collapse =
    "_"))
)
```

Arguments

pdata	data.frame
level_a	parent key columns
level_b	child key columns
name	name of the count column

Value

data.frame of the ‘level_a‘ keys and the count column

See Also

Other preprocessing: INTERNAL_FUNCTIONS_BY_FAMILY, apply_to_response_matrix(), filter_proteins_by_pept
get_robscales(), robust_scale(), scale_with_subset()

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config()
head(prolfqua:::nr_B_in_A(istar$data, "protein_Id", "peptide_Id"))
```

---

nr_children_experiment

Max nr_children across samples per hierarchy unit

Description

Aggregates nr_children per sample (via nr_obs_sample), then takes the max per hierarchy unit.

Usage

```
nr_children_experiment(
  data,
  response,
  hierarchy_keys_depth,
  file_name,
  nr_children_col,
  name_nr_child = "nr_child_exp"
)
```

Arguments

data	data.frame
response	character — intensity column name
hierarchy_keys_depth	character vector — hierarchy columns at current depth
file_name	character — file name column
nr_children_col	character — nr_children column name
name_nr_child	character — output column name

Value

The computed result.

Examples

```
dd <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(dd$data, dd$config)
xd <- nr_children_experiment(lfq$data_long(), lfq$response(),
  lfq$relevant_hierarchy_keys(), lfq$file_name(), lfq$nr_children_col())
stopifnot(min(xd$nr_child_exp) == 1)
```

`nr_features_experiment` *Count distinct child features per hierarchy unit*

Description

Counts the number of distinct child-level entries (e.g. peptides per protein).

Usage

```
nr_features_experiment(
  data,
  hierarchy_keys,
  hierarchy_keys_depth,
  name_nr_child = "nr_child_exp"
)
```

Arguments

`data`	data.frame
`hierarchy_keys`	character vector — all hierarchy column names
`hierarchy_keys_depth`	character vector — hierarchy columns at current depth
`name_nr_child`	character — output column name

Value

The computed result.

Examples

```
dd <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(dd$data, dd$config)
xd <- nr_features_experiment(lfq$data_long(), lfq$hierarchy_keys(),
  lfq$relevant_hierarchy_keys())
stopifnot(min(xd$nr_child_exp) == 1)
```

`nr_obs_sample` *Aggregates e.g. protein abundances from peptide abundances*

Description

Aggregates e.g. protein abundances from peptide abundances

Usage

```
nr_obs_sample(
  data,
  response,
  hierarchy_keys_depth,
  file_name,
  nr_children_col,
  new_child = nr_children_col
)
```

Arguments

`data`	data.frame
`response`	character — intensity column name
`hierarchy_keys_depth`	character vector — hierarchy columns at current depth
`file_name`	character — file name column
`nr_children_col`	character — nr_children column name
`new_child`	character — output column name

Value

The computed result.

Examples

```
dd <- prolfqua::sim_lfq_data_peptide_config()
dd$data <- na.omit(dd$data)

xd <- nr_obs_sample(na.omit(dd$data), dd$config$get_response(),
  dd$config$hierarchy_keys_depth(), dd$config$file_name, dd$config$nr_children)
xd$nr_children |> table()
# xd |> pivot_wider(id_cols = protein_Id, names_from = sample, values_from = nr_children)

dp <- prolfqua::sim_lfq_data_protein_config()
xp <- nr_obs_sample(dp$data, dp$config$get_response(),
  dp$config$hierarchy_keys_depth(), dp$config$file_name, dp$config$nr_children)
# xp
# xp |> pivot_wider(id_cols = protein_Id, names_from = sample, values_from = nrPeptides)
xp$nrPeptides |> table()
```

PACKAGE_DATA *Package Data*

Description

Package Data

Value

A documentation topic.

See Also

Other data: data_checksummarizationrobust87, data_checksummarizerobust69, data_ionstar, prolfqua_data(), x5463yzwer453bbb

pairs_smooth *smoothScatter pairs*

Description

smoothScatter pairs

Usage

```
pairs_smooth(data, legend = FALSE, ...)
```

Arguments

data	data matrix or data.frame as normally passed to pairs
legend	add legend to plots
...	params usually passed to pairs

See Also

also pairs

Other utilities: INTERNAL_FUNCTIONS_BY_FAMILY, get_uniprot_id_from_fasta_header(), is_contaminant(), is_decoy(), matrix_to_tibble(), multigroup_volcano(), panel_cor(), table_facade()

Examples

```
tmp = matrix(rep((1:100),times = 4) + rnorm(100*4,0,3),ncol=4)
pairs_smooth(tmp,main="small data", legend=TRUE)
pairs_smooth(tmp,main="small data")
pairs_smooth(tmp,log="xy",main="small data", legend=TRUE)
```

panel_cor *correlation panel for pairs plot function (used as default in pairs_smooth)*

Description

correlation panel for pairs plot function (used as default in pairs_smooth)

Usage

```
panel_cor(x, y, digits = 2, ...)
```

Arguments

x	numeric data
y	numeric data
digits	number of digits to display
...	not used

See Also

Other utilities: INTERNAL_FUNCTIONS_BY_FAMILY, get_uniprot_id_from_fasta_header(), is_contaminant(), is_decoy(), matrix_to_tibble(), multigroup_volcano(), pairs_smooth(), table_facade()

Examples

```
graphics::plot(1:3, 1:3, type = "n")
panel_cor(1:3, 1:3)
```

pivot_model_contrasts_to_wide *pivot model contrasts matrix to wide format produced by 'contrasts_linfct' and ...*

Description

pivot model contrasts matrix to wide format produced by 'contrasts_linfct' and ...

Usage

```
pivot_model_contrasts_to_wide(
  model_interaction_contrasts,
  subject_id = "protein_Id",
  columns = c("estimate", "p.value", "p.value.adjusted"),
  contrast = "lhs"
)
```

Arguments

model_interaction_contrasts	data.frame with contrast results in long format
subject_id	column name(s) identifying subjects (e.g. protein_Id)
columns	character vector of value columns to pivot wide
contrast	column name containing contrast labels

Value

Contrast definitions or contrast results.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
# this function is used by the contrast classes to implement the to wide method
contrast_df <- data.frame(
  protein_Id = c("P1", "P1", "P2", "P2"),
  lhs = c("A_vs_B", "C_vs_D", "A_vs_B", "C_vs_D"),
  estimate = c(1.0, 0.5, -0.2, 0.7),
  p.value = c(0.01, 0.2, 0.4, 0.05),
  p.value.adjusted = c(0.02, 0.25, 0.4, 0.08)
)
pivot_model_contrasts_to_wide(contrast_df)
```

plot_estimate *Plot feature data and result of aggregation*

Description

Plot feature data and result of aggregation

Usage

```
plot_estimate(lfqdata, lfqdata_agg, show.legend = FALSE)
```

Arguments

lfqdata	LFQData object (original data)
lfqdata_agg	LFQData object (aggregated data)
show.legend	logical, show legend in plot

See Also

Other plotting: ContrastsPlotter, INTERNAL_FUNCTIONS_BY_FAMILY, missigness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), plot_heatmap(), plot_heatmap_cor() plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_na_heatmap(), plot_pca(), plot_raster(), plot_sample_correlation(), upset_interaction_missing_s upset_missing_stats()

Other aggregation: INTERNAL_FUNCTIONS_BY_FAMILY, aggregate_intensity_top_n(), estimate_intensity(), plot_hierarchies_line()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
lfq <- lfq$get_Transformer()$log2()$lfq
bbMed <- estimate_intensity(lfq, method = "medpolish")
lfq_med <- LFQData$new(bbMed$data, bbMed$config)
tmpMed <- plot_estimate(lfq, lfq_med)
stopifnot("ggplot" %in% class(tmpMed$plots[[1]]))
```

plot_heatmap *plot heatmap with annotations*

Description

plot heatmap with annotations

Usage

```
plot_heatmap(
  matrix,
  annotation,
  factor_keys,
  sample_name,
  na_fraction = 0.4,
  show_rownames = FALSE,
  max_rownames_chars = 60,
  max_sample_label_chars = 20,
  ...
)
```

Arguments

matrix	numeric matrix — wide-format intensity data
annotation	data.frame — sample annotation
factor_keys	character vector — factor column names for annotation
sample_name	character — sample name column
na_fraction	maximum fraction of missing values per row. Rows that cannot be meaningfully z-scored are always removed.
show_rownames	if TRUE shows row names, default FALSE
max_rownames_chars	maximum displayed row label length
max_sample_label_chars	maximum displayed sample label length. Labels keep their suffix because sample prefixes are often shared.
...	passed to [ComplexHeatmap::Heatmap()]

See Also

Other plotting: ContrastsPlotter, INTERNAL_FUNCTIONS_BY_FAMILY, missigness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), plot_estimate(), plot_heatmap_cor(), plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribu plot_na_heatmap(), plot_pca(), plot_raster(), plot_sample_correlation(), upset_interaction_missing_s upset_missing_stats()

Examples

```
istar <- sim_lfq_data_protein_config()
lfq <- LFQData$new(istar$data, istar$config)
wide <- lfq$data_wide(as.matrix = TRUE)
p <- plot_heatmap(wide$data, wide$annotation, lfq$factor_keys(), lfq$sample_name())
stopifnot(methods::is(p, "Heatmap"))
```

`plot_heatmap_cor` *plot correlation heatmap with annotations*

Description

plot correlation heatmap with annotations

Usage

```
plot_heatmap_cor(
  matrix,
  annotation,
  factor_keys,
  sample_name,
  R2 = FALSE,
  color = colorRampPalette(c("white", "red"))(1024),
  max_sample_label_chars = 20,
  ...
)
```

Arguments

`matrix`	numeric matrix — wide-format intensity data
`annotation`	data.frame — sample annotation
`factor_keys`	character vector — factor column names for annotation
`sample_name`	character — sample name column
`R2`	logical — plot R-squared instead of correlation
`color`	color palette
`max_sample_label_chars`	maximum displayed sample label length. Labels keep their suffix because sample prefixes are often shared.
`...`	passed to [ComplexHeatmap::Heatmap()]

See Also

Other plotting: `ContrastsPlotter`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `missingness_histogram()`, `missingness_per_condition()`, `missingness_per_condition_cumsum()`, `plot_estimate()`, `plot_heatmap()`, `plot_hierarchies_boxplot_df()`, `plot_hierarchies_line()`, `plot_intensity_distribution`
`plot_na_heatmap()`, `plot_pca()`, `plot_raster()`, `plot_sample_correlation()`, `upset_interaction_missing_s`
`upset_missing_stats()`

Examples

```
istar <- sim_lfq_data_protein_config()
lfq <- LFQData$new(istar$data, istar$config)
wide <- lfq$data_wide(as.matrix = TRUE)
pheat_map <- plot_heatmap_cor(wide$data, wide$annotation,
  lfq$factor_keys(), lfq$sample_name())
stopifnot(methods::is(pheat_map, "Heatmap"))
pheat_map <- plot_heatmap_cor(wide$data, wide$annotation,
```

```
  lfq$factor_keys(), lfq$sample_name(), R2 = TRUE)
stopifnot(methods::is(pheat_map, "Heatmap"))
```

`plot_hierarchies_boxplot` *plot peptides by factors and it's levels.*

Description

plot peptides by factors and it's levels.

