Package 'NADIA'

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Type Package

Title Missing Value-Aware Differential Abundance Analysis of DIA Proteomics Data

Version 0.99.3

Description Provides an end-to-end workflow for differential abundance analysis of protein quantification data, with particular attention to missing values in data-independent acquisition (DIA) proteomics. Quantification reports exported from Spectronaut, DIA-NN and Proteome Discoverer for TMT and label-free experiments (DDA/DIA) are converted into a common data structure, normalised, optionally batch-corrected, imputed and analysed using limma or limpa. The package includes individual and two-stage imputation strategies that treat values assumed to be missing at random and missing not at random separately. Data-driven functions evaluate and rank normalisation and imputation workflows using simulated missingness or spike-in datasets with known ground truth, allowing method selection to be justified for each dataset. Results can be explored through interactive Highcharts visualisations, static ggplot2 and ComplexHeatmap figures, and sortable tables.

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Encoding UTF-8

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BugReports https://github.com/sciordia/NADIA/issues

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NADIA-package *NADIA: Missing Value-Aware DIA Proteomics Analysis*

Description

A complete pipeline for differential protein expression analysis, with particular attention to the missing values that characterise data-independent acquisition. It covers the whole journey from the raw report to the interactive figure.

Details

The package is organised in four blocks:

Preprocessing `preprocess_spectronaut()` for Spectronaut, `preprocess_diann()` for DIA-NN protein-group matrices, `preprocess_tmt()` and `preprocess_lfq()` for Proteome Discoverer. All four return the same `proteomics_data` S3 object, so the rest of the pipeline consumes them unchanged.

Processing `process_proteomics()` coordinates normalization (13 methods), optional batch correction, imputation (19 methods, including the MAR/MNAR hybrids) and differential expression with limma or limpa.

Metrics and benchmarking `normalization_metrics()`, `imputation_metrics()`, `benchmarking_proteomics()` and `benchmarking_multiple()` evaluate and rank method combinations.

Visualization interactive plots with Highcharts (`boxplot_highchart_list()`, `volcano_highchart_list()`, `pca_highchart_list()`), static ones with ggplot2 and ComplexHeatmap (`proteomics_heatmap()`), and tables with reactable (`results_list_reactable()`).

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See Also

Useful links:

- https://github.com/sciordia/NADIA
- https://sciordia.github.io/NADIA/
- Report bugs at https://github.com/sciordia/NADIA/issues

.bc_combat_unfittable *Identify features ComBat cannot fit*

Description

Flags rows that, in any batch, have fewer than 2 finite observations or zero within-batch variance. ComBat's parametric empirical-Bayes estimation divides by the within-batch variance, so such features yield NaN and abort the whole correction (`while (change > conv)` receives NA). These features cannot be batch-corrected anyway (constant within a batch) and should pass through unadjusted.

Usage

```
.bc_combat_unfittable(mat, batch_vec)
```

Arguments

`mat`	Numeric matrix (features x samples).
`batch_vec`	Batch assignment per column.

Value

Logical vector (length nrow(mat)); TRUE = unfittable by ComBat.

.bc_encode_covariates *Encode protected covariates as a numeric design for BERT*

Description

BERT performs no encoding of its own: `BERT::BERT()` collects the `Cov_*` columns with `mod <- data.frame(data[, grepl("Cov", names(data))])` and hands them straight to `sva::ComBat(mod = )` and `limma::removeBatchEffect(design = )`. Its documentation therefore requires integer columns. A character or factor column reaches ComBat as text, which is coerced to double and becomes NA ("NA/NaN/Inf in foreign function call"), and reaches limma as a non-numeric design ("design must be a numeric matrix").

Usage

```
.bc_encode_covariates(df)
```

Arguments

`df`	data.frame of covariate columns (rows = samples).

Details

Numeric columns are passed through unchanged, so a genuinely continuous covariate keeps its meaning. Categorical columns become k-1 treatment-contrast indicators, without an intercept: ComBat builds its own batch design, which already spans the grand mean, and adding an intercept here would make the combined design rank deficient. For a two-level covariate this reproduces the single 0/1 column used in BERT's own examples.

Value

Numeric data.frame with the same rows and one or more columns.

.bc_validate_batch *Validate batch column in colData*

Description

Validate batch column in colData

Usage

```
.bc_validate_batch(se, batch_column)
```

Arguments

se	SummarizedExperiment
batch_column	Character. Column name in colData

.bm_aggregate_metrics *Aggregate metrics by Assay*

Description

Aggregate metrics by Assay

Usage

```
.bm_aggregate_metrics(df, metrics, agg_fun = mean)
```

Arguments

df	Combined opdea data.frame (with Assay column)
metrics	Character vector of metric column names
agg_fun	Aggregation function (mean or median)

Value

data.frame with one row per Assay

.bm_build_extended *Build an extended combined data.frame from opdea + benchmark metrics*

Description

Merges OpDEA metrics and benchmark classification metrics by Assay + Comparison, converts Performance to numeric, and selects the 11 extended metrics for ranking.

Usage

```
.bm_build_extended(opdea_combined, bench_metrics_combined)
```

Arguments

opdea_combined	data.frame from import_opdea_results()
bench_metrics_combined	data.frame from import_benchmark_metrics()

Value

data.frame with columns: Assay, Comparison, and the 11 metrics in .BM_EXTENDED_METRICS

.BM_CLASSIFIED_COLS *Minimum required columns in the combined classified data.frame*

Description

Minimum required columns in the combined classified data.frame

Usage

```
.BM_CLASSIFIED_COLS
```

.BM_CONFUSION_COLS *Required columns in the combined confusion data.frame*

Description

Required columns in the combined confusion data.frame

Usage

```
.BM_CONFUSION_COLS
```

.bm_export_data *Export data.frame to TSV*

Description

Export data.frame to TSV

Usage

```
.bm_export_data(data, filepath)
```

Arguments

data	data.frame
filepath	Output path

.bm_export_gg_plot *Export ggplot2 to PNG*

Description

Export ggplot2 to PNG

Usage

```
.bm_export_gg_plot(gg, filepath, width = 12, height = 8, dpi = 150)
```

Arguments

gg	ggplot2 object
filepath	Output path
width	Width in inches
height	Height in inches
dpi	Resolution

.BM_EXTENDED_METRICS *Extended metrics for combined ranking (all higher = better)*

Description

Extended metrics for combined ranking (all higher = better)

Usage

```
.BM_EXTENDED_METRICS
```

.BM_METRICS *Default metrics for ranking*

Description

Default metrics for ranking

Usage

```
.BM_METRICS
```

.BM_METRICS_REQUIRED_COLS *Required columns in the combined benchmark metrics data.frame*

Description

Required columns in the combined benchmark metrics data.frame

Usage

```
.BM_METRICS_REQUIRED_COLS
```

.bm_performance_to_numeric *Convert Performance (categorical) to numeric score*

Description

Excellent=5, Very Good=4, Good=3, Acceptable=2, Poor=1, NA=0

Usage

```
.bm_performance_to_numeric(x)
```

Arguments

x	Character vector of Performance labels

Value

Numeric vector

.bm_rank_methods *Rank methods by descending metric value*

Description

Rank methods by descending metric value

Usage

```
.bm_rank_methods(agg_df, metrics)
```

Arguments

agg_df	Aggregated data.frame (one row per Assay)
metrics	Character vector of metric column names

Value

data.frame with rank columns and rank_final, sorted by rank_final

.bm_rbind_fill *Row-bind data.frames with heterogeneous columns*

Description

Combines a list of data.frames by the union of their columns, filling missing columns with NA. Unlike `do.call(rbind, ...)`, this tolerates methods whose exported tables carry different column sets (e.g. an external tool like Proteome Discoverer whose classified table keeps its own de_res columns).

Usage

```
.bm_rbind_fill(df_list)
```

.bm_read_tsv *Read a TSV file*

Description

Read a TSV file

Usage

```
.bm_read_tsv(path)
```

Arguments

path	File path

Value

data.frame

.BM_REQUIRED_COLS *Required columns in the combined opdea data.frame*

Description

Required columns in the combined opdea data.frame

Usage

```
.BM_REQUIRED_COLS
```

.bm_validate_bench_metrics *Validate combined benchmark metrics data.frame*

Description

Validate combined benchmark metrics data.frame

Usage

```
.bm_validate_bench_metrics(df)
```

Arguments

df	data.frame to validate

.bm_validate_classified *Validate combined classified data.frame*

Description

Validate combined classified data.frame

Usage

```
.bm_validate_classified(df, p_col = "adj.P.Val")
```

Arguments

df	data.frame to validate
p_col	Name of the p-value column

.bm_validate_confusion *Validate combined confusion data.frame*

Description

Validate combined confusion data.frame

Usage

```
.bm_validate_confusion(df)
```

Arguments

df	data.frame to validate

.bm_validate_opdea *Validate combined opdea data.frame*

Description

Validate combined opdea data.frame

Usage

```
.bm_validate_opdea(df)
```

Arguments

df	data.frame to validate

.classify_all_comparisons *Classify proteins for all comparisons*

Description

Classify proteins for all comparisons

Usage

```
.classify_all_comparisons(de_res, ev, alpha, lfc_thr, p_col)
```

Arguments

de_res	Data frame with DE results
ev	Data frame with expected values
alpha	Significance threshold
lfc_thr	Log fold-change threshold
p_col	P-value column name

Value

Data frame with classification columns for all comparisons

.classify_proteins *Classify proteins for a single comparison*

Description

Assigns truth labels (immutable, biological identity) and predicted labels.

- Species in expected_values -> truth = 1 (spike-in / expected change)
- Species NOT in expected_values -> truth = 0 (background)
- Positive species: predicted = 1 only if significant AND direction matches expected_logFC sign (TP); significant with wrong sign stays predicted = 0 (FN, a detection failure – NOT relabelled as a false positive).
- Negative species: predicted = 1 if significant (any direction -> FP) `truth` is never modified by the prediction, so .compute_auc/.compute_pauc receive the biological ground truth (uncontaminated) for pROC.

Usage

```
.classify_proteins(de_res_comp, ev_comp, alpha, lfc_thr, p_col)
```

Arguments

de_res_comp	DE results for one comparison
ev_comp	Expected values for one comparison
alpha	Significance threshold
lfc_thr	Log fold-change threshold
p_col	P-value column name

Details

Two diagnostic columns are recorded alongside the classification and take no part in any metric. `is_significant` is the significance rule actually used here (p-value AND fold-change threshold), stored so that tables and plots cannot drift from the classification by recomputing it. `direction_error` separates the two kinds of FN: a change that was missed altogether, and a change that was called significant with the sign inverted.

Value

Data frame with added columns: truth, predicted, classification, is_significant, direction_error

.compute_auc *Compute AUC using pROC*

Description

Compute AUC using pROC

Usage

```
.compute_auc(classified_df, p_col)
```

Arguments

classified_df	Classified data frame for one comparison
p_col	P-value column name

Value

AUC value, or NA if the comparison lacks both classes or has fewer than three proteins

.compute_metrics *Compute classification metrics from confusion matrix counts*

Description

Compute classification metrics from confusion matrix counts

Usage

```
.compute_metrics(tp, fp, tn, fn)
```

Arguments

tp	True positives
fp	False positives
tn	True negatives
fn	False negatives

Value

Named numeric vector with metrics

.compute_missing_pct *Compute missing-value percentages per protein*

Description

Four percentages, all measured on the normalized assay, that is, before imputation, and all going from the widest scope to the narrowest:

- MissGlobal: % NAs over every sample in the experiment, including the conditions that take no part in the comparison. It does not depend on the comparison, so a given protein carries the same value in all of them.
- MissComp: % NAs over the replicates of the two conditions being compared only. With more than two conditions this is not the same as MissGlobal.
- MissCND1: % NAs over the samples of Cond1 (numerator, before "-")
- MissCND2: % NAs over the samples of Cond2 (denominator, after "-")

Usage

```
.compute_missing_pct(se, DEPs_results, norm_assay_name)
```

Arguments

se	SummarizedExperiment with normalized assay
DEPs_results	Data frame with DE results (must have Protein.IDs, Comparison)
norm_assay_name	Name of the normalized assay

Value

DEPs_results with MissGlobal, MissComp, MissCND1, MissCND2 columns added

.compute_pauc *Compute partial AUC with McClish correction*

Description

Uses pROC::roc() with partial.auc and partial.auc.correct = TRUE (native McClish correction). Normalized range: 0.5-1.

Usage

```
.compute_pauc(classified_df, p_col, max_fpr = 0.1)
```

Arguments

classified_df	Classified data frame for one comparison
p_col	P-value column name
max_fpr	Maximum false positive rate threshold (default: 0.1)

Value

Corrected partial AUC value, or NA if the comparison lacks both classes or has fewer than three proteins

---

.configure_species_colors *Configure species colors*

Description

Configure species colors

Usage

```
.configure_species_colors(species, colors = NULL)
```

Arguments

species	Character vector of unique species names
colors	Named vector of custom colors (optional)

Value

Named vector of colors per species

.confusion_by_species *Compute confusion matrix by species*

Description

Compute confusion matrix by species

Usage

```
.confusion_by_species(classified_df)
```

Arguments

classified_df	Classified data frame

Value

Data frame with TP/FP/TN/FN counts per Comparison x Species

.confusion_overall *Compute overall confusion matrix per comparison*

Description

Aggregates TP/FP/TN/FN across all species for each comparison.

Usage

```
.confusion_overall(confusion_by_species_df)
```

Arguments

confusion_by_species_df	Data frame from .confusion_by_species()

Value

Data frame with one row per Comparison

.detect_elbow *Detect elbow point via maximum perpendicular distance to LOESS fit*

Description

Given missing_rate (x) and mean_intensity (y), fits a LOESS curve and finds the point of maximum perpendicular distance to the line connecting the first and last fitted points.