Usage

```
plot_hierarchies_boxplot(
  pdata,
  title,
  lfqdata,
  facet_grid_on = NULL,
  beeswarm = TRUE,
  show_mean = TRUE,
  pb
)
```

Arguments

`pdata`	data.frame
`title`	name to show
`lfqdata`	LFQData object
`facet_grid_on`	on which variable to run facet_grid
`beeswarm`	use beeswarm default FALSE
`show_mean`	show mean values
`pb`	progress bar

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
res <- plot_hierarchies_boxplot_df(lfq$data_long(), lfq)
res$boxplot[[1]]

xnested <- lfq$data_long() |>
  dplyr::group_by(across(all_of(lfq$relevant_hierarchy_keys()))) |> tidyr::nest()
p <- plot_hierarchies_boxplot(xnested$data[[1]], xnested$protein_Id[[1]],
  lfq, beeswarm = FALSE, show_mean = TRUE)
p <- plot_hierarchies_boxplot(xnested$data[[1]], xnested$protein_Id[[1]],
  lfq, beeswarm = TRUE)
p
```

`plot_hierarchies_boxplot_df` *generates peptide level plots for all Proteins*

Description

generates peptide level plots for all Proteins

Usage

```
plot_hierarchies_boxplot_df(
  pdata,
  lfqdata,
  hierarchy = lfqdata$relevant_hierarchy_keys(),
  facet_grid_on = NULL
)
```

Arguments

`pdata`	data.frame
`lfqdata`	LFQData object
`hierarchy`	e.g. protein_Id default relevant_hierarchy_keys
`facet_grid_on`	default NULL

See Also

Other plotting: `ContrastsPlotter`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `missigness_histogram()`, `missingness_per_condition()`, `missingness_per_condition_cumsum()`, `plot_estimate()`, `plot_heatmap()`, `plot_heatmap_cor()`, `plot_hierarchies_line()`, `plot_intensity_distribution_violin()`, `plot_na_heatmap()`, `plot_pca()`, `plot_raster()`, `plot_sample_correlation()`, `upset_interaction_missing_s` `upset_missing_stats()`

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
res <- plot_hierarchies_boxplot_df(lfq$data_long(), lfq)
res$boxplot[[1]]

lfq2 <- LFQData$new(
  istar$data |> dplyr::filter(protein_Id %in% sample(protein_Id, 2)),
  istar$config)
res <- plot_hierarchies_boxplot_df(lfq2$data_long(), lfq2)
res$boxplot[[1]]
```

`plot_hierarchies_line` *Plot peptide intensities of protein as a function of the sample and factor*

Description

Plot peptide intensities of protein as a function of the sample and factor

Usage

```
plot_hierarchies_line(res, protein_name, lfqdata, show.legend = FALSE)
```

Arguments

`res`	data.frame
`protein_name`	title of plot
`lfqdata`	LFQData object
`show.legend`	logical, show legend in plot

See Also

Other aggregation: `INTERNAL_FUNCTIONS_BY_FAMILY`, `aggregate_intensity_top_n()`, `estimate_intensity()`, `plot_estimate()`

Other plotting: `ContrastsPlotter`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `missigness_histogram()`, `missingness_per_condition()`, `missingness_per_condition_cumsum()`, `plot_estimate()`, `plot_heatmap()`, `plot_heatmap_cor()`, `plot_hierarchies_boxplot_df()`, `plot_intensity_distribution_viol`
`plot_na_heatmap()`, `plot_pca()`, `plot_raster()`, `plot_sample_correlation()`, `upset_interaction_missing_s`
`upset_missing_stats()`

Examples

```
istar <- sim_lfq_data_peptide_config()
config <- istar$config
analysis <- istar$data

xnested <- analysis |>
  dplyr::group_by(across(all_of(config$hierarchy_keys_depth()))) |>
  tidyr::nest()

lfq <- LFQData$new(analysis, config)
prolfqua::plot_hierarchies_line(xnested$data[[1]], xnested$protein_Id[[1]], lfq)
```

`plot_intensity_distribution_violin` *visualize intensity distributions*

Description

visualize intensity distributions

visualize intensity distributions

Usage

```
plot_intensity_distribution_violin(
  pdata,
  sample_name,
  response,
  is_transformed = FALSE
)

plot_intensity_distribution_density(
  pdata,
  sample_name,
  response,
  is_transformed = FALSE,
  legend = NA,
  max_legend_samples = 16
)
```

Arguments

`pdata`	data.frame
`sample_name`	character — sample column name
`response`	character — intensity column name
`is_transformed`	logical — is intensity log-transformed?
`legend`	show legend. If 'NA', hide automatically when the number of samples is larger than 'max_legend_samples'.
`max_legend_samples`	maximum number of samples for automatic legend display.

See Also

Other plotting: `ContrastsPlotter`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `missingness_histogram()`, `missingness_per_condition()`, `missingness_per_condition_cumsum()`, `plot_estimate()`, `plot_heatmap()`, `plot_heatmap_cor()`, `plot_hierarchies_boxplot_df()`, `plot_hierarchies_line()`, `plot_na_heatmap()`, `plot_pca()`, `plot_raster()`, `plot_sample_correlation()`, `upset_interaction_missing_s` `upset_missing_stats()`

Other plotting: `ContrastsPlotter`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `missingness_histogram()`, `missingness_per_condition()`, `missingness_per_condition_cumsum()`, `plot_estimate()`, `plot_heatmap()`, `plot_heatmap_cor()`, `plot_hierarchies_boxplot_df()`, `plot_hierarchies_line()`, `plot_na_heatmap()`, `plot_pca()`, `plot_raster()`, `plot_sample_correlation()`, `upset_interaction_missing_s` `upset_missing_stats()`

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
plot_intensity_distribution_violin(
  lfq$data_long(), lfq$sample_name(), lfq$response(), lfq$is_transformed())

istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
plot_intensity_distribution_density(
  lfq$data_long(), lfq$sample_name(), lfq$response(), lfq$is_transformed())
```

---

plot_lrt_diagnostics *Write LRT diagnostic plots to PDF*

Description

Writes a histogram of p-values and an empirical CDF to a PDF file. Called by `LR_test` when `path` is non-NULL.

Usage

```
plot_lrt_diagnostics(result, model_name, model_name_int, path)
```

Arguments

`result`	tibble with a `likelihood_ratio_test.pValue` column
`model_name`	name of the full model
`model_name_int`	name of the reduced/interaction model
`path`	directory to write the PDF into

---

plot_na_heatmap *plot heatmap of NA values*

Description

plot heatmap of NA values

Usage

```
plot_na_heatmap(
  matrix,
  annotation,
  factor_keys,
  sample_name,
  limitrows = 10000,
  distance = "binary"
)
```

Arguments

matrix	numeric matrix — wide-format intensity data
annotation	data.frame — sample annotation
factor_keys	character vector — factor column names for annotation
sample_name	character — sample name column
limitrows	max rows to display
distance	distance method for clustering

See Also

Other plotting: ContrastsPlotter, INTERNAL_FUNCTIONS_BY_FAMILY, missingness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), plot_estimate(), plot_heatmap(), plot_heatmap_cor(), plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_pca(), plot_raster(), plot_sample_correlation(), upset_interaction_missing_stats(), upset_missing_stats()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
wide <- lfq$data_wide(as.matrix = TRUE)
tmp <- plot_na_heatmap(wide$data, wide$annotation, lfq$factor_keys(), lfq$sample_name())
stopifnot(methods::is(tmp, "Heatmap"))
```

---

plot_pca *plot PCA*

Description

plot PCA

Usage

```
plot_pca(
  matrix,
  annotation,
  sample_name,
  factor_keys,
  PC = c(1, 2),
  add_txt = FALSE,
  nudge = 0.1
)
```

Arguments

matrix	numeric matrix — wide-format intensity data
annotation	data.frame — sample annotation
sample_name	character — sample name column
factor_keys	character vector — factor column names (first for color, second for shape)
PC	which principal components to plot
add_txt	show sample labels
nudge	label nudge distance

See Also

Other plotting: ContrastsPlotter, INTERNAL_FUNCTIONS_BY_FAMILY, missingness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), plot_estimate(), plot_heatmap(), plot_heatmap_cor(), plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_na_heatmap(), plot_raster(), plot_sample_correlation(), upset_interaction_missing_stats(), upset_missing_stats()

Examples

```
istar <- sim_lfq_data_protein_config(with_missing = TRUE, weight_missing = .8, Nprot = 3000)
lfq <- LFQData$new(istar$data, istar$config)
wide <- lfq$data_wide(as.matrix = TRUE)
tmp <- plot_pca(wide$data, wide$annotation, lfq$sample_name(), lfq$factor_keys(),
  add_txt = TRUE, nudge = 0.01)
stopifnot("ggplot" %in% class(tmp))
tmp <- plot_pca(wide$data, wide$annotation, lfq$sample_name(), lfq$factor_keys())
stopifnot("ggplot" %in% class(tmp))
```

---

plot_raster *plot heatmap without any clustering (use to show NA's)*

Description

plot heatmap without any clustering (use to show NA's)

Usage

```
plot_raster(
  matrix,
  annotation,
  factor_keys,
  sample_name,
  arrange = c("mean", "var"),
  not_na = FALSE,
  show_rownames = FALSE,
  max_rownames_chars = 60,
  max_sample_label_chars = 20,
  ...
)
```

Arguments

matrix	numeric matrix — wide-format intensity data
annotation	data.frame — sample annotation
factor_keys	character vector — factor column names for annotation
sample_name	character — sample name column
arrange	either mean or var
not_na	if true than arrange by nr of NA's first and then by arrange
show_rownames	logical, show row names in heatmap
max_rownames_chars	maximum displayed row label length
max_sample_label_chars	maximum displayed sample label length. Labels keep their suffix because sample prefixes are often shared.
...	additional arguments passed to [ComplexHeatmap::Heatmap()]

See Also

Other plotting: ContrastsPlotter, INTERNAL_FUNCTIONS_BY_FAMILY, missingness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), plot_estimate(), plot_heatmap(), plot_heatmap_cor(), plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_na_heatmap(), plot_pca(), plot_sample_correlation(), upset_interaction_missing_stats(), upset_missing_stats()

Examples

```
istar <- sim_lfq_data_protein_config()
lfq <- LFQData$new(istar$data, istar$config)
wide <- lfq$data_wide(as.matrix = TRUE)
rs <- plot_raster(wide$data, wide$annotation, lfq$factor_keys(), lfq$sample_name())
stopifnot(methods::is(rs, "Heatmap"))
rs <- plot_raster(wide$data, wide$annotation, lfq$factor_keys(), lfq$sample_name(), "var")
stopifnot(methods::is(rs, "Heatmap"))
```

---

plot_sample_correlation

visualize correlation among samples

Description

visualize correlation among samples

Usage

```
plot_sample_correlation(matrix)
```

Arguments

matrix	numeric matrix — wide-format intensity data (samples as columns)

See Also

Other plotting: ContrastsPlotter, INTERNAL_FUNCTIONS_BY_FAMILY, missigness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), plot_estimate(), plot_heatmap(), plot_heatmap_cor(), plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_na_heatmap(), plot_pca(), plot_raster(), upset_interaction_missing_stats(), upset_missing_stats()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
lfq <- lfq$get_Transformer()$log2()$lfq
plot_sample_correlation(lfq$data_wide(as.matrix = TRUE)$data)
```

---

plot_stat_density *plot density distribution or ecdf of sd, mean or CV*

Description

plot density distribution or ecdf of sd, mean or CV

Usage

```
plot_stat_density(
  pdata,
  factor_key,
  stat = c("CV", "meanAbundance", "sd"),
  ggstat = c("density", "ecdf")
)
```

Arguments

pdata	data.frame with statistics
factor_key	character — factor column name for colouring
stat	sd, mean or CV
ggstat	either density or ecdf

See Also

Other stats: INTERNAL_FUNCTIONS_BY_FAMILY, compute_pooled(), lfq_power_t_test_proteins(), lfq_power_t_test_quantiles_V2(), plot_stat_density_median(), plot_stat_violin(), plot_stat_violin_m
plot_stdv_vs_mean(), summarize_stats()

Examples

```
bb1 <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(bb1$data, bb1$config)
res <- lfq$get_Stats()$stats()
plot_stat_density(res, lfq$factor_keys()[1], stat = "meanAbundance")
plot_stat_density(res, lfq$factor_keys()[1], stat = "sd")
plot_stat_density(res, lfq$factor_keys()[1], stat = "CV")
```

plot_stat_density_median

plot density distribution or ecdf of sd, mean or cv given intensity below and above median

Description

plot density distribution or ecdf of sd, mean or cv given intensity below and above median

Usage

```
plot_stat_density_median(
  pdata,
  factor_key,
  stat = c("CV", "meanAbundance", "sd"),
  ggstat = c("density", "ecdf")
)
```

Arguments

pdata	data.frame with statistics
factor_key	character — factor column name for faceting
stat	sd, mean or CV
ggstat	either density or ecdf

See Also

Other stats: INTERNAL_FUNCTIONS_BY_FAMILY, compute_pooled(), lfq_power_t_test_proteins(), lfq_power_t_test_quantiles_V2(), plot_stat_density(), plot_stat_violin(), plot_stat_violin_median() plot_stdv_vs_mean(), summarize_stats()

Examples

```
bb1 <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(bb1$data, bb1$config)
res <- lfq$get_Stats()$stats()
plot_stat_density_median(res, lfq$factor_keys()[1], "CV")
plot_stat_density_median(res, lfq$factor_keys()[1], "meanAbundance")
plot_stat_density_median(res, lfq$factor_keys()[1], "sd")
```

plot_stat_violin

plot Violin plot of sd CV or mean

Description

plot Violin plot of sd CV or mean

Usage

```
plot_stat_violin(
  pdata,
  factor_keys_depth,
  stat = c("CV", "meanAbundance", "sd")
)
```

Arguments

pdata	data.frame with statistics
factor_keys_depth	character vector — factor columns for grouping
stat	either CV, mean or sd

See Also

Other stats: INTERNAL_FUNCTIONS_BY_FAMILY, compute_pooled(), lfq_power_t_test_proteins(), lfq_power_t_test_quantiles_V2(), plot_stat_density(), plot_stat_density_median(), plot_stat_violin_median(), plot_stdv_vs_mean(), summarize_stats()

Examples

```
bb1 <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(bb1$data, bb1$config)
res <- lfq$get_Stats()$stats()
plot_stat_violin(res, lfq$relevant_factor_keys(), stat = "meanAbundance")
plot_stat_violin(res, lfq$relevant_factor_keys(), stat = "sd")
plot_stat_violin(res, lfq$relevant_factor_keys(), stat = "CV")
```

---

plot_stat_violin_median

plot Violin plot of sd CV or mean given intensity lower or above median

---

Description

plot Violin plot of sd CV or mean given intensity lower or above median

Usage

```
plot_stat_violin_median(
  pdata,
  factor_key,
  stat = c("CV", "meanAbundance", "sd")
)
```

Arguments

pdata	data.frame with statistics
factor_key	character — factor column name for x-axis
stat	either CV, mean or sd

See Also

Other stats: INTERNAL_FUNCTIONS_BY_FAMILY, compute_pooled(), lfq_power_t_test_proteins(), lfq_power_t_test_quantiles_V2(), plot_stat_density(), plot_stat_density_median(), plot_stat_violin(), plot_stdv_vs_mean(), summarize_stats()

Examples

```
bb1 <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(bb1$data, bb1$config)
res <- lfq$get_Stats()$stats()
plot_stat_violin_median(res, lfq$factor_keys()[1], stat = "meanAbundance")
```

---

plot_stdv_vs_mean *plot stddev vs mean to asses stability of variance*

Description

plot stddev vs mean to asses stability of variance

Usage

```
plot_stdv_vs_mean(pdata, factor_keys_depth, size = 2000)
```

Arguments

pdata	data.frame with statistics
factor_keys_depth	character vector — factor columns for faceting
size	how many points to sample (since scatter plot to slow for all)

See Also

Other stats: INTERNAL_FUNCTIONS_BY_FAMILY, compute_pooled(), lfq_power_t_test_proteins(), lfq_power_t_test_quantiles_V2(), plot_stat_density(), plot_stat_density_median(), plot_stat_violin(), plot_stat_violin_median(), summarize_stats()

Examples

```
bb1 <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(bb1$data, bb1$config)
res <- lfq$get_Stats()$stats()
plot_stdv_vs_mean(res, lfq$relevant_factor_keys())
```

prolfqua_data *load data from prolfqua*

Description

load data from prolfqua

Usage

```
prolfqua_data(datastr, package = "prolfqua")
```

Arguments

datastr	name of dataset
package	default prolfqua

Value

The computed result.

See Also

Other data: PACKAGE_DATA, data_checksummarizationrobust87, data_checksummarizerobust69, data_ionstar, x5463yzwer453bbb

Examples

```
ionstar <- prolfqua_data("data_ionstar")
names(ionstar)
```

R6_extract_values *Extract all value slots in an R6 object*

Description

Extract all value slots in an R6 object

Usage

```
R6_extract_values(r6class)
```

Arguments

r6class	r6 class

Value

The computed result.

See Also

Other configuration: AnalysisConfiguration, ContrastConfiguration, INTERNAL_FUNCTIONS_BY_FAMILY, complete_cases(), list_to_ContrastConfiguration(), make_interaction_column(), make_reduced_hierarch sample_subset(), separate_hierarchy(), setup_analysis(), table_factors(), table_factors_size()

Examples

```
bb <- sim_lfq_data_peptide_config()
values <- R6_extract_values(bb$config)
names(values)
```

---

rank_peptide_by_intensity

ranks precursor - peptide by intensity.

Description

ranks precursor - peptide by intensity.

Usage

```
rank_peptide_by_intensity(pdata, response, hierarchy_keys)
```

Arguments

pdata	data.frame
response	character — intensity column name
hierarchy_keys	character vector — all hierarchy column names

Value

data.frame

Examples

```
bb <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(bb$data, bb$config)
res <- rank_peptide_by_intensity(lfq$data_long(), lfq$response(), lfq$hierarchy_keys())
X <- res |> dplyr::select(c(lfq$hierarchy_keys(),
 srm_meanInt, srm_meanIntRank)) |> dplyr::distinct()
X |> dplyr::arrange(!!!rlang::syms(c(lfq$hierarchy_keys()[1], "srm_meanIntRank")))
```

register_facade *Register a contrast facade class*

Description

Adds an entry to the prolfqua facade registry so that lookup_facade (and downstream consumers such as prolfquapp::R6_DEAnalyse$build_facade()) can resolve it by short name. Intended for downstream packages that ship additional modelling backends (e.g. prolfquasaint) and want to plug into the same dispatch path as the built-in facades.

Usage

```
register_facade(
  name,
  class,
  needs,
  package = "prolfqua",
  needs_saint_annotation = FALSE,
  ...
)
```

Arguments

name	short method name, e.g. "saint".
class	character; R6 facade class name to instantiate.
needs	one of "same" (facade emits contrasts at the same hierarchy level as its input *e.g.* protein -> protein FC, peptide -> peptide FC) or "nested" (facade takes child-level input and emits parent-level contrasts, *e.g.* peptide -> protein FC).
package	package the facade class lives in. Defaults to "prolfqua".
needs_saint_annotation	TRUE if the backend requires annotation reading in SAINT mode (bait / control columns). Default FALSE.
...	additional fields stored on the registry entry, available to consumers via lookup_facade.

Value

The registered entry (invisibly).

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(),

build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
lookup_facade("lm")$class
# downstream packages call this from .onLoad():
# prolfqua::register_facade("saint", class = "ContrastsSAINTFacade",
#                           needs = "same", package = "prolfquasaint",
#                           needs_saint_annotation = TRUE)
```

`response_matrix_as_tibble` *Takes matrix of responses and converts into tibble*

Description

Takes matrix of responses and converts into tibble

Usage

```
response_matrix_as_tibble(pdata, value, config, data = NULL, sep = "~lfq~")
```

Arguments

pdata	matrix with rownames encoding hierarchy keys
value	name of column to store values in
config	AnalysisConfiguration (needed for column name mapping)
data	optional data.frame to join back to
sep	separator used to unite the hierarchy keys

Examples

```
dd <- prolfqua::sim_lfq_data_peptide_config()
lfqdata <- prolfqua::LFQData$new(dd$data, dd$config)
res <- tidy_to_wide_config(lfqdata, as.matrix = TRUE)

res_scaled <- scale(res$data)
xx <- response_matrix_as_tibble(
  res_scaled, "srm_intensityScaled", lfqdata$get_config()
)
xx <- response_matrix_as_tibble(
  res_scaled, "srm_intensityScaled",
  lfqdata$get_config(), lfqdata$data_long()
```

)

---

robust_scale *robust scale wrapper*

Description

robust scale wrapper

Usage

```
robust_scale(data, dim = 2, preserve_mean = FALSE)
```

See Also

Other preprocessing: INTERNAL_FUNCTIONS_BY_FAMILY, apply_to_response_matrix(), filter_proteins_by_pept
get_robscales(), nr_B_in_A(), scale_with_subset()

Examples

```
mat <- matrix(c(1, 2, 3, 4, 10, 12), nrow = 3)
scaled <- robust_scale(mat)
dim(scaled)
```

---

sample_subset *Sample subset of proteins/peptides/precursors*

Description

Sample subset of proteins/peptides/precursors

Usage

```
sample_subset(size, pdata, hierarchy_keys_depth)
```

Arguments

size	size of sample
pdata	tidy table
hierarchy_keys_depth	character vector — hierarchy columns at current depth

See Also

Other configuration: AnalysisConfiguration, ContrastConfiguration, INTERNAL_FUNCTIONS_BY_FAMILY,
R6_extract_values(), complete_cases(), list_to_ContrastConfiguration(), make_interaction_column(),
make_reduced_hierarchy_config(), separate_hierarchy(), setup_analysis(), table_factors(),
table_factors_size()

Examples

```
bb <- sim_lfq_data_peptide_config(Nprot = 5)
subset <- sample_subset(2, bb$data, bb$config$hierarchy_keys_depth())
length(unique(subset[[bb$config$hierarchy_keys_depth()[1]]]))
```

`scale_with_subset` *Scale data using a subset of the data*

Description

this should reduce the overall variance.