Usage

```
.detect_elbow(missing_rate, mean_intensity)
```

Arguments

missing_rate	Numeric vector of per-protein missing rates
mean_intensity	Numeric vector of per-protein mean intensities (non-NA)

Value

List with r0 (elbow missing rate) and x0 (elbow intensity)

.detect_p_col *Auto-detect p-value column*

Description

Auto-detect p-value column

Usage

```
.detect_p_col(df, preferred = "adj.P.Val")
```

Arguments

df	Data frame
preferred	Preferred column name

Value

Name of the p-value column found

.dispatch_imputation *Central dispatcher for imputation methods*

Description

Central dispatcher for imputation methods

Usage

```
.dispatch_imputation(x, method, method_args = list(), with_value = NA_real_)
```

Arguments

x	Numeric matrix (proteins x samples)
method	Method name (one of .IMP_METHODS_ALL minus "combo")
method_args	Named list of per-method argument lists
with_value	Constant value for method "with"

Value

Imputed matrix

.export_benchmark_data *Export benchmark data to TSV*

Description

Export benchmark data to TSV

Usage

```
.export_benchmark_data(data, filepath)
```

Arguments

data	Data frame to export
filepath	Full file path (with extension)

.export_data *Export data frame to TSV and/or Parquet*

Description

Export data frame to TSV and/or Parquet

Usage

```
.export_data(data, filepath_base, format = "tsv")
```

Arguments

data	Data frame to export
filepath_base	Base path without extension
format	"tsv", "parquet", or "both"

Value

Invisible NULL

.export_gg_plot *Export ggplot2 chart to PNG*

Description

Export ggplot2 chart to PNG

Usage

```
.export_gg_plot(gg, filepath, width = 10, height = 7, dpi = 300)
```

Arguments

gg	ggplot2 object
filepath	Full file path
width	Width in inches (default: 10)
height	Height in inches (default: 7)
dpi	Resolution (default: 300)

.extract_limma_results *Extract results from limma fit*

Description

Extract results from limma fit

Usage

```
.extract_limma_results(
  fit,
  comparisons,
  logFC_up = 1,
  logFC_down = -1,
  alpha = 0.05,
  p_adj = TRUE
)
```

Arguments

fit	limma fit object
comparisons	Comparison vector
logFC_up	Upper logFC threshold for "Up"
logFC_down	Lower logFC threshold for "Down"
alpha	Significance threshold
p_adj	Use adjusted p-value (TRUE) or raw (FALSE)

Value

Data frame with results

.filter_proteins_by_group *Filter proteins by group presence*

Description

Keeps proteins that have enough non-NA values in at least a minimum number of experimental groups.

Usage

```
.filter_proteins_by_group(
  data,
  metadata,
  min_reps = NULL,
  min_groups = 1,
  grouping_column = "Condition"
)
```

Arguments

data	Intensity matrix (proteins x samples)
metadata	Data frame with sample information
min_reps	Minimum replicates with non-NA values per group. If NULL, uses half of the smallest group size.
min_groups	Minimum groups meeting min_reps (default: 1)
grouping_column	Name of grouping column in metadata (default: "Condition")

Value

List with:

- data: Filtered matrix
- keep: Logical vector of kept rows
- summary: Filtering summary

.get_NA_overview *NA overview for a SummarizedExperiment*

Description

NA overview for a SummarizedExperiment

Usage

```
.get_NA_overview(se, assay_name = "log2")
```

Arguments

se	SummarizedExperiment
assay_name	Assay name to evaluate (default: "log2")

Value

Data frame with NA statistics per sample

.harmonize_change *Harmonize Change column values*

Description

Normalizes "Up Regulated" -> "Up", "Down Regulated" -> "Down", "Not Significant" / "No Change" -> "No Change"

Usage

```
.harmonize_change(de_res)
```

Arguments

de_res	Data frame with Change column

Value

Data frame with harmonized Change column

.impute_combo *Mixed combo imputation: configurable MAR + MNAR methods*

Description

Two-stage imputation:

1. MAR/MCAR: dispatched to mar_method
2. MNAR: dispatched to mnar_method

Usage

```
.impute_combo(
  x,
  condition,
  prop_na_in_condition = 1,
  prop_present_in_other_condition = 0,
  min_present_in_other_condition = 1,
  require_n_other_conditions = 1,
  mar_method = "Impseqrob",
  mnar_method = "min",
  method_args = list(),
  with_value = NA_real_
)
```

Arguments

x	Log2 intensity matrix
condition	Condition vector aligned with columns
prop_na_in_condition	Proportion of NA to classify as MNAR (default: 1.0)
prop_present_in_other_condition	Proportion present in other conditions (default: 0.0)
min_present_in_other_condition	Minimum present values (default: 1)
require_n_other_conditions	Required conditions with presence (default: 1)
mar_method	MAR imputation method (default: "Impseqrob")
mnar_method	MNAR imputation method (default: "min")
method_args	Named list of per-method argument lists
with_value	Constant for method "with"

Value

List with x_imputed, mnar_mask, mar_mask, summary

.impute_softHybrid *softHybrid imputation: continuous sigmoid-weighted blend of MAR and MNAR*

Description

Instead of binary MAR/MNAR classification (as in combo), uses a continuous sigmoid function to assign per-protein weights between MAR and MNAR methods. Based on Shi et al. (bioRxiv 2026) softHybridImpute approach.

Usage

```
.impute_softHybrid(
  x,
  mar_method = "Impseqrob",
  mnar_method = "min",
  method_args = list(),
  with_value = NA_real_,
  a = 10,
  b = 5,
  lambda = 0.5,
  r0 = NULL,
  x0 = NULL
)
```

Arguments

x	Numeric matrix (proteins x samples, log2) with NAs
mar_method	MAR imputation method (default: "Impseqrob", deterministic and with no additional dependencies; the impute_proteomics wrapper passes this value). Note: if a stochastic MAR/MNAR method is chosen (e.g. "missForest"), call `set.seed()` before the imputation to reproduce it.
mnar_method	MNAR imputation method (default: "min")
method_args	Named list of per-method argument lists
with_value	Constant value for method "with"
a	Steepness of sigmoid for missing rate (default: 10)
b	Steepness of sigmoid for mean intensity, in SD units (default: 5)
lambda	Balance between missing rate and intensity signals (default: 0.5, in the range 0-1)
r0	Elbow point for missing rate sigmoid (NULL = auto-detect)
x0	Elbow point for intensity sigmoid (NULL = auto-detect)

Value

List with x_imputed, weights (w_mar per protein), elbow (r0, x0), summary

---

.imp_bpca *bpca: Bayesian PCA imputation (pcaMethods)*

Description

bpca: Bayesian PCA imputation (pcaMethods)

Usage

```
.imp_bpca(x, args = list())
```

Arguments

args	list with optional `maxSteps` (default 100). The number of principal components is `ncol(x) - 1`, which `MsCoreUtils` fixes. Delegated to `MsCoreUtils`, which gives identical results (Bioconductor review, #186); this wrapper keeps NADIA's argument names.

.imp_halfmin *halfmin: half of the global observed minimum (the DIA-NN recipe)*

Description

DIA-NN describes it as replacing each missing value with half the observed minimum across all runs. The matrix here is on the log2 scale, so halving the intensity means subtracting 1, not dividing by 2: log2(m / 2) == log2(m) - 1. Dividing the log2 value would give the square root of the minimum intensity, eight times lower than intended on a typical dataset, and its magnitude would depend on where zero happens to fall on the log scale.

Usage

```
.imp_halfmin(x, args = list())
```

.imp_Impseq *Impseq: Sequential imputation (rrcovNA)*

Description

Impseq: Sequential imputation (rrcovNA)

Usage

```
.imp_Impseq(x, args = list())
```

.imp_Impseqrob *Impseqrob: Robust sequential imputation (rrcovNA)*

Description

Impseqrob: Robust sequential imputation (rrcovNA)

Usage

```
.imp_Impseqrob(x, args = list())
```

Arguments

`args`	list with optional `alpha` (default 0.9)

.imp_knn — *knn: k-nearest neighbors imputation (impute)*

Description

knn: k-nearest neighbors imputation (impute)

Usage

```
.imp_knn(x, args = list())
```

Arguments

args	list with optional k (default 10), rowmax (default 0.99), colmax (default 0.99).

.imp_limpa — *limpa: probabilistic imputation with detection probability curve (limpa)*

Description

Uses dpc/dpcCN to estimate a detection probability curve, then dpcQuantByRow to impute protein-level abundances with standard errors. The returned EList is attached as an attribute for downstream dpcDE.

Usage

```
.imp_limpa(x, args = list())
```

Arguments

args	list with optional use_dpcCN (default FALSE), model ("on" or "cn"; defaults to "cn" when use_dpcCN is TRUE and "on" otherwise), dpc.slope (default 0.8), dpc.start (default NULL), iterations (default 2), subset (default 2000), robust (default TRUE), chunk (default 1000), verbose (default FALSE)

.imp_mice *mice: Multiple Imputation by Chained Equations*

Description

mice: Multiple Imputation by Chained Equations

Usage

```
.imp_mice(x, args = list())
```

Arguments

args	list with optional m (default 5), maxit (default 5), method (default "norm") and seed (default NA). NAguideR strategy: no transpose, method="norm", average of m imputations.

Details

With the default seed = NA, mice::mice() draws from the caller's RNG, so set.seed() before impute_proteomics() reproduces a run. A seed passed explicitly is handed to mice::mice(), which then seeds the RNG itself.

.imp_min *Minimum value imputation (global minimum) Delegated to MsCoreUtils, which gives identical results (Bioconductor review, #186); this wrapper keeps NADIA's argument names.*

Description

Minimum value imputation (global minimum) Delegated to MsCoreUtils, which gives identical results (Bioconductor review, #186); this wrapper keeps NADIA's argument names.

Usage

```
.imp_min(x, args = list())
```

.imp_MinDet *MinDet: per-column quantile imputation*

Description

MinDet: per-column quantile imputation

Usage

```
.imp_MinDet(x, args = list())
```

Arguments

args	list with optional q (default 0.01) Delegated to MsCoreUtils, which gives identical results (Bioconductor review, #186); this wrapper keeps NADIA's argument names.

.imp_MinProb *MinProb: Minimum Probability imputation (imputeLCMD)*

Description

MinProb: Minimum Probability imputation (imputeLCMD)

Usage

```
.imp_MinProb(x, args = list())
```

Arguments

args	list with optional q (default 0.01), tune.sigma (default 1) Delegated to MsCoreUtils, which gives identical results (Bioconductor review, #186); this wrapper keeps NADIA's argument names.

.imp_missForest *missForest: Random Forest imputation*

Description

Which unit the forests learn from is set by observations:

- "features" (default): the proteins are the observations and the samples the variables, so each sample is predicted from the other samples, with forests trained over thousands of proteins. This is the default of MsCoreUtils::impute_RF() and the orientation of knn and bpca here.
- "samples": the samples are the observations and every protein is a variable, as NAguideR does. Each forest then trains on at most n - 1 samples, which suits large cohorts only.

Usage

```
.imp_missForest(x, args = list())
```

Arguments

args	list with optional observations ("features", the default, or "samples"), maxiter (default 10), ntree (default 100) and mtry (default floor(sqrt(p)) with "features", the missForest default, and floor(p^(1/3)) with "samples", NAguideR's cube root of the number of proteins). The fit is delegated to MsCoreUtils::impute_RF(), which gives identical results.

Details

Until NADIA 0.99.2 the only orientation was "samples". On nadia_dia (12 samples) with values hidden at random, the RMSE was 0.264 against 0.402, and on the TMT example 0.113 against 0.165 with 24 samples and 0.153 against 0.455 with 12 (Bioconductor review, #186).

This method is stochastic and takes no seed of its own, because missForest::missForest() does not accept one. To reproduce a run, call set.seed() before impute_proteomics(), as for every stochastic method in NADIA.

.imp_MLE *MLE: Maximum Likelihood Estimation (norm)*

Description

MLE: Maximum Likelihood Estimation (norm)

Usage

```
.imp_MLE(x, args = list())
```

Arguments

args	list with optional seed (default NULL). NAguideR strategy: no transpose (features x samples).

Details

norm has an RNG of its own, separate from R's, which norm::rngseed() initialises. When no seed is given, it is drawn from the caller's RNG, so set.seed() before impute_proteomics() reproduces a run here as it does for every other stochastic method. A seed passed explicitly is handed to norm::rngseed() unchanged. One limitation belongs to norm and no seed removes it: its generator keeps state that rngseed() does not reset, so a second MLE imputation in the same R session differs from the first even with the same seed. A script run in a fresh session is reproducible.

.imp_PI *PI: Perseus-style imputation (down-shifted normal distribution)*

Description

PI: Perseus-style imputation (down-shifted normal distribution)

Usage

```
.imp_PI(x, args = list())
```

Arguments

args	list with optional width (default 0.3) and downshift (default 1.8).

Details

The imputed values are drawn with rnorm() from the caller's RNG. To reproduce a run, call set.seed() before impute_proteomics().

.imp_QRILC *QRILC: Quantile Regression Imputation of Left-Censored data (imputeLCMD)*

Description

QRILC: Quantile Regression Imputation of Left-Censored data (imputeLCMD)

Usage

```
.imp_QRILC(x, args = list())
```

Arguments

args	list with optional tune.sigma (default 1) Delegated to MsCoreUtils, which gives identical results (Bioconductor review, #186); this wrapper keeps NA-DIA's argument names.

.imp_with *with: replace NAs with user-specified constant*

Description

with: replace NAs with user-specified constant

Usage

```
.imp_with(x, args = list())
```

Arguments

args	list with with_value Delegated to MsCoreUtils, which gives identical results (Bioconductor review, #186); this wrapper keeps NADIA's argument names.

.imp_zero *zero: replace NAs with 0 Delegated to* MsCoreUtils*, which gives identical results (Bioconductor review, #186); this wrapper keeps NADIA's argument names.*

Description

zero: replace NAs with 0 Delegated to MsCoreUtils, which gives identical results (Bioconductor review, #186); this wrapper keeps NADIA's argument names.

Usage

```
.imp_zero(x, args = list())
```

.im_acc_oi *ACC_OI – Correlation of Original and Imputed at masked positions*

Description

Pearson correlation between the true values and the imputed values, evaluated ONLY at the artificially masked cells (pooled across all features and columns). Higher is better.

Usage

```
.im_acc_oi(true_mat, imp_mat, na_mask)
```

Arguments

true_mat	Numeric matrix (ground truth)
imp_mat	Numeric matrix (imputed)
na_mask	Logical matrix

Details

Note: the previous version correlated the WHOLE row (true vs imputed), which differs in only 1-2 masked cells -> correlation ~1 regardless of the imputation quality, making the metric non-discriminative. Restricting it to the masked cells measures the real accuracy.