Usage

```
scale_with_subset(lfqdata, lfqsubset, preserve_mean = FALSE, colname = NULL)
```

Arguments

`lfqdata`	LFQData object with full dataset
`lfqsubset`	LFQData object with subset for computing scales
`preserve_mean`	default FALSE - sets mean to zero
`colname`	name of the scaled intensity column; default NULL uses `<response>_subset_scaled`

Value

list with data, scales, and colname

See Also

Other preprocessing: `INTERNAL_FUNCTIONS_BY_FAMILY`, `apply_to_response_matrix()`, `filter_proteins_by_pept`
`get_robscales()`, `nr_B_in_A()`, `robust_scale()`

Examples

```
bb <- sim_lfq_data_peptide_config(Nprot = 100)
lfqdata <- LFQData$new(bb$data, bb$config)
lfqdata <- lfqdata$get_Transformer()$log2()$lfq
s1 <- get_robscales(lfqdata)
res <- scale_with_subset(lfqdata, lfqdata)
cfg <- lfqdata$get_config()$clone(deep = TRUE)
cfg$set_response(res$colname)
lfqres <- LFQData$new(res$data, cfg)
s2 <- get_robscales(lfqres)
stopifnot(abs(mean(s1$mads) - mean(s2$mads)) < 1e-6)
```

script_copy_helper_vec *copy script files and other from a package to workdir*

Description

copy script files and other from a package to workdir

Usage

```
script_copy_helper_vec(
  runscripts,
  workdir = getwd(),
  packagename = "prolfqua",
  overwrite = TRUE
)
```

Arguments

runscripts	paths of the files relative to the package root (or inst/)
workdir	directory to copy the files to
packagename	package to copy the files from
overwrite	overwrite existing files in workdir, default TRUE

Value

paths of the copied files

Examples

```
copied <- script_copy_helper_vec("CITATION", workdir = tempdir())
basename(copied)
```

separate_hierarchy *Separates hierarchy columns into starting columns*

Description

Separates hierarchy columns into starting columns

Usage

```
separate_hierarchy(data, config)
```

Arguments

data	data.frame
config	AnalysisConfiguration

See Also

Other configuration: AnalysisConfiguration, ContrastConfiguration, INTERNAL_FUNCTIONS_BY_FAMILY, R6_extract_values(), complete_cases(), list_to_ContrastConfiguration(), make_interaction_column(), make_reduced_hierarchy_config(), sample_subset(), setup_analysis(), table_factors(), table_factors_size()

Examples

```
bb <- sim_lfq_data_protein_config()
dt <- separate_hierarchy(bb$data, bb$config)
base::setdiff(colnames(dt) ,colnames(bb$data))
stopifnot(ncol(dt) >= ncol(bb$data))
```

---

setup_analysis *Setup a tidy table compatible with a AnalysisConfiguration*

Description

Extracts columns relevant for a configuration from a data frame and create new columns e.g. sampleName column etc.

Usage

```
setup_analysis(data, configuration, debug = FALSE)
```

Arguments

data	data.frame
configuration	AnalysisConfiguration
debug	if FALSE (default) and any hierarchy-key/sample combination has more than one observation, stop with an informative error. If TRUE, warn and return the diagnostic count table (inspect rows where n > 1) instead.

Value

A tibble with the columns relevant for configuration (sample, hierarchy, factor and response columns). Stops if any hierarchy-key/sample combination is observed more than once (unless debug = TRUE).

See Also

Other configuration: AnalysisConfiguration, ContrastConfiguration, INTERNAL_FUNCTIONS_BY_FAMILY, R6_extract_values(), complete_cases(), list_to_ContrastConfiguration(), make_interaction_column(), make_reduced_hierarchy_config(), sample_subset(), separate_hierarchy(), table_factors(), table_factors_size()

Examples

```
# Example with a normValue column (e.g., creatinine)
set.seed(1234)
data <- sim_lfq_data(Nprot = 10, PEPTIDE = TRUE, N = 4)
data$nr_children <- 1
data$isotopeLabel <- "light"
data$qValue <- 0

# Add creatinine values per sample (not per protein/peptide)
sample_creatinine <- data |> dplyr::select(sample) |> dplyr::distinct() |>
  dplyr::mutate(creatinine = rnorm(dplyr::n(), mean = 100, sd = 10))
data <- dplyr::inner_join(data, sample_creatinine, by = "sample")

config <- AnalysisConfiguration$new()
config$file_name = "sample"
config$factors["group_"] = "group"
config$hierarchy[["protein_Id"]] = c("proteinID", "idtype2")
config$hierarchy[["peptide_Id"]] = "peptideID"
config$set_response("abundance")
config$norm_value = "creatinine"

adata <- setup_analysis(data, config)
```

---

sigma.rfit_prolfqua *Scale estimate for an augmented rfit fit*

Description

Returns the rank-based scale ‘tauhat‘. This stands in for the residual standard deviation of an ‘lm‘; it does not affect the Wald std.error or p-value (those come from ‘vcov()‘), but it is reported and used as the per- protein variance estimate if results are passed to limma/eBayes moderation.

Usage

```
## S3 method for class 'rfit_prolfqua'
sigma(object, ...)
```

Arguments

`object`	an ‘rfit_prolfqua‘ fit
`...`	ignored

Value

the rank-based scale estimate ‘tauhat‘.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste

ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
fit <- strategy_rfit("Sepal.Length ~ Species")$model_fun(iris)
sigma(fit)
```

---

sigma.rlm *Residual scale estimate for rlm objects*

Description

`stats::sigma` returns `NA` for `rlm` objects. This S3 method computes a weighted residual scale estimate instead.

Usage

```
## S3 method for class 'rlm'
sigma(object, ...)
```

Arguments

`object`	an `rlm` object
`...`	ignored

Value

numeric scalar

`sim_build_models_lm` *build dataframe with models for testing*

Description

build dataframe with models for testing

Usage

```
sim_build_models_lm(
  model = c("parallel2", "parallel3", "factors", "interaction"),
  Nprot = 10,
  with_missing = TRUE,
  weight_missing = 1
)
```

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
modi <- sim_build_models_lm(model = "interaction", weight_missing = 1)
stopifnot(dim(modi$model_df) == c(10,9))
mod2 <- sim_build_models_lm(model = "parallel2", weight_missing = 1)
mod2$model_df$linear_model[[1]]
mod3 <- sim_build_models_lm(model = "parallel3", weight_missing = 1)
modf <- sim_build_models_lm(model = "factors", weight_missing = 1)
```

`sim_build_models_lmer` *build lmer model from simulated data*

Description

build lmer model from simulated data

Usage

```
sim_build_models_lmer(
  model = c("parallel2", "parallel3", "factors", "interaction"),
  Nprot = 10,
  with_missing = TRUE,
  weight_missing = 1
)
```

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
modi <- sim_build_models_lmer(model = "interaction", weight_missing = 1)
stopifnot(sum(modi$model_df$has_model_fit) == 6)
mod2 <- sim_build_models_lmer(model = "parallel2", weight_missing = 1)
stopifnot(sum(mod2$model_df$has_model_fit) == 6)
mod4 <- sim_build_models_lmer(model = "parallel3", weight_missing = 1)
stopifnot(sum(mod4$model_df$has_model_fit) == 6)
modf <- sim_build_models_lmer(model = "factors", weight_missing = 1)
stopifnot(sum(modf$model_df$has_model_fit) == 6)
```

sim_build_models_logistf *build dataframe with models for testing*

Description

build dataframe with models for testing

Usage

```
sim_build_models_logistf(
  model = c("parallel2", "parallel3", "factors", "interaction"),
  Nprot = 10,
  with_missing = TRUE,
  weight_missing = 1,
  peptide = FALSE
)
```

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
modi <- sim_build_models_logistf(model = "interaction", weight_missing = 1)
stopifnot(dim(modi$model_df) == c(10,9))
mod2 <- sim_build_models_logistf(model = "parallel2", weight_missing = 1)
mod2$model_df$linear_model[[1]]
mod3 <- sim_build_models_logistf(model = "parallel3", weight_missing = 1)
modf <- sim_build_models_logistf(model = "factors", weight_missing = 1)

mod3 <- sim_build_models_logistf(model = "parallel3", weight_missing = 1, peptide=TRUE)
modf <- sim_build_models_logistf(model = "factors", weight_missing = 1, peptide=TRUE)
```

`sim_lfq_data` *simulate protein level data with two groups*

Description

simulate protein level data with two groups

Usage

```
sim_lfq_data(
  Nprot = 20,
  N = 4,
  fc = list(A = c(D = -2, U = 2, N = 0), B = c(D = 1, U = -4)),
  prop = list(A = c(D = 10, U = 10), B = c(D = 5, U = 20)),
  mean_prot = 20,
  sdlog = log(1.2),
  probability_of_success = 0.3,
  PEPTIDE = FALSE
)
```

Arguments

`Nprot`	number of proteins
`N`	group size
`fc`	D - down regulation N - matrix, U - regulation
`prop`	proportion of down (D), up (U) and not regulated (N)
`mean_prot`	mean protein abundance on the natural scale
`sdlog`	standard deviation of the log-normal abundance distribution
`probability_of_success`	probability of success for the geometric distribution of peptide counts
`PEPTIDE`	if TRUE, simulate peptide-level data; if FALSE, protein-level

Value

A data frame containing simulated LFQ data.