Value

Numeric scalar (Pearson correlation over masked cells)

`.im_introduce_na` *Introduce artificial NAs into a complete-case matrix*

Description

Takes a matrix with no NAs (ground truth) and introduces NAs at random or mimicking the NA pattern from a reference matrix.

Usage

```
.im_introduce_na(mat, na_prop = 0.2, pattern = "random", ref_mat = NULL)
```

Arguments

`mat`	Numeric matrix (proteins x samples), no NAs (ground truth)
`na_prop`	Numeric (0-1). Proportion of values to set as NA. Default 0.20. Only used when `pattern = "random"`; ignored when `pattern = "from_data"`.
`pattern`	Character: `"random"` for uniform random NAs, or `"from_data"` to replicate NAguideR's simulation strategy using the actual NA structure from `ref_mat`.
`ref_mat`	Numeric matrix. Reference matrix with real NAs, used when `pattern = "from_data"`. Ignored otherwise.

Details

When `pattern = "from_data"`, replicates the NAguideR strategy (Wang et al., DOI:10.1093/nar/gkz903): the proportion of affected rows and the per-column NA distribution are derived entirely from `ref_mat`, so `na_prop` is ignored.

Value

Named list:

`mat_with_na`	Matrix with artificial NAs introduced
`na_mask`	Logical matrix (TRUE = artificially set to NA)
`true_mat`	Original complete matrix (unchanged)
`summary`	List with n_total, n_na, na_rate, rows_affected, row_ratio (from_data only)

.im_method_factor *Order Method as factor (consistent with Normalization_Metrics.R pattern)*

Description

Order Method as factor (consistent with Normalization_Metrics.R pattern)

Usage

```
.im_method_factor(df, method_levels)
```

Arguments

df	data.frame with Method column
method_levels	Character vector of method names in desired order

Value

data.frame with Method as ordered factor

.im_nrmse *NRMSE – Normalized Root Mean Squared Error*

Description

Computes NRMSE between true and imputed values at positions indicated by the NA mask. Lower is better.

Usage

```
.im_nrmse(true_mat, imp_mat, na_mask)
```

Arguments

true_mat	Numeric matrix (ground truth, complete)
imp_mat	Numeric matrix (imputed from artificially-NA'd version)
na_mask	Logical matrix (TRUE = position was set to NA)

Value

Numeric scalar (NRMSE)

.im_pss *PSS – Procrustes Statistical Shape analysis*

Description

PCA on both true and imputed matrices (transposed: samples as rows), retain components up to 95% cumulative variance, then Procrustes SS. Requires vegan (optional). Lower is better.

Usage

```
.im_pss(true_mat, imp_mat)
```

Arguments

true_mat	Numeric matrix (ground truth, proteins x samples)
imp_mat	Numeric matrix (imputed)

Value

Numeric scalar (Procrustes SS), or NA if vegan not available

.im_reimpute *Re-impute a matrix with multiple methods*

Description

Iterates over a vector of imputation method names, calling `.dispatch_imputation()` from Imputation.R for each. Also supports combo and softHybrid methods via `combo_methods` parameter. Methods that fail are omitted with a warning.

Usage

```
.im_reimpute(
  mat_with_na,
  methods = character(0),
  combo_methods = list(),
  condition = NULL,
  method_args = list(),
  with_value = NA_real_,
  verbose = TRUE
)
```

Arguments

mat_with_na	Numeric matrix with artificial NAs
methods	Character vector of individual method names
combo_methods	Named list of combo/softHybrid configurations. Each element is a list with: `mode` ("combo" or "softHybrid", default "combo"), `mar_method`, `mnar_method`, and optionally other parameters. The list name is used as the method label.

condition	Factor or character vector of conditions (required for combo methods, ignored for individual methods).
method_args	Named list of per-method argument lists
with_value	Constant for method "with"
verbose	Logical. Print progress. Default TRUE.

Value

Named list of imputed matrices (one per successful method)

.im_rmse_per_feature *Per-feature RMSE for SOR computation*

Description

For each row (feature) with artificial NAs, computes RMSE between true and imputed values. Returns a named numeric vector.

Usage

```
.im_rmse_per_feature(true_mat, imp_mat, na_mask)
```

Arguments

true_mat	Numeric matrix (ground truth)
imp_mat	Numeric matrix (imputed)
na_mask	Logical matrix

Value

Named numeric vector of per-feature RMSE

.load_proteomics_data *Create SummarizedExperiment from proteomics data*

Description

Create SummarizedExperiment from proteomics data

Usage

```
.load_proteomics_data(
  data,
  metadata,
  protein_column = "ProteinGroups",
  gene_column = "GeneNames",
  condition_column = "Condition",
  label_column = "Column"
)
```

Arguments

data	Data frame with proteins and intensity values
metadata	Data frame with sample information
protein_column	Protein ID column name
gene_column	Gene name column name
condition_column	Condition column name in metadata
label_column	Sample label column name in metadata

Value

SummarizedExperiment with assays: raw, log2

.mnar_mask_by_condition *MNAR mask by condition with evidence in other conditions*

Description

Identifies MNAR candidate cells: NA in one condition but with sufficient presence in other conditions.

Usage

```
.mnar_mask_by_condition(
  x,
  condition,
  prop_na_in_condition = 1,
  prop_present_in_other_condition = 0,
  min_present_in_other_condition = 1,
  require_n_other_conditions = 1,
  drop_empty_levels = TRUE
)
```

Arguments

x	Intensity matrix (proteins x samples)
condition	Condition vector aligned with columns
prop_na_in_condition	Minimum proportion of NA in the condition (default: 1.0 = 100%)
prop_present_in_other_condition	Minimum proportion of non-NA in other condition (default: 0.0)
min_present_in_other_condition	Minimum absolute non-NA count in other condition (default: 1)
require_n_other_conditions	Number of other conditions that must meet criteria (default: 1)
drop_empty_levels	Drop empty factor levels (default: TRUE)

Value

Logical matrix of same dimensions indicating MNAR cells

.nm_condition_number *Condition number of the covariance matrix (via PCA eigenvalues)*

Description

Ratio of the largest to smallest non-zero eigenvalue from PCA of the sample covariance matrix. High values indicate numerical instability or multicollinearity.

Usage

```
.nm_condition_number(mat)
```

Arguments

`mat`	Numeric matrix (proteins x samples), no NAs.

Value

Numeric scalar >= 1 (Inf if smallest eigenvalue is zero).

.nm_cophenetic_cor *MDS cophenetic correlation*

Description

Pearson correlation between the original Euclidean distances and the distances in the 2D MDS projection. Uses scaled data (consistent with `nm_plot_mds`).

Usage

```
.nm_cophenetic_cor(mat)
```

Arguments

`mat`	Numeric matrix (proteins x samples), no NAs.

Value

Numeric scalar (-1 to 1).

.nm_cumvar_pc2 *Cumulative variance explained by PC1 and PC2*

Description

Percentage of total variance captured by the first two principal components.

Usage

```
.nm_cumvar_pc2(mat)
```

Arguments

mat	Numeric matrix (proteins x samples), no NAs.

Value

Numeric scalar (0-100).

.nm_hopkins *Hopkins statistic for clustering tendency*

Description

Manual implementation of the Hopkins statistic. Values > 0.5 suggest non-random clustering structure; values near 0.5 indicate uniform distribution.

Usage

```
.nm_hopkins(mat, n_sample = 10L)
```

Arguments

mat	Numeric matrix (proteins x samples), no NAs.
n_sample	Integer. Number of points to sample (default 10, capped at ncol - 1).

Details

The random reference points and the sampled data points are drawn from the caller's RNG, so the statistic is reproducible only after `set.seed()`.

Value

Numeric scalar (0-1).

.nm_intragroup_cor *Intra-group Pearson correlations*

Description

Computes pairwise Pearson correlations between all sample pairs within each group, using complete observations only.

Usage

```
.nm_intragroup_cor(mat, groups, method = "pearson")
```

Arguments

mat	Numeric matrix (proteins x samples)
groups	Factor or character vector of group labels

Value

Numeric vector of correlation values

.nm_mds1_var_pct *Percentage of variance explained by MDS dimension 1*

Description

Computes the percentage of variance captured by the first MDS dimension, using only positive eigenvalues from classical MDS (`cmdscale(eig = TRUE)`). Uses scaled data (consistent with `nm_plot_mds`).

Usage

```
.nm_mds1_var_pct(mat)
```

Arguments

mat	Numeric matrix (proteins x samples), no NAs.

Value

Numeric scalar (0-100).

.nm_mds_gof *MDS goodness-of-fit*

Description

GOF[1] from `cmdscale()` with `eig = TRUE`: proportion of variance retained in the 2D MDS projection. Uses scaled data (consistent with `nm_plot_mds`).

Usage

```
.nm_mds_gof(mat)
```

Arguments

`mat`	Numeric matrix (proteins x samples), no NAs.

Value

Numeric scalar (0-1).

.nm_pc1_f_ratio *PC1 F-ratio (between-group / within-group variance on PC1 scores)*

Description

One-way ANOVA F-statistic on PC1 scores grouped by condition. Higher values indicate better group separation along PC1.

Usage

```
.nm_pc1_f_ratio(mat, groups)
```

Arguments

`mat`	Numeric matrix (proteins x samples), no NAs.
`groups`	Factor or character vector of group labels.

Value

Numeric scalar (0-Inf).

.nm_pc1_var_pct *PC1 variance percentage*

Description

Percentage of total variance explained by the first principal component.

Usage

```
.nm_pc1_var_pct(mat)
```

Arguments

mat	Numeric matrix (proteins x samples), no NAs.

Value

Numeric scalar (0-100).

.nm_pcv *Per-protein CV averaged across groups (PRONE-style PCV)*

Description

For each protein, computes CV = 100 * SD / |mean| within each group, then averages across groups. Returns one value per protein.

Usage

```
.nm_pcv(mat, groups)
```

Arguments

mat	Numeric matrix (proteins x samples), log2 scale
groups	Factor or character vector of group labels (length = ncol(mat))

Value

Named numeric vector, one value per protein

.nm_permanova_r2 *PERMANOVA R^2 via vegan::adonis2*

Description

Proportion of variance in Euclidean distances explained by the grouping. Requires the vegan package (optional).

Usage

```
.nm_permanova_r2(mat, groups)
```

Arguments

mat	Numeric matrix (proteins x samples), no NAs.
groups	Factor or character vector of group labels.

Details

`adonis2()` obtains its p-value by permuting the group labels with the caller's RNG, so the p-value is reproducible only after `set.seed()`. `R2` is deterministic.

Value

Named list with `R2` and `p_value`, or NA if vegan unavailable.

.nm_pev *Per-protein variance averaged across groups (PRONE-style PEV)*

Description

For each protein, computes variance within each group, then averages across groups. Returns one value per protein.

Usage

```
.nm_pev(mat, groups)
```

Arguments

mat	Numeric matrix (proteins x samples)
groups	Factor or character vector of group labels

Value

Named numeric vector, one value per protein

.nm_pmad *Per-protein MAD averaged across groups (PRONE-style PMAD)*

Description

For each protein, computes MAD = median(|x - median(x)|) within each group, then averages across groups. Returns one value per protein.

Usage

```
.nm_pmad(mat, groups)
```

Arguments

mat	Numeric matrix (proteins x samples)
groups	Factor or character vector of group labels

Value

Named numeric vector, one value per protein

.nm_silhouette_avg *Average silhouette width*

Description

Mean silhouette width when samples are clustered by condition labels. Requires the cluster package (optional).

Usage

```
.nm_silhouette_avg(mat, groups)
```

Arguments

mat	Numeric matrix (proteins x samples), no NAs.
groups	Factor or character vector of group labels.

Value

Numeric scalar (-1 to 1), or NA if cluster unavailable.

.nm_spectral_entropy *Spectral entropy of PCA eigenvalues*

Description

Normalized Shannon entropy of the eigenvalue distribution from PCA. Values near 0 indicate variance concentrated in few components; values near 1 indicate uniform spread across all components.

Usage

```
.nm_spectral_entropy(mat)
```

Arguments

mat	Numeric matrix (proteins x samples), no NAs.

Value

Numeric scalar (0-1).

.nm_to_long *Reshape SE assays to long data.frame for ggplot2*

Description

Reshape SE assays to long data.frame for ggplot2

Usage

```
.nm_to_long(se, assay_names = NULL, condition_col = "Condition")
```

Arguments

se	SummarizedExperiment object
assay_names	Character vector of assay names to include. NULL = all.
condition_col	Column name in colData with condition labels.

Value

data.frame with columns: Method, Sample, Condition, Protein, Value

.pca_compute_scores *Compute PCA scores from a SE assay*

Description

Compute PCA scores from a SE assay

Usage

```
.pca_compute_scores(
  se,
  assay_name,
  na_action = "complete",
  fill_value = -1,
  center = TRUE,
  scale. = TRUE,
  verbose = TRUE
)
```

Arguments

se	SummarizedExperiment
assay_name	Character. Assay to use.
na_action	Character: "complete" (remove rows with NAs) or "fill".
fill_value	Numeric. Replacement for NAs when na_action="fill".
center	Logical. Center variables before PCA (default TRUE).
scale.	Logical. Scale variables before PCA (default TRUE).
verbose	Logical.

Value

List with: scores (data.frame PC1, PC2, Sample + colData), pct_var (numeric vector of % variance per PC), n_proteins (integer).

.perform_limma *Run limma analysis*

Description

Run limma analysis

Usage

```
.perform_limma(
  data,
  condition_vector,
  comparisons,
  covariate = NULL,
  block = NULL,
  eBayes_trend = TRUE,
  eBayes_robust = TRUE
)
```

Arguments

data	Log2 intensity matrix
condition_vector	Condition vector aligned with columns
comparisons	Comparison vector
covariate	Optional covariate for the model
eBayes_trend	Use trend estimation in eBayes (default: TRUE)
eBayes_robust	Use robust estimation in eBayes (default: TRUE)

Value

limma fit object

.perform_limpa_de *Run limpa dpcDE analysis*

Description

Uses limpa::dpcDE with precision weights from the EList (standard errors) produced by dpcQuantByRow. The EList is stored in SE metadata by impute_proteomics() when imp_method="limpa".