Examples

```
res <- sim_lfq_data(Nprot = 10)
res <- sim_lfq_data(Nprot = 10, PEPTIDE = TRUE)
res <- sim_lfq_data(Nprot = 10, N=4)
```

`sim_lfq_data_2factor_config` *Simulate data, protein, with config with 2 factors Treatment and Background*

Description

Simulate data, protein, with config with 2 factors Treatment and Background

Usage

```
sim_lfq_data_2factor_config(
  Nprot = 10,
  with_missing = TRUE,
  weight_missing = 0.2,
  PEPTIDE = FALSE,
  seed = 1234,
  TWO = TRUE
)
```

Arguments

`Nprot`	number of proteins to simulate
`with_missing`	add missing values, default TRUE
`weight_missing`	controls proportion of missing values; greater weight means more missingness
`PEPTIDE`	if TRUE, simulate peptide-level data; if FALSE, protein-level
`seed`	seed for reproducibility, if NULL no seed is set.
`TWO`	use two factors for modelling

Value

A list containing simulated data and an analysis configuration.

Examples

```
x <- sim_lfq_data_2factor_config(PEPTIDE= FALSE)
dim(x$data)
stopifnot("data.frame" %in% class(x$data))
stopifnot("AnalysisConfiguration" %in% class(x$config))
x <- sim_lfq_data_2factor_config(PEPTIDE = TRUE)

head(x$data)
x <- sim_lfq_data_2factor_config(PEPTIDE = TRUE, TWO = TRUE)
names(x)
nrow(x$data) > 10
x$data$Treatment |> table()
```

sim_lfq_data_peptide_config

Simulate data, protein and peptide, with config

Description

Simulate data, protein and peptide, with config

Usage

```
sim_lfq_data_peptide_config(
  Nprot = 10,
  with_missing = TRUE,
  weight_missing = 0.2,
  seed = 1234,
  N = 4
)
```

Arguments

Nprot	number of proteins to simulate
with_missing	add missing values, default TRUE
weight_missing	controls proportion of missing values; greater weight means more missingness
seed	seed for reproducibility, if NULL no seed is set.
N	number of replicates per group

Value

A list containing simulated data and an analysis configuration.

Examples

```
x <- sim_lfq_data_peptide_config()
stopifnot("data.frame" %in% class(x$data))
stopifnot("AnalysisConfiguration" %in% class(x$config))
```

sim_lfq_data_protein_config

Simulate data, protein, with config

Description

Simulate data, protein, with config

Usage

```
sim_lfq_data_protein_config(
  Nprot = 10,
  with_missing = TRUE,
  weight_missing = 0.2,
  seed = 1234,
  paired = FALSE
)
```

Arguments

Nprot	number of proteins to simulate
with_missing	add missing values, default TRUE
weight_missing	controls proportion of missing values; greater weight means more missingness
seed	seed for reproducibility, if NULL no seed is set.
paired	if TRUE, add a paired subject factor to the design

Value

A list containing simulated data and an analysis configuration.

Examples

```
x <- sim_lfq_data_protein_config()
stopifnot("data.frame" %in% class(x$data))
stopifnot("AnalysisConfiguration" %in% class(x$config))
x <- sim_lfq_data_protein_config(with_missing = FALSE)

stopifnot(sum(is.na(x$data$abundance)) == 0)
xp <- sim_lfq_data_protein_config(with_missing = FALSE, paired = TRUE)
stopifnot(length(xp$config$factors) == 2)
stopifnot(nrow(xp$data) == nrow(x$data))
```

---

sim_make_model_lm *make interaction model for examples*

Description

make interaction model for examples

Usage

```
sim_make_model_lm(
  model = c("parallel2", "parallel3", "factors", "interaction")
)
```

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
m <- sim_make_model_lm()
mi <- sim_make_model_lm("interaction")
stopifnot(length(coefficients(summary(mi))[,"Estimate"]) == 4)
mf <- sim_make_model_lmer("factors")
m2 <- sim_make_model_lmer("parallel2")
m3 <- sim_make_model_lmer("parallel3")
```

---

sim_make_model_lmer *make interaction model for examples*

Description

make interaction model for examples

Usage

```
sim_make_model_lmer(
  model = c("parallel2", "parallel3", "factors", "interaction")
)
```

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter,

ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
mf <- sim_make_model_lmer("factors")
mi <- sim_make_model_lmer("interaction")
```

`StrategyBase` *Base class for per-subject model strategies*

Description

Base class for per-subject model strategies

Base class for per-subject model strategies

Details

Holds the fields, constructor and default methods shared by `StrategyLM`, `StrategyRLM`, `StrategyLmer`, `StrategyRfit`, `StrategyLogistf` and `StrategyBinomial`. A subclass implements the private `fit(x)` method and overrides only the methods that differ.

Value

An R6 class generator.

Public fields

`formula` model formula

`model_name` name of model

`anova_df` ANOVA extractor, see `AnovaExtractor`

Methods

Public methods:

- StrategyBase$new()
- StrategyBase$model_fun()
- StrategyBase$isSingular()
- StrategyBase$contrast_fun()
- StrategyBase$df_residual()
- StrategyBase$sigma()
- StrategyBase$clone()

Method `new()`**:** Create a new strategy

Usage:

```
StrategyBase$new(modelstr, model_name = "Model")
```

Arguments:

`modelstr` model formula string

`model_name` name of model

Method `model_fun()`**:** Fit the model to one subject's data. A failed fit returns the error message.

Usage:

```
StrategyBase$model_fun(x, pb)
```

Arguments:

`x` data.frame for one subject

`pb` optional progress bar

Method `isSingular()`**:** Check if model is singular (NA coefficients or df < 2)

Usage:

```
StrategyBase$isSingular(model)
```

Arguments:

`model` fitted model

Method `contrast_fun()`**:** Compute contrasts from fitted model

Usage:

```
StrategyBase$contrast_fun(...)
```

Arguments:

`...` passed to compute_contrast

Method `df_residual()`**:** Get residual degrees of freedom

Usage:

```
StrategyBase$df_residual(model)
```

Arguments:

`model` fitted model

Method `sigma()`**:** Get residual standard error

Usage:

```
StrategyBase$sigma(model)
```

Arguments:

`model` fitted model

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
StrategyBase$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

`StrategyBinomial` *Quasibinomial detection-count strategy*

Description

Quasibinomial detection-count strategy

Quasibinomial detection-count strategy

Details

Fits detected and undetected child-feature counts for each parent feature using `glm` with a quasi-binomial family. The symmetric pseudo-count stabilizes fits under complete separation; it is not equivalent to Firth's bias-reducing penalty.

Value

An R6 class generator.

Super class

`prolfqua::StrategyBase` -> `StrategyBinomial`

Public fields

`prior_count` symmetric pseudo-count added to both outcomes

Methods

Public methods:

- `StrategyBinomial$new()`
- `StrategyBinomial$clone()`

Method `new()`**:** Create a quasibinomial count strategy. `sigma()` is the Pearson residual scale used by `vcov()`.

Usage:

```
StrategyBinomial$new(
  modelstr,
  prior_count = 0.1,
  model_name = "binomial_nested"
)
```

Arguments:

`modelstr` right-hand-side model formula, for example `"~ group_"`

`prior_count` non-negative symmetric pseudo-count

`model_name` model identity

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
StrategyBinomial$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
dat <- data.frame(
  group_ = factor(rep(c("A", "B"), each = 4)),
  detected = c(1, 2, 1, 3, 4, 5, 3, 5),
  undetected = c(4, 3, 4, 2, 1, 0, 2, 0)
)
strategy <- StrategyBinomial$new("~ group_")
fit <- strategy$model_fun(dat)
coefficients(fit)
```

`StrategyLimma` *R6 class for limma modelling strategy*

Description

R6 class for limma modelling strategy

R6 class for limma modelling strategy

Details

Analogous to `strategy_lm` but for limma's matrix-based pipeline. Consumed by `build_model_limma`.

Value

An R6 class generator.

Public fields

`formula` model formula

`model_name` name of model

`trend` logical, passed to `eBayes`

`robust` logical, passed to `eBayes`

`weights` either a character string (column name) or a numeric matrix

Methods

Public methods:

- StrategyLimma$new()
- StrategyLimma$clone()

Method `new()`**:** Create a new StrategyLimma

Usage:

```
StrategyLimma$new(
  modelstr,
  model_name = "limma",
  trend = FALSE,
  robust = FALSE,
  weights = NULL
)
```

Arguments:

`modelstr`, `model_name`, `trend`, `robust`, `weights` see strategy_limma

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
StrategyLimma$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
strat <- StrategyLimma$new("abundance ~ group_")
strat$formula
strat$model_name
```

`StrategyLimpa` *R6 class for limpa modelling strategy*

Description

R6 class for limpa modelling strategy

R6 class for limpa modelling strategy

Details

Consumed by `build_model_limpa`. Configures the `limpa::voomaLmFitWithImputation` call: formula for the design matrix, trend/robust flags for `eBayes`, and optional vooma plotting parameters.

Value

An R6 class generator.

Public fields

`formula` model formula

`model_name` name of model

`trend` logical, passed to `eBayes`

`robust` logical, passed to `eBayes`

`plot` logical, plot the vooma mean-variance trend

`span` lowess smoother span for vooma trend (NULL = auto)

Methods

Public methods:

- `StrategyLimpa$new()`
- `StrategyLimpa$clone()`

Method `new()`**:** Create a new StrategyLimpa

Usage:

```
StrategyLimpa$new(
  modelstr,
  model_name = "limpa",
  trend = FALSE,
  robust = FALSE,
  plot = FALSE,
  span = NULL
)
```

Arguments:

`modelstr`, `model_name`, `trend`, `robust`, `plot`, `span` see `strategy_limpa`

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
StrategyLimpa$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
strat <- StrategyLimpa$new("abundance ~ group_")
strat$formula
strat$model_name
```

StrategyLM *Linear model strategy (R6 class)*

Description

Linear model strategy (R6 class)

Linear model strategy (R6 class)

Details

Encapsulates everything needed to fit per-protein linear models and extract contrasts: the formula, model fitting function, singularity check, contrast computation, ANOVA, and residual statistics.

Value

An R6 class generator.

Super class

prolfqua::StrategyBase -> StrategyLM

Public fields

`weights` optional character string naming a column in the data containing per-observation weights, passed to `lm`.

Methods

Public methods:

- `StrategyLM$new()`
- `StrategyLM$clone()`

Method `new()`**:** Create a new StrategyLM

Usage:

```
StrategyLM$new(modelstr, model_name = "Model", weights = NULL)
```

Arguments:

`modelstr` model formula string

`model_name` name of model

`weights` optional character string naming a column in the data containing per-observation weights

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
StrategyLM$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu` `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste` `ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRLM`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf` `compute_borrowed_variance()`, `compute_borrowed_variance_limma()`, `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_res` `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()` `new_imputed_model()`, `pivot_model_contrasts_to_wide()`, `register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median` `vcov.rfit_prolfqua()`

Examples

```
strat <- StrategyLM$new("Intensity ~ condition", model_name = "parallel design")
strat$formula
strat$weights
```

`StrategyLmer` *Linear mixed-effects model strategy (R6 class)*

Description

Linear mixed-effects model strategy (R6 class)

Linear mixed-effects model strategy (R6 class)

Details

Encapsulates everything needed to fit per-protein linear mixed-effects models via `lmer` and extract contrasts.

Value

An R6 class generator.

Super class

`prolfqua::StrategyBase` -> `StrategyLmer`

Methods

Public methods:

- `StrategyLmer$isSingular()`
- `StrategyLmer$contrast_fun()`
- `StrategyLmer$clone()`

Method `isSingular()`**:** Check if model is singular

Usage:

```
StrategyLmer$isSingular(model)
```

Arguments:

`model` fitted model

Method `contrast_fun()`**:** Compute contrasts from fitted model

Usage:

```
StrategyLmer$contrast_fun(...)
```

Arguments:

`...` passed to `compute_lmer_contrast`

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
StrategyLmer$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
istar <- prolfqua::sim_lfq_data_peptide_config(Nprot = 10, with_missing = FALSE)
istar <- prolfqua::LFQData$new(istar$data, istar$config)
istar$set_data(istar$data_long() |> dplyr::group_by(protein_Id) |>
  dplyr::mutate(abundanceC = abundance - mean(abundance)) |> dplyr::ungroup())
strat <- StrategyLmer$new("abundanceC ~ group_ + (1|peptide_Id)",
  model_name = "random_example")
mod <- build_model(istar, strat)
sum(mod$model_df$has_model_fit)
```

StrategyLogistf *Firth's logistic regression strategy (R6 class)*

Description

Firth's logistic regression strategy (R6 class)

Firth's logistic regression strategy (R6 class)

Details

Encapsulates everything needed to fit per-protein Firth's bias-reduced logistic regression via logistf and extract contrasts.