Usage

```
.perform_limpa_de(
  elist,
  condition_vector,
  comparisons,
  covariate = NULL,
  block = NULL,
  eBayes_trend = FALSE,
  eBayes_robust = FALSE
)
```

Arguments

elist	EList from limpa (with $E and $weights)
condition_vector	Condition vector aligned with columns
comparisons	Comparison vector
covariate	Optional covariate for the model
eBayes_trend	Use trend estimation in eBayes (default: FALSE, vooma already models the trend)
eBayes_robust	Use robust estimation in eBayes (default: FALSE, voomaLmFitWithImputation already handles imputed proteins)

Value

limma MArrayLM fit object

.prefilter_by_na_prop *Pre-filter proteins by NA proportion*

Description

Removes proteins with more than max_na_prop fraction of NAs. With max_na_prop = NULL (the default) nothing is removed, so every imputation method sees the same set of proteins: combo never applied this filter, and having the single methods apply it made the same argument mean different things depending on imp_method.

Usage

```
.prefilter_by_na_prop(x, max_na_prop = NULL)
```

Arguments

x	Numeric matrix
max_na_prop	Maximum NA proportion, or NULL to disable the filter (default).

Value

List with keep (logical vector), summary

`.prefilter_by_rules` *Pre-filter proteins by MNAR rules (for combo mode)*

Description

Keeps a protein if: (A) It has MNAR in >= 1 condition, OR (B) It has sufficient signal in >= require_n_other_conditions conditions

Usage

```
.prefilter_by_rules(
  x,
  condition,
  prop_na_in_condition = 0.51,
  prop_present_in_other_condition = 0.5,
  min_present_in_other_condition = 1,
  require_n_other_conditions = 1
)
```

Arguments

`x`	Log2 intensity matrix
`condition`	Condition vector
`prop_na_in_condition`	NA proportion for MNAR (default: 0.51)
`prop_present_in_other_condition`	Required present proportion (default: 0.5)
`min_present_in_other_condition`	Minimum present values (default: 1)
`require_n_other_conditions`	Required conditions (default: 1)

Value

List with keep, summary

`.prepare_benchmark_data` *Prepare benchmark data*

Description

Filters de_res by assay and comparisons, validates inputs, resolves p-value column.

Usage

```
.prepare_benchmark_data(
  de_res,
  expected_values,
  alpha = 0.05,
  lfc_thr = 0,
  p_col = "adj.P.Val",
  comparisons = NULL,
  assay = NULL,
  species_df = NULL
)
```

Arguments

de_res	Data frame with DE results (must include Species column)
expected_values	Data frame with expected values
alpha	Significance threshold
lfc_thr	Log fold-change threshold
p_col	P-value column name
comparisons	Comparisons to include (NULL = all)
assay	Assay to filter (NULL = all)
species_df	Data frame with Protein.IDs and Species columns (optional). If provided, Species is merged into de_res. If NULL, de_res must already contain a Species column.

Value

List with filtered de_res, expected_values, and resolved p_col

---

.prepare_metadata *Prepare metadata from proteomics_data object*

Description

Prepare metadata from proteomics_data object

Usage

```
.prepare_metadata(preprocessing, covariate_df = NULL)
```

Arguments

preprocessing	A `proteomics_data` object, from any of the preprocess_*() functions

Value

Data frame with columns: Column, Condition, Replicate

.prepare_pca_input *Prepare PCA input with differential expression information*

Description

Prepare PCA input with differential expression information

Usage

```
.prepare_pca_input(se, DEPs_results, assay_name, alpha = 0.05)
```

Arguments

se	SummarizedExperiment
DEPs_results	Data frame with DE results
assay_name	Assay name to use
alpha	Significance threshold for sig_any

Value

Data frame with intensities and adjP columns per comparison

.prepare_protein_data *Prepare protein data from proteomics_data object*

Description

Prepare protein data from proteomics_data object

Usage

```
.prepare_protein_data(preprocessing)
```

Arguments

preprocessing	A proteomics_data object, from any of the preprocess_*() functions

Value

Data frame with columns: ProteinGroups, GeneNames, UniqPepts, and intensity columns

.pvca_categorize *Categorize PVCA labels as technical, biological, interaction, or residual*

Description

Categorize PVCA labels as technical, biological, interaction, or residual

Usage

```
.pvca_categorize(
  pvca_df,
  technical_factors,
  biological_factors,
  variance_threshold = 0.01
)
```

.pvca_export_gg_plot *Export a ggplot2 plot to file*

Description

Export a ggplot2 plot to file

Usage

```
.pvca_export_gg_plot(gg, filepath, width = 10, height = 6, dpi = 150)
```

.pvca_prepare_matrix *Extract and prepare the abundance matrix, handling NAs*

Description

Extract and prepare the abundance matrix, handling NAs

Usage

```
.pvca_prepare_matrix(
  se,
  assay_name,
  na_action = "complete",
  fill_value = -1,
  verbose = TRUE
)
```

.pvca_run *Core PVCA algorithm using lme4*

Description

1. PCA on the expression matrix
2. Retain PCs explaining >= pca_threshold cumulative variance
3. For each retained PC, fit lme4 mixed model with factors as random effects
4. Extract variance components, weight by PC variance proportion

Usage

```
.pvca_run(mat, annot_df, factors, pca_threshold = 0.6, verbose = TRUE)
```

Arguments

mat	Numeric matrix (proteins x samples)
annot_df	data.frame with factor columns (rows = samples)
factors	Character vector of factor names
pca_threshold	Numeric (0-1)
verbose	Logical

Value

data.frame with columns: label, weights

.pvca_safe_interactions *Check which interaction terms are safe (n_levels < n_obs)*

Description

Returns only interactions whose combined factor levels are strictly less than the number of observations. This prevents lme4 from failing on saturated random effects (e.g., Condition:Patient in paired designs).

Usage

```
.pvca_safe_interactions(annot_df, factors, verbose = TRUE)
```

Arguments

annot_df	data.frame with factor columns
factors	Character vector of main effect names
verbose	Logical

Value

Character vector of safe interaction terms (e.g., "A:B")

`.pvca_validate_factors` *Validate that factors exist in colData*

Description

Validate that factors exist in colData

Usage

```
.pvca_validate_factors(se, factors)
```

`.rename_rownames_from_rd` *Rename rownames using IDs column*

Description

Rename rownames using IDs column

Usage

```
.rename_rownames_from_rd(x_df, rd, id_col = "IDs")
```

Arguments

`x_df`	Matrix or data frame with rownames as ProteinGroups
`rd`	rowData data frame with IDs column
`id_col`	Name of IDs column (default: "IDs")

Value

Data frame with renamed rownames

`.run_DE` *Run differential expression analysis*

Description

Internal function that coordinates DE analysis with limma.

Usage

```
.run_DE(
  se,
  comparisons,
  assay_name = NULL,
  condition_column = NULL,
  logFC = TRUE,
  logFC_up = 1,
  logFC_down = -1,
  p_adj = TRUE,
  alpha = 0.05,
  eBayes_trend = TRUE,
  eBayes_robust = TRUE,
  de_method = "limma",
  covariate_column = NULL,
  bio_replicate_column = NULL
)
```

Arguments

se	SummarizedExperiment with processed data
comparisons	Comparisons to perform (result of .specify_comparisons)
assay_name	Assay name to use. If NULL, uses the last available
condition_column	Condition column. If NULL, uses SE metadata
logFC	Apply logFC filter (default: TRUE)
logFC_up	Upper logFC threshold (default: 1)
logFC_down	Lower logFC threshold (default: -1)
p_adj	Use adjusted p-value (default: TRUE)
alpha	Significance threshold (default: 0.05)
eBayes_trend	Use trend estimation in eBayes (default: TRUE)
eBayes_robust	Use robust estimation in eBayes (default: TRUE)
de_method	DE method: "limma" or "limpa" (default: "limma")
covariate_column	Column name(s) in colData for paired/blocked design. Single string or character vector for multiple covariates (default: NULL)

Value

Data frame with DE results

.se_to_long *Convert SummarizedExperiment to long format*

Description

Convert SummarizedExperiment to long format

Usage

```
.se_to_long(se, assay_names = NULL)
```

Arguments

se	SummarizedExperiment
assay_names	Assay names to include. If NULL, uses all

Value

Data frame in long format

.sigmoid *Sigmoid function*

Description

Sigmoid function

Usage

```
.sigmoid(x, k, x0)
```

Arguments

x	Numeric vector
k	Steepness parameter
x0	Midpoint (inflection point)

Value

Numeric vector in (0, 1)

.specify_comparisons *Generate comparisons for differential analysis*

Description

Generate comparisons for differential analysis

Usage

```
.specify_comparisons(se, condition_column = NULL, control = NULL)
```

Arguments

se	SummarizedExperiment
condition_column	Condition column (if NULL, uses SE metadata)
control	Control condition. If NULL, generates all pairwise comparisons

Value

Factor with comparisons in "Treatment-Control" format

.summarize_significant_proteins *Summarize significant proteins per comparison and species*

Description

Generates a summary table with counts of significant and non-significant proteins broken down by species and direction (up/down), plus derived percentages and ratios.

Usage

```
.summarize_significant_proteins(classified_df)
```

Arguments

classified_df	Data frame from .classify_all_comparisons() with columns: Comparison, Species, logFC, truth, predicted, classification, is_significant and direction_error

Details

Significance is read from the `is_significant` column rather than recomputed, so this table can never disagree with the classification it summarizes. It used to apply only `p <= alpha`, ignoring `lfc_thr` entirely, which made the counts here larger than the ones behind the metrics whenever a fold-change threshold was in force.

Value

Data frame with per-comparison summary

.trimmed_sd_cv *Compute trimmed SD and CV*

Description

Compute trimmed SD and CV

Usage

```
.trimmed_sd_cv(x, trim = 0.1)
```

Arguments

x	Numeric vector
trim	Proportion to trim from each side (default: 0.1)

Value

Named list with trimmed_sd and trimmed_cv

.validate_de_res *Validate required columns in DE results*

Description

Validate required columns in DE results

Usage

```
.validate_de_res(de_res)
```

Arguments

de_res	Data frame with differential expression results

Value

Invisible TRUE if valid, stops with error otherwise

.validate_expected_values *Validate expected_values*

Description

`expected_values` is the ground truth of the benchmark: it decides which species are positives and which direction counts as a correct detection. A malformed row does not produce an error further down, it produces a plausible-looking benchmark, so every failure mode below is rejected here.

Usage

```
.validate_expected_values(ev)
```

Arguments

`ev`	Data frame with expected values

Value

Invisible TRUE if valid, stops with error otherwise

.validate_species_df *Validate and de-duplicate the species mapping*

Description

`species_df` is joined to the DE results on `Protein.IDs`, so a repeated identifier multiplies the rows of every comparison it appears in and inflates the counts the metrics are built from. The mapping is therefore reduced to one row per protein before the join: exact repeats are dropped, and an identifier claimed by two different species is an error, because there is no way to know which side of the truth table the protein belongs to.

Usage

```
.validate_species_df(species_df)
```

Arguments

`species_df`	Data frame with Protein.IDs and Species columns

Value

The mapping reduced to the two columns, one row per protein

.zero_to_missing *Convert zero values to NA*

Description

Replaces 0 values in a matrix or data frame with NA. Useful for DIA-NN data where 0 indicates non-detection.

Usage

```
.zero_to_missing(data)
```

Arguments

data	Numeric matrix or data frame

Value

Object of same type with 0 converted to NA

batch_correct_proteomics *Batch Correction with BERT*

Description

Applies BERT batch effect correction to a normalized assay in a SummarizedExperiment. BERT uses hierarchical tree decomposition to handle missing values, making it suitable for pre-imputation batch correction on protein-level proteomics data.

Usage

```
batch_correct_proteomics(
  se,
  assay_name,
  batch_column = "Batch",
  corrected_assay_name = "BERT",
  algorithm = "ComBat",
  ComBat_mode = 1,
  covariates = NULL,
  qualitycontrol = FALSE,
  verbose = TRUE
)
```

Arguments

se	SummarizedExperiment with a normalized assay.
assay_name	Character. Name of the input assay to correct (e.g., "cycloess").
batch_column	Character. Column in colData(se) containing batch assignments (default "Batch").
corrected_assay_name	Character. Name for the new corrected assay added to the SE (default "BERT").
algorithm	Character: "ComBat" (default), "limma", or "ref".
ComBat_mode	Integer 1-4 controlling ComBat behavior: 1 = parametric + mean+variance, 2 = parametric + mean-only, 3 = non-parametric + mean+variance, 4 = non-parametric + mean-only.
covariates	Character vector of column names from colData(se) to protect during batch correction (default NULL). These are mapped to BERT's Cov_1, Cov_2, ... format internally. BERT uses those columns directly as the design matrix and encodes nothing itself, so categorical columns are converted to indicator variables here; numeric columns are passed through unchanged and act as continuous covariates. IMPORTANT: for ComBat/limma, include here the biological variable of interest (e.g. the condition) in order to PRESERVE it; otherwise ComBat removes all batch-associated variance and can erase biological signal when condition and batch are confounded. Protecting covariates needs at least two non-missing values of a protein in every combination of batch and covariate level. Proteins that lack them are corrected for the batch alone, without protecting the covariates, so that none of their measured values is lost; BERT itself would set them to missing. With a balanced design (every condition equally represented in every batch) this is harmless; when batch and condition are unbalanced, it can remove part of the biological signal of those proteins. Their names are listed in `metadata(se)$batch_correction`.
qualitycontrol	Logical. Compute ASW (Average Silhouette Width) quality metrics for raw vs corrected data (default FALSE).
verbose	Logical (default TRUE).

Value

SummarizedExperiment with the new corrected assay added, and `metadata(se)$batch_correction`, a list naming the features kept unadjusted (`unadjusted`, no variance within a batch) and those corrected for the batch only (`batch_only`). If BERT returns fewer features than the input, the SE is subsetted to match and a warning is issued.