Value

An R6 class generator.

Super class

prolfqua::StrategyBase -> StrategyLogistf

Methods

Public methods:

- StrategyLogistf$new()
- StrategyLogistf$df_residual()
- StrategyLogistf$sigma()
- StrategyLogistf$clone()

Method `new()`**:** Create a new StrategyLogistf

Usage:

```
StrategyLogistf$new(modelstr, model_name = "logistf")
```

Arguments:

`modelstr` model formula string

`model_name` name of model

Method `df_residual()`**:** Get residual degrees of freedom

Usage:

```
StrategyLogistf$df_residual(model)
```

Arguments:

`model` fitted model

Method `sigma()`**:** Get residual standard error (always 1 for logistic)

Usage:

```
StrategyLogistf$sigma(model)
```

Arguments:

`model` fitted model

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
StrategyLogistf$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(),

build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf
compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(),
compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(),
get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(),
linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res
model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma()
new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(),
sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(),
sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median
vcov.rfit_prolfqua()

Examples

```
strat <- StrategyLogistf$new("bin_resp ~ condition")
strat$formula
```

StrategyRfit *Rank-based regression strategy (R6 class)*

Description

Rank-based regression strategy (R6 class)

Rank-based regression strategy (R6 class)

Details

Encapsulates everything needed to fit per-protein rank-based linear models via `rfit` and extract Wald contrasts. The fit is augmented (model frame, terms, `rfit_prolfqua` subclass) so it satisfies the same `coef()` / `vcov()` / `terms()` contract as `lm`.

Unlike `StrategyLM`, `rfit` takes no observation weights, so `nr_children` weighting is not supported by this backend.

Value

An R6 class generator.

Super class

`prolfqua::StrategyBase` -> `StrategyRfit`

Methods

Public methods:

- `StrategyRfit$new()`
- `StrategyRfit$clone()`

Method `new()`**:** Create a new StrategyRfit. Residual df and scale come from `df.residual()` and `sigma()` of the augmented fit.

Usage:

```
StrategyRfit$new(modelstr, model_name = "rfit")
```

Arguments:

`modelstr` model formula string

`model_name` name of model

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
StrategyRfit$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf compute_borrowed_variance(), compute_borrowed_variance_limma(), compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_res model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma() new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median vcov.rfit_prolfqua()

Examples

```
strat <- StrategyRfit$new("Intensity ~ condition", model_name = "parallel design")
strat$formula
```

StrategyRLM *Robust linear model strategy (R6 class)*

Description

Robust linear model strategy (R6 class)

Robust linear model strategy (R6 class)

Details

Encapsulates everything needed to fit per-protein robust linear models via `rlm` and extract contrasts.

Value

An R6 class generator.

Super class

`prolfqua::StrategyBase` -> `StrategyRLM`

Methods

Public methods:

- `StrategyRLM$sigma()`
- `StrategyRLM$clone()`

Method `sigma()`**:** Get the robust scale estimate used by `vcov()`
Returns `model$s`, the robust scale `MASS::rlm` builds its `vcov()` / `summary()` standard errors from. This must match the scale embedded in `vcov()` so that `ContrastsModerated`'s `sigma / sqrt(var.post)` rescaling stays coherent; `stats::sigma()` returns the ordinary-residual scale instead and would distort moderated `rlm` statistics.

Usage:

```
StrategyRLM$sigma(model)
```

Arguments:

`model` fitted model

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
StrategyRLM$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu` `ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste` `ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`, `StrategyLogistf`, `StrategyRfit`, `build_contrast_analysis()`, `build_model()`, `build_model_glm_peptide()`, `build_model_glm_protein()`, `build_model_impute()`, `build_model_limma()`, `build_model_limma_impute()`, `build_model_limma_voom()`, `build_model_limma_voom_impute()`, `build_model_limpa()`, `build_model_logistf` `compute_borrowed_variance()`, `compute_borrowed_variance_limma()`, `compute_contrast()`, `compute_lmer_contrast()`, `df.residual.rfit_prolfqua()`, `get_anova_df()`, `get_complete_model_fit()`, `get_p_values_pbeta()`, `group_label()`, `impute_from_model()`, `impute_refit_singular()`, `linfct_from_model()`, `linfct_matrix_contrasts()`, `list_facades()`, `lookup_facade()`, `merge_contrasts_res` `model_analyse()`, `model_summary()`, `moderated_p_deqms()`, `moderated_p_deqms_long()`, `moderated_p_limma()` `new_imputed_model()`, `pivot_model_contrasts_to_wide()`, `register_facade()`, `sigma.rfit_prolfqua()`, `sim_build_models_lm()`, `sim_build_models_lmer()`, `sim_build_models_logistf()`, `sim_make_model_lm()`, `sim_make_model_lmer()`, `strategy_limma()`, `strategy_limpa()`, `strategy_logistf()`, `summary_ROPECA_median` `vcov.rfit_prolfqua()`

Examples

```
strat <- StrategyRLM$new("Intensity ~ condition", model_name = "parallel design")
strat$formula
```

`strategy_binomial` *Create a quasibinomial detection-count strategy*

Description

Create a quasibinomial detection-count strategy

Usage

```
strategy_binomial(modelstr, prior_count = 0.1, model_name = "binomial_nested")
```

Arguments

`modelstr`	right-hand-side model formula
`prior_count`	non-negative symmetric pseudo-count
`model_name`	model identity

Value

A `StrategyBinomial` object.

Examples

```
strategy <- strategy_binomial("~ group_", prior_count = 0.1)
strategy$formula
```

`strategy_limma` *Create limma modelling strategy*

Description

Wrapper that returns a `StrategyLimma` R6 object.

Usage

```
strategy_limma(
  modelstr,
  model_name = "limma",
  trend = FALSE,
  robust = FALSE,
  weights = NULL
)
```

Arguments

modelstr	model formula as string (e.g. "abundance ~ group_")
model_name	name of model
trend	logical, passed to eBayes
robust	logical, passed to eBayes
weights	either a character string (column name in annotation for per-sample weights) or a numeric matrix (proteins x samples) passed to lmFit. Default NULL (no weights).

Value

The computed result.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
strat <- strategy_limma("abundance ~ group_")
strat$formula
strat$model_name
```

---

strategy_limpa *Create limpa modelling strategy*

Description

Wrapper that returns a StrategyLimpa R6 object.

Usage

```
strategy_limpa(
  modelstr,
  model_name = "limpa",
  trend = FALSE,
  robust = FALSE,
  plot = FALSE,
  span = NULL
)
```

Arguments

modelstr	model formula as string (e.g. "abundance ~ group_")
model_name	name of model
trend	logical, passed to eBayes
robust	logical, passed to eBayes
plot	logical, plot the vooma mean-variance trend
span	lowess smoother span (NULL = auto)

Value

The computed result.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_logistf(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
strat <- strategy_limpa("abundance ~ group_")
strat$formula
strat$model_name
```

`strategy_logistf` *Create Firth's logistic regression strategy*

Description

Convenience wrapper that creates a `StrategyLogistf` object.

Convenience wrapper that creates a `StrategyRfit` object.

Convenience wrapper that creates a `StrategyLmer` object.

Convenience wrapper that creates a `StrategyLM` object.

Convenience wrapper that creates a `StrategyRLM` object.

Usage

```
strategy_logistf(modelstr, model_name = "logistf")

strategy_rfit(modelstr, model_name = "rfit")

strategy_lmer(modelstr, model_name = "Model")

strategy_lm(modelstr, model_name = "Model", weights = NULL)

strategy_rlm(modelstr, model_name = "Model")
```

Arguments

`modelstr`	model formula
`model_name`	name of model
`weights`	optional character string naming a column in the data containing per-observation weights, passed to `lm`. Default `NULL` (unweighted).

Value

a `StrategyLogistf` object

a `StrategyRfit` object

a `StrategyLmer` object

a `StrategyLM` object

a `StrategyRLM` object

See Also

Other modelling: `AnovaExtractor`, `Contrasts`, `ContrastsDEqMSFacade`, `ContrastsDEqMSVoomFacade`, `ContrastsFacadeBase`, `ContrastsFirth`, `ContrastsFirthFacade`, `ContrastsFirthNestedFacade`, `ContrastsLMFacade`, `ContrastsLMImputeFacade`, `ContrastsLimma`, `ContrastsLimmaFacade`, `ContrastsLimmaImpu`
`ContrastsLimmaVoomFacade`, `ContrastsLimmaVoomImputeFacade`, `ContrastsLimpaFacade`, `ContrastsLimpaNeste`
`ContrastsLmerNestedFacade`, `ContrastsModerated`, `ContrastsModeratedDEqMS`, `ContrastsPlotter`, `ContrastsRLMFacade`, `ContrastsROPECA`, `ContrastsROPECANestedFacade`, `ContrastsRfitFacade`, `ContrastsRfitImputeFacade`, `ContrastsTable`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `LR_test()`, `Model`, `ModelFirth`, `ModelLimma`, `StrategyLM`, `StrategyLimma`, `StrategyLimpa`, `StrategyLmer`,

StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_, compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu, ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste, ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_, compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu, ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste, ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_, compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide(), register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), summary_ROPECA_median_p_scaled(), vcov.rfit_prolfqua()