Examples

```
data(nadia_dia)

# nadia_dia has no batch information, so the example builds a plausible one:
# two digestion batches crossed with the three conditions.
cov <- data.frame(Column = nadia_dia$metadata$Coding,
                  Batch = rep(c("b1", "b2"),
                              length.out = nrow(nadia_dia$metadata)),
                  stringsAsFactors = FALSE)
res <- process_proteomics(nadia_dia, covariate_df = cov, verbose = FALSE)

# BERT removes the batch effect and adds a "BERT" assay, leaving the
# original one untouched
```

```
se <- batch_correct_proteomics(res$se_proc, assay_name = "Impseqrob_min",
                               batch_column = "Batch", verbose = FALSE)
SummarizedExperiment::assayNames(se)

# On a real experiment you would normally pass the biological variable of
# interest in `covariates`, so that ComBat preserves it instead of removing
# it along with the batch effect. Before imputation, a protein that lacks
# two values in some batch-by-condition cell is corrected for the batch only.
```

`benchmarking_multiple` *Multiple-method OpDEA Benchmarking*

Description

Orchestrator that imports, ranks, visualizes, and exports results from multiple normalization/imputation method combinations.

Usage

```
benchmarking_multiple(
  opdea_combined = NULL,
  confusion_combined = NULL,
  classified_combined = NULL,
  bench_metrics_combined = NULL,
  results_dir = NULL,
  pattern = "benchmark_opdea_metrics\\.tsv$",
  method_names = NULL,
  recursive = TRUE,
  strip_prefix = "benchmark_",
  metrics = .BM_METRICS,
  extended_metrics = .BM_EXTENDED_METRICS,
  p_col = "adj.P.Val",
  plots = "all",
  verbose = TRUE,
  output_dir = NULL,
  export_plots = TRUE,
  export_tables = TRUE,
  plot_width = 12,
  plot_height = 8,
  plot_dpi = 150
)
```

Arguments

`opdea_combined` Optional pre-built data.frame with columns: Assay, Comparison, nMCC, G_mean, pAUC_001, pAUC_005, pAUC_010. If NULL, results are imported from `results_dir`.

`confusion_combined` Optional pre-built data.frame with columns: Assay, Comparison, TP, FP, TN, FN. If NULL and `results_dir` is provided, imported from `benchmark_confusion_overall.tsv` files.

`classified_combined`
: Optional pre-built data.frame with columns: Assay, Comparison, truth, and a p-value column. If NULL and `results_dir` is provided, imported from `benchmark_classified.tsv` files. Used for multi-method ROC curves.

`bench_metrics_combined`
: Optional pre-built data.frame, the `metrics_table` of several `benchmarking_proteomics()` runs stacked with an Assay column. Columns: Assay, Comparison, Sensitivity, Specificity, Precision, NPV, F1, Accuracy, MCC, Performance. If NULL and `results_dir` is provided, imported from `benchmark_metrics.tsv` files. Used for extended 11-metric ranking.

`results_dir`
: Parent directory containing benchmark subfolders (each with `benchmark_opdea_metrics.tsv`). Used only if `opdea_combined` is NULL.

`pattern`
: Regex for opdea metrics filename (default: `"benchmark_opdea_metrics\.tsv$"`)

`method_names`
: Optional Assay names for file import

`recursive`
: Search subdirectories? (default: TRUE)

`strip_prefix`
: Prefix removed from each `Assay` name (default "benchmark_"), so folder-derived names in `results_dir` mode match the in-memory ones (e.g. "benchmark_Rlr_none_BERT" -> "Rlr_none_BERT"). Set to NULL or "" to keep the full folder name. Harmless when the prefix is absent.

`metrics`
: Character vector of metrics for OpDEA ranking (default: all 5 OpDEA metrics)

`extended_metrics`
: Character vector of metrics for extended ranking (default: all 11 classification + OpDEA metrics)

`p_col`
: P-value column name for ROC curves (default: "adj.P.Val")

`plots`
: Which plots to generate: "all" or character vector of names. Valid names: "ranking_heatmap_mean", "ranking_heatmap_median", "ranking_bars_mean", "ranking_bars_median", "metrics_heatmap_mean", "metrics_heatmap_median", "metrics_comparison", "extended_ranking_bars", "extended_ranking_heatmap"

`verbose`
: Print progress messages (default: TRUE)

`output_dir`
: Directory for exporting results (NULL = no export)

`export_plots`
: Export plots as PNG (default: TRUE)

`export_tables`
: Export tables as TSV (default: TRUE)

`plot_width`
: Plot width in inches (default: 12)

`plot_height`
: Plot height in inches (default: 8)

`plot_dpi`
: Plot resolution (default: 150)

Value

Named list with:

opdea_combined Combined input data.frame

mean_aggregated Mean of metrics per Assay

median_aggregated Median of metrics per Assay

mean_ranking Ranking table (mean-based)

median_ranking Ranking table (median-based)

gg_ranking_heatmap_mean Heatmap of ranks (mean)

gg_ranking_heatmap_median Heatmap of ranks (median)

gg_ranking_bars_mean Bar chart of final rank (mean)

gg_ranking_bars_median Bar chart of final rank (median)

gg_metrics_heatmap_mean Heatmap of metric values (mean)

gg_metrics_heatmap_median Heatmap of metric values (median)

gg_metrics_comparison Boxplot distributions

ranking_by_comparison Named list of ranking data.frames per comparison

ranking_by_comparison_combined data.frame with all per-comparison rankings

gg_ranking_heatmap_by_comp Named list of heatmaps per comparison

gg_ranking_bars_by_comp Named list of bar charts per comparison

confusion_combined Combined confusion data.frame (if available)

gg_confusion_stacked Faceted confusion stacked bars (if available)

gg_confusion_stacked_by_comp Named list of confusion plots per comparison

classified_combined Combined classified data.frame (if available)

gg_roc_by_comp Named list of ROC plots per comparison (if available)

gg_roc_zoom_by_comp Named list of ROC zoom plots per comparison (if available)

extended_combined Merged classification + OpDEA data (if bench_metrics available)

extended_mean_aggregated Mean-aggregated extended metrics per Assay

extended_ranking Extended ranking table (11 metrics, mean-based)

gg_extended_ranking_bars Bar chart of extended ranking

gg_extended_ranking_heatmap Heatmap of extended ranking

parameters List of parameters used

Examples

```
data(nadia_dia)
sp <- utils::read.delim(system.file("extdata", "nadia_dia_spikein.tsv.gz",
                                    package = "NADIA"))
ev <- data.frame(Comparison = rep(c("B-A", "D-A"), each = 2),
                 Species = c("ECOLI", "YEAST"),
                 expected_logFC = c(1, -0.58, 2, -3.3))
root <- file.path(tempdir(), "nadia_bench")
for (nm in c("cycloess", "quantile")) {
  de <- process_proteomics(nadia_dia, norm_method = nm,
                           verbose = FALSE)$DEPs_results
  de$Species <- sp$PG.OrganismId[match(de$Protein.IDs, sp$PG.ProteinGroups)]
  benchmarking_proteomics(de, ev, output_dir = file.path(root, nm),
                          verbose = FALSE)
}
result <- benchmarking_multiple(results_dir = root, verbose = FALSE)
result$mean_ranking
result$gg_ranking_bars_mean
```

benchmarking_proteomics *Benchmark Proteomics Differential Expression Results*

Description

Evaluates the reliability of DE results by comparing them against known ground truth (multi-species spike-in experiments). Computes classification metrics, dispersion statistics, and generates visualizations.

Usage

```
benchmarking_proteomics(
  de_res,
  expected_values,
  alpha = 0.05,
  lfc_thr = 0,
  p_col = "adj.P.Val",
  comparisons = NULL,
  assay = NULL,
  output_dir = NULL,
  verbose = TRUE,
  species_colors = NULL,
  species_df = NULL
)
```

Arguments

de_res	Data frame with DE results. Required columns: Protein.IDs, logFC, P.Value, adj.P.Val, Change, Comparison. Optional: Gene.Names, Assay, Species (if not using species_df).
expected_values	Data frame with expected values. Required columns: Comparison, Species, expected_logFC.
alpha	Significance threshold (default: 0.05)
lfc_thr	Log fold-change threshold (default: 0)
p_col	P-value column to use (default: "adj.P.Val")
comparisons	Comparisons to include (NULL = all)
assay	Assay to filter (NULL = all)
output_dir	Directory for exported files (NULL = no export)
verbose	Print progress messages (default: TRUE)
species_colors	Named vector of colors per species (optional)
species_df	Data frame with Protein.IDs and Species columns (optional). If NULL, de_res must already contain a Species column.

Value

List with:

- metrics_table: Classification metrics per comparison
- confusion_by_species: Confusion matrix per Comparison x Species
- confusion_overall: Confusion matrix aggregated per Comparison
- dispersion_metrics: Dispersion stats per Comparison x Species
- classified_df: Full classified data frame
- gg_heatmap: ggplot2 performance heatmap
- gg_confusion_by_species: ggplot2 confusion matrix heatmap (by species)
- gg_confusion_overall: ggplot2 confusion matrix heatmap (aggregated)
- gg_auc_bars: ggplot2 AUC bar chart
- gg_metrics_bars: ggplot2 grouped metrics bar chart
- gg_signif_bars: ggplot2 significant proteins stacked bars (absolute)
- hc_volcano_list: Named list of Highcharter volcano plots (empty if the suggested package highcharter is not installed)
- parameters: List of parameters used

Examples

```
data(nadia_dia)
de <- process_proteomics(nadia_dia, verbose = FALSE)$DEPs_results
sp <- utils::read.delim(system.file("extdata", "nadia_dia_spikein.tsv.gz",
                                    package = "NADIA"))
species_df <- data.frame(Protein.IDs = sp$PG.ProteinGroups,
                         Species = sp$PG.OrganismId)
ev <- data.frame(Comparison = rep(c("B-A", "D-A"), each = 2),
                 Species = c("ECOLI", "YEAST"),
                 expected_logFC = c(1, -0.58, 2, -3.3))
bench <- benchmarking_proteomics(de, ev, species_df = species_df,
                                 verbose = FALSE)
bench$metrics_table
bench$gg_heatmap
```

---

boxplot_highchart_list

Interactive Highcharts Boxplot for Proteomics

Description

Interactive Highcharts Boxplot for Proteomics

Usage

```
boxplot_highchart_list(
  data,
  assays = NULL,
  color_by = "Condition",
  group_order = NULL,
  palette = NULL,
  title = NULL,
  subtitle = NULL,
  show_outliers = TRUE,
  outlier_jitter = 0.15,
  outlier_size = 3,
  box_width = 20,
  horizontal = TRUE,
  height = NULL
)
```

Arguments

data	Data frame with columns: Column, Assay, Intensity, Condition
assays	Vector of assays to include (NULL = all of them)
color_by	Column used for colouring (default: "Condition")
group_order	Order of the groups/conditions
palette	Colour palette: NULL for the default; "pkg::name" for a palette from paletteer; "brewer:Name", or the bare name, for an RColorBrewer palette; or a vector of colours, unnamed or named after the groups. A palette with fewer colours than groups is interpolated.
title	Chart title (optional). Use {assay} as a placeholder (e.g. "Boxplot: {assay}" -> "Boxplot: ImpSeqRob_Min")
subtitle	Chart subtitle (optional). Use {assay} as a placeholder
show_outliers	Show outliers lying outside the whiskers (default: TRUE)
outlier_jitter	Amount of horizontal jitter applied to the outliers (default: 0.15)
outlier_size	Radius of the outlier points (default: 3)
box_width	Width of the boxplot boxes in pixels (default: 20)
horizontal	Horizontal orientation (default: TRUE)
height	Chart height in pixels

Value

List of highchart objects (one per assay)

Examples

```
if (requireNamespace("highcharter", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)

  # One boxplot per assay; keep only the imputed one
  hc_list <- boxplot_highchart_list(
```

```
    res$BoxPlot_Input,
    assays      = "Impseqrob_min",
    group_order = c("A", "B", "D"),
    title       = "Boxplot: {assay}"
  )
  names(hc_list)
}
```

`build_clustering_matrix` *Build the clustering matrix aggregated by condition*

Description

Build the clustering matrix aggregated by condition

Usage

```
build_clustering_matrix(
  intensity_matrix,
  sample_metadata,
  selected_features,
  condition_order = NULL,
  aggregate = c("median", "mean"),
  verbose = TRUE
)
```

Arguments

`intensity_matrix`	Intensity matrix (features x samples)
`sample_metadata`	DataFrame with SampleID, Condition
`selected_features`	Vector of features to include
`condition_order`	Condition order (NULL = alphabetical order)
`aggregate`	Aggregation method: "median" or "mean"
`verbose`	Print progress messages (default: TRUE)

Value

Matrix of aggregated intensities (features x conditions)

build_long_output *Build the output table in LONG format*

Description

Creates one row per FeatureID-Cluster combination where membership >= min_membership. This lets a protein appear in several clusters (soft clustering).

Usage

```
build_long_output(cl, eset_std, conditions, min_membership)
```

Arguments

cl	Mfuzz clustering object
eset_std	Standardised ExpressionSet (with z-scores)
conditions	Vector of condition names
min_membership	Minimum membership threshold

Value

DataFrame in long format

build_pca_scores *Build a PCA scores data frame from data in long format*

Description

Build a PCA scores data frame from data in long format

Usage

```
build_pca_scores(
  pca_input,
  mode = c("all", "any", "specific"),
  alpha = 0.05,
  comparison = NULL,
  subset_label = NULL,
  center = TRUE,
  scale. = TRUE,
  filter_samples_to_comparison = FALSE,
  cond_col = "Condition"
)
```

Arguments

pca_input	Data frame in long format with columns: • SampleID: Sample identifier • FeatureID: Protein/feature identifier • Intensity: Intensity value (log2) • Condition: Experimental condition • Replicate: Replicate number (optional) • sig_any: Logical flagging significance in any comparison (for mode="any") • adjP_*: Adjusted p-value columns, one per comparison (for mode="specific")
mode	Protein filtering mode: "all", "any", or "specific"
alpha	Significance threshold for mode "specific" (default: 0.05)
comparison	Name of the comparison for mode "specific" (e.g. "B-A")
subset_label	Custom label for the subset (optional)
center	Center the data before PCA (default: TRUE)
scale.	Scale the data before PCA (default: TRUE)
filter_samples_to_comparison	Restrict samples to the conditions involved in the specific comparison (default: FALSE)
cond_col	Name of the condition column (default: "Condition")

Value

Data frame with columns: SampleID, PC1, PC2, PC1_Perc, PC2_Perc, Subset, Condition, Replicate

Examples

```
data(nadia_dia)
res <- process_proteomics(nadia_dia, verbose = FALSE)

# Scores and the variance explained by the first two components
scores <- build_pca_scores(res$PCA_Input, mode = "all")
head(scores)
unique(scores[c("PC1_Perc", "PC2_Perc")])
```

---

cluster_centroids_highchart

Centroid plot for all the clusters

Description

Builds a comparative plot with the centroids of all the clusters.

Usage

```
cluster_centroids_highchart(
  data,
  conditions = NULL,
  clusters = NULL,
  min_membership = NULL,
  centroid_summary = c("mean", "median"),
  palette = NULL,
  line_width = 2.5,
  show_markers = TRUE,
  title = NULL,
  height = NULL
)
```

Arguments

data	Pattern Profiler DataFrame (LONG format)
conditions	Vector of condition names
clusters	Clusters to include (NULL = all)
min_membership	Membership filter applied before computing the centroids
centroid_summary	Method: "mean" or "median"
palette	Colour palette: NULL for the default; "pkg::name" for a palette from paletteer; "brewer:Name", or the bare name, for an RColorBrewer palette; or a vector of colours. A palette with fewer colours than clusters is interpolated.
line_width	Line width (default: 2.5)
show_markers	Show markers on the points (default: TRUE)
title	Custom title
height	Plot height

Value

highchart object

Examples

```
if (requireNamespace("highcharter", quietly = TRUE) &&
    requireNamespace("Mfuzz", quietly = TRUE) &&
    requireNamespace("e1071", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)
  pp <- pattern_profiler_analysis(res$se_proc, res$DEPs_results,
                                  assay_name = "Impseqrob_min",
                                  auto_select_c = FALSE, c = 3,
                                  verbose = FALSE)

  # All the cluster centroids on one chart
  hc <- cluster_centroids_highchart(pp$long_output,
                                    conditions = c("A", "B", "D"),
                                    centroid_summary = "median")
  print(class(hc))
```

```
}
```

`cluster_profile_highchart` *Cluster profile plot with Highcharts*

Description

Builds an interactive plot showing the expression profiles of the proteins in a given cluster.

Usage

```
cluster_profile_highchart(
  data,
  cluster,
  conditions = NULL,
  min_membership = NULL,
  show_centroid = TRUE,
  centroid_summary = c("mean", "median"),
  cluster_color = NULL,
  line_width = 1,
  line_opacity = 0.4,
  centroid_width = 3,
  title = NULL,
  height = NULL
)
```

Arguments

`data`	Pattern Profiler DataFrame (LONG format)
`cluster`	Number of the cluster to plot
`conditions`	Vector of condition names (order for the X axis)
`min_membership`	Additional membership filter (NULL = no filter)
`show_centroid`	Show the centroid line (default: TRUE)
`centroid_summary`	Method for the centroid: "mean" or "median"
`cluster_color`	Cluster colour (NULL = automatic)
`line_width`	Width of the profile lines (default: 1)
`line_opacity`	Opacity of the lines (default: 0.4)
`centroid_width`	Width of the centroid line (default: 3)
`title`	Custom title (optional)
`height`	Plot height in pixels

Value

highchart object

Examples

```
if (requireNamespace("highcharter", quietly = TRUE) &&
    requireNamespace("Mfuzz", quietly = TRUE) &&
    requireNamespace("e1071", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)
  pp <- pattern_profiler_analysis(res$se_proc, res$DEPs_results,
                                  assay_name = "Impseqrob_min",
                                  auto_select_c = FALSE, c = 3,
                                  verbose = FALSE)

  hc <- cluster_profile_highchart(pp$long_output, cluster = 1,
                                  conditions = c("A", "B", "D"))
  print(class(hc))
}
```

---

cluster_profile_highchart_list

List of cluster profile plots with Highcharts

Description

Builds a list of interactive plots for all the clusters.

Usage

```
cluster_profile_highchart_list(
  data,
  conditions = NULL,
  clusters = NULL,
  min_membership = NULL,
  show_centroid = TRUE,
  centroid_summary = c("mean", "median"),
  palette = NULL,
  line_width = 1,
  line_opacity = 0.4,
  centroid_width = 3,
  height = NULL
)
```

Arguments

data	Pattern Profiler DataFrame (LONG format)
conditions	Vector of condition names
clusters	Vector of clusters to plot (NULL = all)
min_membership	Minimum membership filter
show_centroid	Show the centroid line (default: TRUE)
centroid_summary	Method for the centroid: "mean" or "median"

palette	Colour palette: NULL for the default; "pkg::name" for a palette from paletteer; "brewer:Name", or the bare name, for an RColorBrewer palette; or a vector of colours. A palette with fewer colours than clusters is interpolated.
line_width	Width of the profile lines (default: 1)
line_opacity	Opacity of the lines (default: 0.4)
centroid_width	Width of the centroid line (default: 3)
height	Height of each plot in pixels

Value

Named list of highchart objects

Examples

```
if (requireNamespace("highcharter", quietly = TRUE) &&
    requireNamespace("Mfuzz", quietly = TRUE) &&
    requireNamespace("e1071", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)
  pp <- pattern_profiler_analysis(res$se_proc, res$DEPs_results,
                                  assay_name = "Impseqrob_min",
                                  auto_select_c = FALSE, c = 3,
                                  verbose = FALSE)

  hc_profiles <- cluster_profile_highchart_list(pp$long_output,
                                                conditions = c("A", "B", "D"))
  print(names(hc_profiles))
}
```

---

compute_confidence_ellipse

Compute the confidence ellipse per group

Description

Computes the coordinates of a confidence ellipse based on the chi-squared distribution, similar to FactoMineR::coord.ellipse and ggplot2::stat_ellipse.

Usage

```
compute_confidence_ellipse(
  scores_df,
  group_col = "Condition",
  level = 0.95,
  npoints = 100
)
```

Arguments

scores_df	Data frame with columns PC1, PC2 and the grouping column
group_col	Name of the grouping column (default: "Condition")
level	Confidence level (default: 0.95)
npoints	Number of points used to draw the ellipse (default: 100)

Value

List of data frames, each one with columns: group, x, y

---

compute_hulls *Compute the convex hull (enclosing polygon) per group*

Description

Compute the convex hull (enclosing polygon) per group

Usage

```
compute_hulls(scores_df, group_col = "Condition")
```

Arguments

scores_df	Data frame with columns PC1, PC2 and the grouping column
group_col	Name of the grouping column (default: "Condition")

Value

List of data frames, each one with columns: group, x, y

---

configure_cluster_palette *Configure the colour palette for the clusters*

Description

Configure the colour palette for the clusters

Usage

```
configure_cluster_palette(n_clusters, palette = NULL)
```

Arguments

n_clusters	Number of clusters
palette	Colour palette: NULL for the default; "pkg::name" for a palette from paletteer; "brewer:Name", or the bare name, for an RColorBrewer palette; or a vector of colours. A palette with fewer colours than clusters is interpolated.

Value

Vector of colours named by cluster

---

create_expression_set *Create an ExpressionSet for Mfuzz*

Description

Create an ExpressionSet for Mfuzz

Usage

```
create_expression_set(mat, feature_info = NULL)
```

Arguments

mat	Expression matrix (features x conditions)
feature_info	DataFrame with feature information (optional)

Value

ExpressionSet object

---

deps_with_clusters *Differential abundance with the Pattern Profiler cluster of each protein*

Description

Joins the differential-abundance results to the soft clustering, giving the table a functional-enrichment or over-representation analysis needs: the statistics that say which proteins moved, and the cluster that says which pattern they follow.

Usage

```
deps_with_clusters(
  DEPs_results,
  pattern_profiler,
  assignment = c("primary", "all"),
  min_membership = NULL,
  comparison = NULL,
  significant_only = FALSE
)
```

Arguments

DEPs_results	Differential-abundance results, the DEPs_results element of process_proteomics(). Needs at least Protein.IDs and Comparison.
pattern_profiler	Result of pattern_profiler_analysis(), or NULL for no clustering at all, in which case the three cluster columns are returned as NA and the shape of the table is unchanged.
assignment	"primary" (default) for one row per protein and comparison, carrying the cluster of highest membership; "all" for one row per protein, comparison and cluster.
min_membership	Optional extra membership threshold. It can only be stricter than the one the analysis ran with: pairs below that one were discarded when long_output was built and cannot be recovered here. A protein left with no cluster keeps its row, with NA.
comparison	Optional character vector of comparisons to keep. The default, NULL, keeps them all.
significant_only	Keep only the rows classified Up or Down. The classification is the one the analysis made, with its own alpha and logFC_threshold; nothing is recomputed here.

Details

The join is a left join from the results, so **every protein that was tested survives it**, with or without a cluster. That matters more than it looks: the complete set of tested proteins is the background an enrichment is computed against, and a protein with no cluster – one that was never selected for the clustering, or that the clustering dropped – belongs in that background rather than in the bin.

Clustering is fuzzy, so a protein can belong to several clusters at once. assignment decides what to do about it. "primary" keeps only the dominant pattern of each protein and returns exactly one row per protein and comparison, which is what most enrichment tools expect. "all" keeps every association above the threshold, which is the honest representation of a soft clustering and the one to use when the analysis downstream can weight by membership.

Value

A data frame with the columns of DEPs_results followed by Cluster, Membership and ClusterRank (1 is the protein's dominant cluster).

See Also

nadia_deps_with_clusters() for the same table read from a .nadia file, and pattern_profiler_analysis() for the clustering.

Examples

```
data(nadia_dia)
res <- process_proteomics(nadia_dia, verbose = FALSE)

# Without a clustering the shape is the same and the clusters are NA.
fi <- deps_with_clusters(res$DEPs_results, NULL)
head(fi)
```

```
if (requireNamespace("Mfuzz", quietly = TRUE) &&
    requireNamespace("Biobase", quietly = TRUE) &&
    requireNamespace("e1071", quietly = TRUE)) {
    pp <- pattern_profiler_analysis(res$se_proc, res$DEPs_results,
                                    assay_name = "Impseqrob_min",
                                    verbose = FALSE)

    primary <- deps_with_clusters(res$DEPs_results, pp)
    nrow(primary) == nrow(res$DEPs_results)   # the background is intact

    soft <- deps_with_clusters(res$DEPs_results, pp, assignment = "all")
    table(soft$ClusterRank)
}
```

`detect_condition_columns` *Detect the condition columns (z-scores)*

Description

Detect the condition columns (z-scores)

Usage

```
detect_condition_columns(data)
```

Arguments

`data`	Pattern Profiler DataFrame

Value

Vector with the names of the condition columns

`de_analysis_proteomics` *Perform differential expression analysis on proteomics data*

Description

Coordinates comparison specification, limma analysis, and result extraction.

Usage

```
de_analysis_proteomics(
  se,
  assay_name = NULL,
  comparisons = NULL,
  control = NULL,
  logFC_threshold = 0,
  alpha = 0.05,
  p_adj = TRUE,
  eBayes_trend = NULL,
  eBayes_robust = NULL,
  de_method = "limma",
  covariate_column = NULL,
  bio_replicate_column = NULL,
  condition_column = "Condition",
  verbose = TRUE
)
```

Arguments

se	SummarizedExperiment with imputed assay (output of impute_proteomics)
assay_name	Assay name to use. If NULL, uses the last available assay
comparisons	Comparisons to perform. If NULL, auto-generates (pairwise or vs control)
control	Control condition. If NULL, generates all pairwise comparisons
logFC_threshold	LogFC threshold for significance (default: 0)
alpha	Adjusted p-value threshold (default: 0.05)
p_adj	Use adjusted p-value (default: TRUE)
eBayes_trend	Use trend estimation in eBayes (default: TRUE, recommended for proteomics)
eBayes_robust	Use robust estimation in eBayes (default: TRUE, recommended for proteomics)
de_method	DE method: "limma" (default) or "limpa" (probabilistic, requires imp_method="limpa")
covariate_column	Column name(s) in colData for paired/blocked design. Single string (e.g., "Subject") or character vector (e.g., c("Subject", "Batch")). Default: NULL
bio_replicate_column	Column name in colData identifying biological replicates (e.g., "Patient", "Subject"). Used with limma::duplicateCorrelation() to account for technical replicates or paired designs via random effect blocking. Default: NULL
condition_column	Condition column name (default: "Condition")
verbose	Print progress messages (default: TRUE)

Value

List with:

- DEPs_results: Data frame with differential expression results
- comparisons: Comparisons performed
- assay_name: Assay name used

Examples

```
data(nadia_dia)
norm <- normalize_proteomics(nadia_dia, norm_method = "cycloess",
                             verbose = FALSE)
imp  <- impute_proteomics(norm$se, normalized_assay_name = "cycloess",
                          verbose = FALSE)

# All pairwise comparisons
de <- de_analysis_proteomics(imp$se, assay_name = "Impseqrob_min",
                             verbose = FALSE)
head(de$DEPs_results[, c("Protein.IDs", "Comparison", "logFC", "adj.P.Val")])

# Or every condition against a single control
de2 <- de_analysis_proteomics(imp$se, assay_name = "Impseqrob_min",
                              control = "A", verbose = FALSE)
unique(de2$DEPs_results$Comparison)
```

`evaluate_cluster_range`

Evaluate a range of cluster numbers

Description

Evaluate a range of cluster numbers

Usage

```
evaluate_cluster_range(
  eset_std,
  c_range = 2:10,
  m = NULL,
  n_starts = 3L,
  verbose = TRUE
)
```

Arguments

`eset_std`	Standardised ExpressionSet
`c_range`	Vector of cluster numbers to evaluate
`m`	Fuzziness parameter
`n_starts`	Number of random starts per candidate number of clusters; the metrics are averaged over them. Drawn from the caller's RNG.
`verbose`	Show progress

Value

DataFrame with the metrics per number of clusters

extract_se_data *Extract data from a SummarizedExperiment*

Description

Retrieves the intensity matrix, the feature IDs and the sample metadata from a SummarizedExperiment object.