Examples

```
tmp <- strategy_logistf("bin_resp ~ condition", model_name = "parallel design")
tmp$formula

istar <- prolfqua::sim_lfq_data_peptide_config(Nprot = 10, with_missing = TRUE,
  weight_missing = 0.5, seed = 3)
istar$data <- encode_bin_resp(LFQData$new(istar$data, istar$config))
istar$config$bin_resp <- "bin_resp"
istar <- LFQData$new(istar$data, istar$config)
df <- istar$summarize_hierarchy()
df2 <- df[df[[ncol(df)]] > 1, ]
```

```
istar2 <- istar$get_subset(df2)
istar2$data_long() |>
  dplyr::group_by(protein_Id) |>
  tidyr::nest() -> nestProtein
modelFunction <- strategy_logistf("bin_resp ~ group_ + peptide_Id",
  model_name = "random_example")
modelFunction$model_fun(nestProtein$data[[1]])
modelFunction$model_fun(nestProtein$data[[4]])
tmp <- strategy_rfit("Intensity ~ condition", model_name = "parallel design")
tmp$formula
modelFunction <- strategy_lmer("abundanceC ~ group_ + (1|peptide_Id)",
  model_name = "random_example")
modelFunction$formula
tmp <- strategy_lm("Intensity ~ condition", model_name = "parallel design")
tmp$formula
tmp$weights
tmp <- strategy_rlm("Intensity ~ condition", model_name = "parallel design")
tmp$formula
```

`summarize_hierarchy` *Summarize hierarchy counts*

Description

E.g compute number of peptides for each protein

Usage

```
summarize_hierarchy(
  pdata,
  hierarchy_keys,
  isotope_label = "isotopeLabel",
  hierarchy = hierarchy_keys,
  factors = character()
)
```

Arguments

`pdata`	data.frame
`hierarchy_keys`	character vector — all hierarchy column names
`isotope_label`	character — isotope label column name
`hierarchy`	character vector — hierarchy level to group by (default hierarchy_keys)
`factors`	character vector — factor columns to include

See Also

Other summary: `HierarchyCountsSample`, `INTERNAL_FUNCTIONS_BY_FAMILY`, `hierarchy_counts()`

Examples

```
bb <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(bb$data, bb$config)
summarize_hierarchy(lfq$data_long(), lfq$hierarchy_keys(), lfq$isotope_label())
summarize_hierarchy(lfq$data_long(), lfq$hierarchy_keys(), lfq$isotope_label(),
 factors = character())
summarize_hierarchy(lfq$data_long(), lfq$hierarchy_keys(), lfq$isotope_label(),
 hierarchy = lfq$relevant_hierarchy_keys())
```

`summarize_stats` *Compute mean, sd, and CV for all Peptides, or proteins, for all interactions and all samples.*

Description

Compute mean, sd, and CV for all Peptides, or proteins, for all interactions and all samples.

summarize stats output (compute quantiles)

Usage

```
summarize_stats(lfqdata, factor_key = lfqdata$relevant_factor_keys())

summarize_stats_quantiles(
  stats_res,
  factor_keys_depth,
  stats = c("sd", "CV"),
  probs = c(0.1, 0.25, 0.5, 0.75, 0.9)
)
```

Arguments

`lfqdata`	LFQData object
`factor_key`	character vector — factor columns to group by (default: relevant_factor_keys)
`stats_res`	result of running ‘summarize_stats‘
`factor_keys_depth`	character vector — factor columns at current depth
`stats`	summarize either sd or CV
`probs`	for which quantiles 10, 20 etc.

See Also

Other stats: `INTERNAL_FUNCTIONS_BY_FAMILY`, `compute_pooled()`, `lfq_power_t_test_proteins()`, `lfq_power_t_test_quantiles_V2()`, `plot_stat_density()`, `plot_stat_density_median()`, `plot_stat_violin()`, `plot_stat_violin_median()`, `plot_stdv_vs_mean()`

Other stats: `INTERNAL_FUNCTIONS_BY_FAMILY`, `compute_pooled()`, `lfq_power_t_test_proteins()`, `lfq_power_t_test_quantiles_V2()`, `plot_stat_density()`, `plot_stat_density_median()`, `plot_stat_violin()`, `plot_stat_violin_median()`, `plot_stdv_vs_mean()`

Examples

```
bb <- prolfqua::sim_lfq_data_protein_config()
lfq <- LFQData$new(bb$data, bb$config)
res1 <- summarize_stats(lfq)

res2 <- prolfqua::sim_lfq_data_2factor_config()
res2$config$factor_depth <- 2
lfq2 <- LFQData$new(res2$data, res2$config)
stats <- summarize_stats(lfq2)
stopifnot(nrow(stats) == 40)

stats <- summarize_stats(lfq2, factor_key = lfq2$factor_keys()[1])
stopifnot(nrow(stats) == 20)
stats <- summarize_stats(lfq2, factor_key = lfq2$factor_keys()[2])
stopifnot(nrow(stats) == 20)
stats <- summarize_stats(lfq2, factor_key = NULL)
stopifnot(nrow(stats) == 10)
library(ggplot2)
bb1 <- prolfqua::sim_lfq_data_peptide_config()
lfq <- LFQData$new(bb1$data, bb1$config)
stats_res <- summarize_stats(lfq)
sq <- summarize_stats_quantiles(stats_res, lfq$relevant_factor_keys())
sq <- summarize_stats_quantiles(stats_res, lfq$relevant_factor_keys(), stats = "CV")
sq <- summarize_stats_quantiles(stats_res, lfq$relevant_factor_keys(), stats = "sd")
xx <- summarize_stats_quantiles(stats_res, lfq$relevant_factor_keys(), probs = seq(0, 1, by = 0.1))
ggplot2::ggplot(xx$long, aes(x = probs, y = quantiles, color = group_)) + geom_line() + geom_point()
```

---

summarize_stats_factors

compute var sd etc for all factor levels

Description

compute var sd etc for all factor levels

Usage

```
summarize_stats_factors(lfqdata)
```

Arguments

lfqdata	LFQData object

Value

The computed result.

Examples

```
res2 <- prolfqua::sim_lfq_data_2factor_config()
res2$config$factor_depth <- 2
lfq2 <- LFQData$new(res2$data, res2$config)
xx <- summarize_stats_factors(lfq2)
stopifnot(nrow(xx) == 80)
stopifnot(length(unique(xx$interaction)) == (2 + 2 + 2 * 2))
```

---

summary_ROPECA_median_p_scaled

compute protein level fold changes and p.values (using beta distribution) takes p-value of the scaled p-value

---

Description

compute protein level fold changes and p.values (using beta distribution) takes p-value of the scaled p-value

Usage

```
summary_ROPECA_median_p_scaled(
  contrasts_data,
  contrast = "contrast",
  subject_id = "protein_Id",
  estimate = "diff",
  statistic = "statistic",
  p.value = "moderated.p.value",
  max.n = 10
)
```

Arguments

contrasts_data	data frame
contrast	name of column with contrast identifier
subject_id	name of column with typically protein Id
estimate	name of column with effect size estimate
statistic	statistic name of column with statistic (typically t-statistics)
p.value	name of column with moderated.p.value
max.n	used to limit the number of peptides in probability computation.

Value

data.frame with columns

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), vcov.rfit_prolfqua()

Examples

```
set.seed(10)
nrPep <- 10000
nrProtein <- 800
p.value <- runif(nrPep)
estimate <- rnorm(nrPep)
avgAbd <- runif(nrPep)
protein_Id <- sample(1:800, size = nrPep,
  replace = TRUE, prob = dexp(seq(0,5,length = 800)))

plot(table(table(protein_Id)))

testdata <- data.frame(contrast = "contrast1",
  protein_Id = protein_Id,
  estimate = estimate,
  pseudo_estimate = estimate,
  p.value = p.value,
  avgAbd = avgAbd )

xx30 <- summary_ROPECA_median_p_scaled(testdata,
                                       subject_id = "protein_Id",
                                       estimate = "estimate",
                                       p.value = "p.value",
                                       max.n = 30)

xx2 <- summary_ROPECA_median_p_scaled(testdata,
                                       subject_id = "protein_Id",
                                       estimate = "estimate",
                                       p.value = "p.value",
                                       max.n = 1)

testthat::expect_equal(mad(xx2$estimate, na.rm = TRUE),0.384409, tolerance = 1e-4)
```

```
testthat::expect_equal(median(xx2$estimate), -0.006874857, tolerance = 1e-4)
testthat::expect_equal(xx2$beta.based.significance[1],0.819, tolerance = 1e-3)
testthat::expect_equal(xx2$beta.based.significance[2],0.9234362,tolerance = 1e-3)

# Uniform distribution
hist(testdata$p.value)
hist(xx30$median.p.scaled, breaks = 20)
hist(xx2$median.p.scaled, breaks = 20)
# shows that beta.based.significance has NO uniform distribution
# although H0 is true for all cases.

hist(xx30$beta.based.significance, breaks = 20)
hist(xx2$beta.based.significance, breaks = 20)

hist(xx2$median.p.value, breaks = 20)
hist(xx2$beta.based.significance, breaks = 20)
hist(estimate)
```

`table_facade` *table facade to easily switch implementations*

Description

table facade to easily switch implementations

Usage

```
table_facade(df, caption, digits = getOption("digits"), kable = TRUE)
```

Arguments

`df`	data.frame to display
`caption`	table caption
`digits`	number of digits (default from options)
`kable`	if TRUE use knitr::kable

Value

The requested plot, table, or transformed object.