Usage

```
extract_se_data(se_proc, assay_name = NULL, verbose = TRUE)
```

Arguments

se_proc	SummarizedExperiment object
assay_name	Name of the assay to use (NULL = first available)
verbose	Print progress messages (default: TRUE)

Value

List with:

- intensity_matrix: features x samples matrix
- feature_ids: vector of protein IDs
- sample_metadata: DataFrame with SampleID, Condition, etc.

filter_significant_features *Filter features by significance*

Description

Filter features by significance

Usage

```
filter_significant_features(
  feature_info,
  filter_mode = c("any", "all", "specific"),
  comparison = NULL,
  alpha = 0.05,
  verbose = TRUE
)
```

Arguments

feature_info	DataFrame with significance columns
filter_mode	Selection mode: • "any": features significant in AT LEAST one comparison (uses sig_any). • "all": ALL features, with no significance filtering (it does NOT mean "significant in every comparison"). • "specific": significant in the comparison given by comparison.
comparison	Specific comparison (for mode="specific")
alpha	Significance threshold
verbose	Print progress messages (default: TRUE)

Value

Vector of the selected FeatureIDs

---

get_annotation_palette *Build the Colour Palette for Categorical Annotations*

Description

Build the Colour Palette for Categorical Annotations

Usage

```
get_annotation_palette(levels, palette = NULL)
```

Arguments

levels	Vector of levels (categories)
palette	Colour palette: NULL for the default; "pkg::name" for a palette from paletteer; "brewer:Name", or the bare name, for an RColorBrewer palette; or a vector of colours, unnamed or named after the groups. A palette with fewer colours than levels is interpolated.

Value

Named vector of colours

get_heatmap_palette *Build the Colour Palette for the Heatmap Values*

Description

Build the Colour Palette for the Heatmap Values

Usage

```
get_heatmap_palette(palette = NULL, n = 11, reverse = FALSE)
```

Arguments

palette	Palette for the values, used as a colour ramp: NULL for the default (blue-white-red); "pkg::name" for a palette from paletteer; "brewer:Name", or the bare name, for an RColorBrewer palette (up to n colours); or a vector of colours.
n	Number of colours to generate
reverse	Reverse the palette (default: FALSE)

Value

Vector of colours, or a colorRamp2 function

import_imp_matrices *Import imputed matrices into a SummarizedExperiment*

Description

Reads all TSV files matching a pattern from a directory, one assay per file. Each TSV must have column 1 as protein identifier and remaining columns as sample names matching the sample_col in the metadata file.

Usage

```
import_imp_matrices(
  tsv_dir,
  metadata_path,
  pattern = "matrix_log2_.*\\.tsv$",
  method_names = NULL,
  condition_col = "Condition",
  sample_col = "Column"
)
```

Arguments

tsv_dir	Character. Directory containing the TSV files.
metadata_path	Character. Path to a TSV or CSV file with at minimum columns sample_col and condition_col.
pattern	Character. Regex to filter files in tsv_dir. Default: "matrix_log2_.*\\.tsv$".
method_names	Character vector. Assay names to assign (in order). NULL (default) = extracted from file names between matrix_log2_ and .tsv.
condition_col	Character. Column in metadata with condition/group labels.
sample_col	Character. Column in metadata with sample names.

Value

A SummarizedExperiment with one assay per TSV, colData from metadata, and rowData containing Protein.IDs.

Examples

```
# Round trip: write the imputed matrices out, then read them back in
data(nadia_dia)
res <- process_proteomics(nadia_dia, export_dir = tempdir(),
                          export_format = "tsv", verbose = FALSE)

meta <- file.path(tempdir(), "metadata.tsv")
utils::write.table(
  data.frame(Column = res$se_proc$Column, Condition = res$se_proc$Condition,
             Replicate = res$se_proc$Replicate),
  meta, sep = "\t", row.names = FALSE, quote = FALSE)

se <- import_imp_matrices(tsv_dir = tempdir(), metadata_path = meta)
SummarizedExperiment::assayNames(se)
```

---

import_norm_matrices *Import normalized matrices into a SummarizedExperiment*

Description

Reads all TSV files matching a pattern from a directory, one assay per file. Each TSV must have column 1 named ProteinGroups and remaining columns as sample names matching the sample_col in the metadata file.

Usage

```
import_norm_matrices(
  tsv_dir,
  metadata_path,
  pattern = "matrix_log2_.*\\.tsv$",
  method_names = NULL,
  condition_col = "Condition",
  sample_col = "Column"
)
```

Arguments

tsv_dir	Character. Directory containing the normalized TSV files.
metadata_path	Character. Path to a TSV or CSV file with at minimum columns sample_col and condition_col.
pattern	Character. Regex to filter files in tsv_dir. Default: "matrix_log2_.*\\.tsv$".
method_names	Character vector. Assay names to assign (in order). NULL (default) = extracted from file names between matrix_log2_ and .tsv.
condition_col	Character. Column in metadata with condition/group labels.
sample_col	Character. Column in metadata with sample names.

Value

A SummarizedExperiment with one assay per TSV, colData from metadata, and rowData containing Protein.IDs.

Examples

```
data(nadia_dia)
se <- nm_prepare_se(nadia_dia, verbose = FALSE)
se <- nm_run_normalizations(se, methods = c("cycloess", "MAD"), verbose = FALSE)

# Write the normalized assays as TSVs, then read them back into a new SE
tsv_dir <- file.path(tempdir(), "nm_matrices")
dir.create(tsv_dir, showWarnings = FALSE)
for (a in c("cycloess", "MAD")) {
  m <- SummarizedExperiment::assay(se, a)
  utils::write.table(
    data.frame(ProteinGroups = rownames(m), m, check.names = FALSE),
    file.path(tsv_dir, paste0("matrix_log2_", a, ".tsv")),
    sep = "\t", row.names = FALSE, quote = FALSE)
}
meta_path <- file.path(tsv_dir, "metadata.tsv")
utils::write.table(as.data.frame(SummarizedExperiment::colData(se)), meta_path,
                   sep = "\t", row.names = FALSE, quote = FALSE)

se_nm <- import_norm_matrices(tsv_dir, meta_path)
SummarizedExperiment::assayNames(se_nm)
```

---

imputation_metrics *Generate imputation quality metric plots and ranking*

Description

Computes NRMSE, SOR, PSS, ACC_OI via ground-truth simulation, then generates up to 6 diagnostic plots. Each plot is wrapped in tryCatch() so that a failure in one does not abort all.

Usage

```
imputation_metrics(
  se,
  assay_name = NULL,
  methods = .IM_BENCH_METHODS,
  combo_methods = list(),
  condition_col = "Condition",
  na_prop = 0.2,
  pattern = "random",
  method_args = list(),
  with_value = NA_real_,
  plots = "all",
  verbose = TRUE,
  output_dir = NULL,
  export_plots = TRUE,
  export_tables = TRUE,
  plot_width = 12,
  plot_height = 8,
  plot_dpi = 150
)
```

Arguments

se	SummarizedExperiment (from `import_imp_matrices()` or pipeline).
assay_name	Character. Assay name to use as starting point. NULL (default) = first assay.
methods	Character vector of individual methods to benchmark. Default: `.IM_BENCH_METHODS` (15 methods). Use `NULL` or `character(0)` to skip individual methods when only using combo_methods.
combo_methods	Named list of combo/softHybrid configurations. Each element is a list with: `mode` ("combo" or "softHybrid", default "combo"), `mar_method`, `mnar_method`. The list name is used as the method label in results. Default: empty list (no combo methods).
condition_col	Character. Column in colData for combo methods. Default `"Condition"`.
na_prop	Numeric (0-1). Proportion of artificial NAs. Default 0.20. Only used when `pattern = "random"`. Ignored when `pattern = "from_data"` (NA proportion is derived from the data, replicating NAguideR).
pattern	Character. `"random"` or `"from_data"`. Default `"random"`.
method_args	Named list of per-method argument lists.
with_value	Constant for method `"with"`.
plots	Character vector of plot names or `"all"` (default). Valid: `"nrmse"`, `"sor"`, `"pss"`, `"acc_oi"`, `"ranking"`, `"metrics"`.
verbose	Logical. Print progress. Default TRUE.
output_dir	Character. Path to export directory. If `NULL` (default), no files are exported. When set, tables (TSV) and/or plots (PNG) are saved to this directory (created if needed).
export_plots	Logical. Export plots as PNG when `output_dir` is set. Default `TRUE`.
export_tables	Logical. Export tables as TSV when `output_dir` is set. Default `TRUE`.
plot_width	Numeric. Width in inches for exported plots. Default `12`.

plot_height	Numeric. Height in inches for exported plots. Default 8.
plot_dpi	Numeric. Resolution for exported plots. Default 150.

Value

Named list of ggplot objects (or NULL for failed plots), plus metrics_table: a data.frame with one row per method and the columns NRMSE, SOR, PSS, ACC_OI and Rank_Mean.

Reproducibility

The cells masked to build the ground truth are drawn from the caller's RNG, and so are the imputations of the stochastic methods (MinProb, QRILC, PI, mice, missForest, MLE). Call set.seed() beforehand to reproduce a run.

Examples

```
data(nadia_dia)
se <- im_prepare_se(nadia_dia, norm_method = "cycloess", verbose = FALSE)

# The default sweeps 15 methods; a handful is enough to illustrate it
set.seed(42)
res <- imputation_metrics(se, methods = c("min", "zero", "knn"),
                          plots = "ranking", verbose = FALSE)
res$metrics_table

# Two-stage combos can be compared alongside the individual methods
res2 <- imputation_metrics(se, methods = c("min", "knn"),
  combo_methods = list(
    "Impseq+min" = list(mar_method = "Impseq", mnar_method = "min")),
  plots = "ranking", verbose = FALSE)
res2$metrics_table$Method
```

---

impute_proteomics *Impute proteomics data*

Description

Complete imputation pipeline with 19 methods. Four pathways:

Usage

```
impute_proteomics(
  se,
  normalized_assay_name = "cycloess",
  imputed_assay_name = NULL,
  imp_method = "combo",
  mar_method = "Impseqrob",
  mnar_method = "min",
  prop_na_mnar = 0.51,
  prop_present_mar = 0.5,
  min_present_mar = 1,
  require_n_conditions = 1,
```

```
  max_na_prop = NULL,
  method_args = list(),
  with_value = NA_real_,
  verbose = TRUE
)
```

Arguments

se	SummarizedExperiment with normalized assay
normalized_assay_name	Name of the normalized assay to use (default: "cycloess")
imputed_assay_name	Name for the imputed assay. If NULL, it is built from the method: combo gives <mar_method>_<mnar_method>, softHybrid gives softHybrid_<mar_method>_<mnar_method>, and any single method gives its own name.
imp_method	Imputation method (default: "combo"). One of: "combo", "softHybrid", "bpca", "knn", "mice", "missForest", "Impseq", "Impseqrob", "QRILC", "MLE", "MinDet", "MinProb", "PI", "min", "halfmin", "zero", "with", "limpa", "none". "halfmin" is the DIA-NN half-minimum recipe: since the assay is on the log2 scale, halving the intensity means one unit below the global observed minimum.
mar_method	MAR method for combo/softHybrid mode (default: "Impseqrob")
mnar_method	MNAR method for combo/softHybrid mode (default: "min")
prop_na_mnar	NA proportion threshold for MNAR classification (default: 0.51)
prop_present_mar	Present proportion for MAR (default: 0.5)
min_present_mar	Minimum present values for MAR (default: 1)
require_n_conditions	Number of conditions required with presence (default: 1)
max_na_prop	Maximum NA proportion above which a protein is removed before imputation. NULL (the default) disables the filter, so every method receives the same proteins.
method_args	Named list of per-method argument lists (e.g., list(knn = list(k = 10), bpca = list(nPcs = 3))). For missForest, observations = "samples" fits the forests on the samples, as NAguideR does, instead of on the proteins (the default).
with_value	Constant value for imp_method="with" (default: NA_real_)
verbose	Print progress messages (default: TRUE)

Details

- imp_method = "none": no imputation
- imp_method = "combo": two-stage MAR+MNAR with binary classification
- imp_method = "softHybrid": sigmoid-weighted MAR+MNAR blend (continuous)
- Any other method: apply to all NAs (no MAR/MNAR distinction)

Value

List with:

- se: SummarizedExperiment with imputed assay added

- x_imputed: Raw imputed matrix (for direct export)
- prefilter_summary: Pre-filtering summary
- imputation_summary: Imputation statistics
- mnar_mask: MNAR mask matrix (combo only, NULL otherwise)
- mar_mask: MAR mask matrix (combo only, NULL otherwise)

Examples

```
data(nadia_dia)
norm <- normalize_proteomics(nadia_dia, norm_method = "cycloess",
                             verbose = FALSE)

# Default: two-stage combo, Impseqrob for MAR and min for MNAR
imp <- impute_proteomics(norm$se, normalized_assay_name = "cycloess",
                         verbose = FALSE)
SummarizedExperiment::assayNames(imp$se)
sum(is.na(SummarizedExperiment::assay(imp$se, "Impseqrob_min")))

# Any single method works too, and per-method options go in method_args
imp2 <- impute_proteomics(norm$se, normalized_assay_name = "cycloess",
                          imp_method = "knn",
                          method_args = list(knn = list(k = 15)),
                          verbose = FALSE)
SummarizedExperiment::assayNames(imp2$se)
```

---

im_prepare_se *Build a SummarizedExperiment for imputation benchmarking*

Description

Convenience function that creates a SE from a `proteomics_data` object and applies the winning normalization method (from normalization benchmarking). The result is ready for `imputation_metrics()`.