See Also

Other utilities: `INTERNAL_FUNCTIONS_BY_FAMILY`, `get_uniprot_id_from_fasta_header()`, `is_contaminant()`, `is_decoy()`, `matrix_to_tibble()`, `multigroup_volcano()`, `pairs_smooth()`, `panel_cor()`

Examples

```
table_facade(head(iris, 3), caption = "Iris preview")
```

table_factors *Table of distinct factors (sample annotation)*

Description

Table of distinct factors (sample annotation)

Usage

```
table_factors(pdata, file_name, sample_name, factor_keys)
```

Arguments

pdata	data.frame
file_name	character — file name column
sample_name	character — sample name column
factor_keys	character vector — factor column names

See Also

Other configuration: AnalysisConfiguration, ContrastConfiguration, INTERNAL_FUNCTIONS_BY_FAMILY, R6_extract_values(), complete_cases(), list_to_ContrastConfiguration(), make_interaction_column(), make_reduced_hierarchy_config(), sample_subset(), separate_hierarchy(), setup_analysis(), table_factors_size()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
xx <- table_factors(lfq$data_long(), lfq$file_name(), lfq$sample_name(), lfq$factor_keys())
xt <- xx |> dplyr::group_by(!!!rlang::syms(lfq$factor_keys())) |>
 dplyr::summarize(n = dplyr::n())
stopifnot(all(xt$n == 4))
```

table_factors_size *Table of distinct factors with group sizes*

Description

Table of distinct factors with group sizes

Usage

```
table_factors_size(
  pdata,
  file_name,
  sample_name,
  factor_keys,
  factor_keys_depth
)
```

Arguments

pdata	data.frame
file_name	character — file name column
sample_name	character — sample name column
factor_keys	character vector — all factor column names
factor_keys_depth	character vector — factor columns at current depth

See Also

Other configuration: AnalysisConfiguration, ContrastConfiguration, INTERNAL_FUNCTIONS_BY_FAMILY, R6_extract_values(), complete_cases(), list_to_ContrastConfiguration(), make_interaction_column(), make_reduced_hierarchy_config(), sample_subset(), separate_hierarchy(), setup_analysis(), table_factors()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
xx <- table_factors_size(lfq$data_long(), lfq$file_name(),
  lfq$sample_name(), lfq$factor_keys(), lfq$relevant_factor_keys())
stopifnot(all(xx$n == 4))
```

---

tidy_to_wide_config *transform long to wide*

Description

transform long to wide

Usage

```
tidy_to_wide_config(
  lfqdata,
  as.matrix = FALSE,
  file_name = FALSE,
  sep = "~lfq~",
  value = lfqdata$response()
)
```

Arguments

lfqdata	LFQData object
as.matrix	if TRUE return matrix, otherwise data.frame
file_name	if TRUE use file_name as column labels, otherwise sample_name
sep	separator for row IDs when as.matrix = TRUE
value	column name to pivot (default: lfqdata$response())

Value

list with data, rowdata, and annotation (colData)

Examples

```
dd <- prolfqua::sim_lfq_data_peptide_config()
lfqdata <- prolfqua::LFQData$new(dd$data, dd$config)
res <- tidy_to_wide_config(lfqdata)
testthat::expect_equal(nrow(res$rowdata), nrow(res$data))
testthat::expect_equal(ncol(res$data) - ncol(res$rowdata) , nrow(res$annotation))
res <- tidy_to_wide_config(lfqdata, as.matrix = TRUE)
stopifnot(all(dim(res$data) == c(28,  12)))
stopifnot(all(dim(res$annotation) == c(12,  4)))
stopifnot(all(dim(res$rowdata) == c(28, 3)))

res <- scale(res$data)
tidy_to_wide_config(lfqdata, value = lfqdata$nr_children_col())

res <- lfqdata$get_Aggregator("medpolish")
x <- res$aggregate()
towide <- tidy_to_wide_config(x, value = x$nr_children_col())

dd <- prolfqua::sim_lfq_data_protein_config()
lfqprot <- prolfqua::LFQData$new(dd$data, dd$config)
xt <- tidy_to_wide_config(lfqprot, value = lfqprot$nr_children_col())
xt$data
```

---

transform_work_intensity

Transform intensity column by applying a function

Description

Transform intensity column by applying a function

Usage

```
transform_work_intensity(pdata, response, .func, .funcname = NULL)
```

Arguments

pdata	data.frame
response	character, name of the response column to transform
.func	function to transform intensities e.g. log2
.funcname	name of function (used for creating new column name)

Value

list with ‘data‘ (data.frame) and ‘colname‘ (new column name)

Examples

```
istar <- sim_lfq_data_peptide_config()
config <- istar$config
res <- transform_work_intensity(
  istar$data, config$get_response(), .func = log2
)
stopifnot("log2_abundance" %in% colnames(res$data))
res <- transform_work_intensity(
  istar$data, config$get_response(), .func = asinh
)
stopifnot("asinh_abundance" %in% colnames(res$data))
```

---

upset_interaction_missing_stats

UpSetR plot from interaction_missing_stats

Description

UpSetR plot from interaction_missing_stats

Usage

```
upset_interaction_missing_stats(lfqdata, tr = 2)
```

Arguments

lfqdata	LFQData object
tr	if less than tr observations in condition then missing

Value

The computed result.

See Also

Other plotting: ContrastsPlotter, INTERNAL_FUNCTIONS_BY_FAMILY, missingness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), plot_estimate(), plot_heatmap(), plot_heatmap_cor(), plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_na_heatmap(), plot_pca(), plot_raster(), plot_sample_correlation(), upset_missing_stats()

Other imputation: get_contrast(), missingness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), upset_missing_stats()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
pups <- upset_interaction_missing_stats(lfq)
stopifnot(ncol(pups$data) == 5)
UpSetR::upset(pups$data, order.by = "freq", nsets = pups$nsets)
```

upset_missing_stats *prepare dataframe for UpSetR plot for all samples*

Description

prepare dataframe for UpSetR plot for all samples

Usage

```
upset_missing_stats(lfqdata)
```

Arguments

lfqdata	LFQData object

See Also

Other plotting: ContrastsPlotter, INTERNAL_FUNCTIONS_BY_FAMILY, missigness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), plot_estimate(), plot_heatmap(), plot_heatmap_cor(), plot_hierarchies_boxplot_df(), plot_hierarchies_line(), plot_intensity_distribution_violin(), plot_na_heatmap(), plot_pca(), plot_raster(), plot_sample_correlation(), upset_interaction_missing_stats()

Other imputation: get_contrast(), missigness_histogram(), missingness_per_condition(), missingness_per_condition_cumsum(), upset_interaction_missing_stats()

Examples

```
istar <- sim_lfq_data_peptide_config()
lfq <- LFQData$new(istar$data, istar$config)
pups <- upset_missing_stats(lfq)
UpSetR::upset(pups$data, order.by = "freq", nsets = pups$nsets)
```

vcov.rfit_prolfqua *Named variance-covariance matrix for an augmented rfit fit*

Description

‘Rfit::vcov.rfit‘ returns an unnamed matrix; ‘compute_contrast()‘ indexes the covariance by coefficient name, so this method restores the dimnames from ‘coef()‘.

Usage

```
## S3 method for class 'rfit_prolfqua'
vcov(object, ...)
```

Arguments

object	an ‘rfit_prolfqua‘ fit
...	passed to the next method

Value

the rfit covariance matrix with row/column names set to the coefficient names.

See Also

Other modelling: AnovaExtractor, Contrasts, ContrastsDEqMSFacade, ContrastsDEqMSVoomFacade, ContrastsFacadeBase, ContrastsFirth, ContrastsFirthFacade, ContrastsFirthNestedFacade, ContrastsLMFacade, ContrastsLMImputeFacade, ContrastsLimma, ContrastsLimmaFacade, ContrastsLimmaImpu ContrastsLimmaVoomFacade, ContrastsLimmaVoomImputeFacade, ContrastsLimpaFacade, ContrastsLimpaNeste ContrastsLmerNestedFacade, ContrastsModerated, ContrastsModeratedDEqMS, ContrastsPlotter, ContrastsRLMFacade, ContrastsROPECA, ContrastsROPECANestedFacade, ContrastsRfitFacade, ContrastsRfitImputeFacade, ContrastsTable, INTERNAL_FUNCTIONS_BY_FAMILY, LR_test(), Model, ModelFirth, ModelLimma, StrategyLM, StrategyLimma, StrategyLimpa, StrategyLmer, StrategyLogistf, StrategyRLM, StrategyRfit, build_contrast_analysis(), build_model(), build_model_glm_peptide(), build_model_glm_protein(), build_model_impute(), build_model_limma(), build_model_limma_impute(), build_model_limma_voom(), build_model_limma_voom_impute(), build_model_limpa(), build_model_logistf(), compute_borrowed_variance(), compute_borrowed_variance_ compute_contrast(), compute_lmer_contrast(), df.residual.rfit_prolfqua(), get_anova_df(), get_complete_model_fit(), get_p_values_pbeta(), group_label(), impute_from_model(), impute_refit_singular(), linfct_from_model(), linfct_matrix_contrasts(), list_facades(), lookup_facade(), merge_contrasts_results(), model_analyse(), model_summary(), moderated_p_deqms(), moderated_p_deqms_long(), moderated_p_limma(), new_imputed_model(), pivot_model_contrasts_to_wide() register_facade(), sigma.rfit_prolfqua(), sim_build_models_lm(), sim_build_models_lmer(), sim_build_models_logistf(), sim_make_model_lm(), sim_make_model_lmer(), strategy_limma(), strategy_limpa(), strategy_logistf(), summary_ROPECA_median_p_scaled()

Examples

```
fit <- strategy_rfit("Sepal.Length ~ Species")$model_fun(iris)
vcov(fit)
```

`volcano_plotly` *volcano plotly*

Description

volcano plotly

Usage

```
volcano_plotly(
  .data,
  effect = "fc",
  significance = "BFDR",
  contrast = "condition",
  proteinID = "Prey",
  color = "modelName",
  palette = NULL,
  xintercept = c(-2, 2),
  yintercept = 0.1,
  minsignificance = NULL,
```

```
  title_size = 25,
  group = "BB"
)
```

Arguments

.data	data frame
effect	effect size x-axis
significance	significance
contrast	column with contrast labels
proteinID	column with protein ids
color	column used for colouring points
palette	named colour vector for the colour aesthetic
xintercept	vertical abline at x
yintercept	horizontal abline at y
minsignificance	optional minimum significance value (floor for -log10 axis). If NULL, only exact zero and negative values are replaced with the smallest positive observed value in the same score column.
title_size	font size of the subplot title annotation
group	crosstalk group name for linked brushing

Value

The requested plot, table, or transformed object.

Examples

```
data <- data.frame(fc = c(-1,0,1,2,8), BFDR = c(0.01,1, 0.01, 0.005,0),
condition = rep("A",5), Prey = LETTERS[1:5], modelName = c("A","A","B","A","A"))

dataB <- data.frame(fc = c(-1,0,1,2,8), BFDR = c(0.01,1, 0.01, 0.005,0),
condition = rep("B",5), Prey = LETTERS[1:5],modelName = c("A","A","B","B","B"))
data <- dplyr::bind_rows(data, dataB)
bc <- volcano_plotly(data, xintercept = 1, yintercept= 0.01, palette = c(A = "black" , B = "red"))
bc |> plotly::subplot()
```

---

which_missing *add missing values to x vector based on the values of x*

Description

add missing values to x vector based on the values of x

Usage

```
which_missing(x, weight_missing = 0.2)
```

Arguments

x	vector of intensities
weight_missing	greater weight more missing

Value

A logical vector indicating which values are missing.

Examples

```
which_missing(2**rnorm(10,2,0.4))
```

---

x5463yzwer453bbb *Factor annotation of 36 samples*

Description

Sample annotation table with two factors (‘factor_A‘: MI / MINOCA, ‘factor_B‘: sampling time T0 / T150 / T300), used to demonstrate how contrasts are derived from the factor levels. See ‘inst/script/README.md‘ for its origin.

Usage

```
x5463yzwer453bbb
```

Format

A tibble with 36 rows and the columns ‘Relative Path‘, ‘Name‘, ‘Group‘, ‘factor_A‘, ‘factor_B‘.

See Also

Other data: PACKAGE_DATA, data_checksummarizationrobust87, data_checksummarizerobust69, data_ionstar, prolfqua_data()

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