Usage

```
im_prepare_se(
  preprocessing,
  norm_method = NULL,
  pc1_rank = NULL,
  min_reps = NULL,
  min_groups = 1,
  covariate_df = NULL,
  norm_method_args = list(),
  include_log2 = TRUE,
  verbose = TRUE
)
```

Arguments

preprocessing	A proteomics_data object, from any of the preprocess_*() functions.
norm_method	Character scalar. Normalization method name (e.g. "cycloess"). If provided, used directly. Default NULL.
pc1_rank	The pc1_rank data.frame returned by normalization_metrics(). The first row's Method column is used as winner. Ignored if norm_method is provided. Default NULL.
min_reps	Minimum replicates with non-NA values per group for protein filtering. If NULL, auto-computed as half the smallest group. Default NULL.
min_groups	Minimum groups meeting min_reps (default: 1).
covariate_df	Optional covariate data.frame for paired designs (must contain a Column column). Default NULL.
norm_method_args	Named list of per-method arguments for normalization. Default list().
include_log2	Logical. Include the baseline "log2" assay in the returned SE. Default TRUE. Ignored when the method is "log2" itself, whose only assay is the baseline.
verbose	Logical. Print progress messages. Default TRUE.

Details

Internally calls nm_prepare_se() to build the baseline SE with assay "log2", then applies the chosen normalization via .norm_dispatch().

Value

SummarizedExperiment with assays "log2" (optional) + winner method; only "log2" when that is the method.

Examples

```
data(nadia_dia)

# Option A: name the normalization to benchmark imputation on
se <- im_prepare_se(nadia_dia, norm_method = "cycloess", verbose = FALSE)
SummarizedExperiment::assayNames(se)

# Option B: let the winner of normalization_metrics() decide. That function
# takes a SummarizedExperiment, so the baseline is built first.
se_base <- nm_prepare_se(nadia_dia, verbose = FALSE)
nm <- normalization_metrics(se_base,
                            methods = c("cycloess", "quantile", "MAD"),
                            plots = "pc1_ranking", verbose = FALSE)
nm$pc1_rank
se2 <- im_prepare_se(nadia_dia, pc1_rank = nm$pc1_rank, verbose = FALSE)
SummarizedExperiment::assayNames(se2)
```

merge_significance_info

Merge significance information from DEPs_results

Description

Converts DEPs_results (long format) into wide format with one adjP_* column per comparison, and computes sig_any.

Usage

```
merge_significance_info(
  feature_ids,
  DEPs_results,
  assay_name,
  alpha = 0.05,
  verbose = TRUE
)
```

Arguments

feature_ids	Vector of feature IDs
DEPs_results	DataFrame with columns Protein.IDs, adj.P.Val, Comparison, Assay
assay_name	Name of the assay used to filter DEPs_results
alpha	Significance threshold (default: 0.05)
verbose	Print progress messages (default: TRUE)

Value

DataFrame with FeatureID, adjP_*, sig_any

nadia_add_pattern_profiler

Add a Pattern Profiler run to an existing `.nadia` *file*

Description

The clustering is an optional extra step, so it is written separately: this adds it to a file that already holds the analysis, and refuses to create one from scratch.

Usage

```
nadia_add_pattern_profiler(
  file,
  pattern_profiler,
  overwrite = FALSE,
  verbose = TRUE
)
```

Arguments

file	Path to an existing .nadia file.
pattern_profiler	Object from pattern_profiler_analysis().
overwrite	Replace a clustering already in the file.
verbose	Print progress.

Value

The path, invisibly.

See Also

write_nadia()

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
    data(nadia_dia)
    res <- process_proteomics(nadia_dia, verbose = FALSE)
    f <- file.path(tempdir(), "pp.nadia")
    write_nadia(f, nadia_dia, res, verbose = FALSE)

    # pp <- pattern_profiler_analysis(res$se_proc, res$DEPs_results)
    # nadia_add_pattern_profiler(f, pp)

    unlink(f)
}
```

---

nadia_connect *Open a connection to a .nadia file*

Description

For querying the file directly with SQL or dplyr. Most users want read_nadia() instead; this is the way in when the file is larger than memory or when a specific query beats loading everything.

Usage

```
nadia_connect(file, read_only = TRUE)
```

Arguments

file	Path to a .nadia file.
read_only	Open without write access. TRUE by default, which is also what allows several processes to read the same file at once.

Details

The caller owns the connection and must close it with DBI::dbDisconnect(con, shutdown = TRUE).

Value

A DBI connection.

See Also

read_nadia(), nadia_tables()

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
    data(nadia_dia)
    f <- file.path(tempdir(), "query.nadia")
    write_nadia(f, nadia_dia,
                process_proteomics(nadia_dia, verbose = FALSE),
                verbose = FALSE)

    con <- nadia_connect(f)
    DBI::dbGetQuery(con, "SELECT COUNT(*) AS n FROM proteins")
    DBI::dbDisconnect(con, shutdown = TRUE)

    unlink(f)
}
```

---

nadia_deps_with_clusters

Differential abundance with clusters, from a `.nadia` *file*

Description

The file's own answer to deps_with_clusters(). The join lives in the file as the view v_deps_pattern_profiler, so this reads a table rather than building one, and a client that is not R gets the same table from the same SQL. The filters are the ones deps_with_clusters() applies, and the two functions return identical results for the same arguments.

Usage

```
nadia_deps_with_clusters(
  db,
  assignment = c("primary", "all"),
  min_membership = NULL,
  comparison = NULL,
  significant_only = FALSE
)
```

Arguments

db	A nadia_db from read_nadia(), or the path to a .nadia file.
assignment	"primary" (default) for one row per protein and comparison, carrying the cluster of highest membership; "all" for one row per protein, comparison and cluster.
min_membership	Optional extra membership threshold. It can only be stricter than the one the analysis ran with.

`comparison` Optional character vector of comparisons to keep.

`significant_only`
Keep only the rows classified `Up` or `Down`.

Details

The table is read on demand rather than by `read_nadia()`, because it is as long as the number of proteins times comparisons times clusters and there is no reason to carry it around unasked.

Value

A data frame with the columns of `DEPs_results` followed by `Cluster`, `Membership` and `ClusterRank`, or `NULL` if the file holds no differential-abundance results. A file with results but no clustering returns the same shape with the three cluster columns `NA`.

See Also

`deps_with_clusters()`, `nadia_add_pattern_profiler()`

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
    data(nadia_dia)
    res <- process_proteomics(nadia_dia, verbose = FALSE)

    f <- file.path(tempdir(), "functional.nadia")
    write_nadia(f, nadia_dia, res, verbose = FALSE)

    head(nadia_deps_with_clusters(f))

    unlink(f)
}
```

---

nadia_dia *Example DIA experiment, already preprocessed*

Description

Output of `preprocess_spectronaut()` on a trimmed Spectronaut report, ready to feed `process_proteomics()` and the rest of the pipeline without having to read the source file again.

Usage

```
data(nadia_dia)
```

Format

An S3 object of class `c("spectronaut_data", "proteomics_data", "list")` with three elements:

`metadata` Data frame of 12 rows and 7 columns, one row per injection: `R.FileName`, `R.Condition`, `R.Replicate`, `Coding` and the three identification counts reported by Spectronaut (`R.PrecursorsIdentified`, `R.StrippedSequencesIdentified`, `R.ProteinGroupsIdentified`).

`protein_id` Data frame of 2,000 rows by 52 columns holding the identification information of every protein group.

`protein_quant` Data frame of 2,000 rows by 44 columns: eight annotation columns plus, for each of the 12 samples, the number of precursors and of stripped sequences used for quantification and the intensity (`PG.Quantity_<condition>_<replicate>`).

Details

The data come from a quantitative proteomics experiment acquired on an Orbitrap Exploris at the Proteomics Facility of the Centro Nacional de Biotecnologia (CNB-CSIC) and processed with Spectronaut v20. The original experiment has 16 injections of the same digest split across four conditions (A-D) of four replicates each, and 10,437 protein groups.

So that the package examples run quickly, three conditions (A, B and D) and a random sample of 2,000 protein groups are kept. Three and not two conditions are retained because the soft-clustering in `pattern_profiler_analysis()` groups profiles across conditions, and with only two points per profile there is no pattern left to cluster.

The sample is drawn at random, with a fixed seed, rather than picking the best-covered proteins. That matters: **8.1 % of the intensities are missing and 72.2 % of the proteins are complete**, closely matching the 7.9 % and 72.1 % of the full experiment. Selecting the most-quantified proteins instead would yield a dataset with no missing values at all, in which every imputation method returns the input unchanged, and in which 87 % of the proteins come out differentially expressed instead of the 31 % of the full data.

The full recipe is in `system.file("scripts", "make_extdata.R", package = "NADIA")`. The trimmed report this object is derived from is also distributed as a file, in `system.file("extdata", "nadia_dia_report.tsv.gz", package = "NADIA")`, so that `preprocess_spectronaut()` can be run end to end.

Source

Proteomics Facility, Centro Nacional de Biotecnologia (CNB-CSIC).

Examples

```
data(nadia_dia)
nadia_dia

# The three conditions and their four replicates
table(nadia_dia$metadata$R.Condition)

# Proteins and intensity columns
dim(nadia_dia$protein_quant)
grep("^PG.Quantity_", colnames(nadia_dia$protein_quant), value = TRUE)

# Missing values, which is what the package is about. A Spectronaut report is
# long, one row per run and protein group, and where a protein was not
# quantified the row is simply absent; the pivot to wide format is what turns
# those absences into NA.
quant <- as.matrix(nadia_dia$protein_quant[
  grep("^PG.Quantity_", colnames(nadia_dia$protein_quant))])
round(100 * mean(is.na(quant)), 1)
```

`nadia_export_parquet` *Export the tables of a* `.nadia` *file to Parquet*

Description

A way out to an open, stable format. DuckDB reads its own files back a long way, but Parquet is the safer bet for something that has to be readable in ten years by software nobody has written yet, and it is what a repository will expect alongside a publication.

Usage

```
nadia_export_parquet(db, dir, views = TRUE, verbose = TRUE)
```

Arguments

`db`	A `nadia_db` from `read_nadia()`, or the path to a file.
`dir`	Directory to write to; created if it does not exist.
`views`	Export the reconstructed canonical tables (`TRUE`, the default) or the underlying storage tables (`FALSE`).
`verbose`	Print progress.

Value

The paths written, invisibly.

See Also

`read_nadia()`, `write_nadia()`

Examples

```
if (requireNamespace("duckdb", quietly = TRUE) &&
    requireNamespace("arrow", quietly = TRUE)) {
    data(nadia_dia)
    f <- file.path(tempdir(), "export.nadia")
    write_nadia(f, nadia_dia, verbose = FALSE)

    out <- file.path(tempdir(), "nadia_parquet_export")
    nadia_export_parquet(f, out, verbose = FALSE)
    list.files(out)

    unlink(c(f, out), recursive = TRUE)
}
```

nadia_pattern_profiler *Rebuild the Pattern Profiler table from a* .nadia *file*

Description

Rebuild the Pattern Profiler table from a .nadia file

Usage

```
nadia_pattern_profiler(db)
```

Arguments

db	A nadia_db from read_nadia().

Value

The long_output data frame, ready for cluster_profile_highchart_list(), or NULL if the file holds no clustering.

See Also

read_nadia(), nadia_add_pattern_profiler()

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
    data(nadia_dia)
    f <- file.path(tempdir(), "nopp.nadia")
    write_nadia(f, nadia_dia, verbose = FALSE)

    is.null(nadia_pattern_profiler(read_nadia(f)))

    unlink(f)
}
```

nadia_preprocessing *Rebuild the preprocessing object from a* .nadia *file*

Description

Returns an object indistinguishable from what the preprocess_*() function that wrote the file produced – Spectronaut, DIA-NN, TMT or label-free – so it can be fed straight to process_proteomics() or to the table functions.

Usage

```
nadia_preprocessing(db)
```

Arguments

db	A nadia_db from read_nadia().

Value

A proteomics_data object with metadata, protein_id and protein_quant.

See Also

read_nadia(), nadia_result()

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
    data(nadia_dia)
    f <- file.path(tempdir(), "pre.nadia")
    write_nadia(f, nadia_dia, verbose = FALSE)

    pre <- nadia_preprocessing(read_nadia(f))
    identical(pre$protein_id, nadia_dia$protein_id)

    unlink(f)
}
```

---

nadia_result *Rebuild the processing result from a* .nadia *file*

Description

Returns a proteomics_result with everything process_proteomics() returns, the SummarizedExperiment included, so that every plotting function in the package works from the file directly:

Usage

```
nadia_result(db)
```

Arguments

db	A nadia_db from read_nadia().

Details

```
db  <- read_nadia("experiment.nadia")
res <- nadia_result(db)
volcano_highchart_list(res$DEPs_results)
pca_highchart_list(res$PCA_Input)
```

Value

A proteomics_result object, or an error if the file holds only the preprocessing step.

See Also

read_nadia(), nadia_preprocessing()

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
    data(nadia_dia)
    res <- process_proteomics(nadia_dia, verbose = FALSE)
    f <- file.path(tempdir(), "result.nadia")
    write_nadia(f, nadia_dia, res, verbose = FALSE)

    back <- nadia_result(read_nadia(f))
    identical(back$DEPs_results, res$DEPs_results)
    class(volcano_highchart_list(back$DEPs_results)[[1]])

    unlink(f)
}
```

---

nadia_skill_path *Locate the NADIA agent skill*

Description

Returns the directory holding the agent skill that ships with NADIA. The skill documents the analysis pipeline for a coding assistant: which function to call at each stage, how to choose between the normalisation and imputation methods, what to verify afterwards, and the mistakes the package's defaults invite. It is plain Markdown, so any assistant can read it, and it follows the layout Claude expects for a skill: a `SKILL.md` entry point that points at the files under `reference/` and `scripts/`.

Usage

```
nadia_skill_path(...)
```

Arguments

`...`	Character path segments below the skill directory, passed on to `base::system.file()`. With no arguments the directory itself is returned.

Details

To use it with Claude Code, copy the directory into the skills folder of a project (`.claude/skills/nadia/`) or of the user (`~/.claude/skills/nadia/`). The examples below print the command that does it.

Value

A single character string: the absolute path, or `""` when the skill cannot be found, which is what `system.file()` returns for a missing file.

See Also

`vignette("NADIA")` for the same pipeline written for a person.

Examples

```
# Where the skill lives
nadia_skill_path()

# Its entry point, and the files it refers to
nadia_skill_path("SKILL.md")
list.files(nadia_skill_path(), recursive = TRUE)

# Install it for Claude Code, for the current user
cat(sprintf(
    "cp -R '%s' ~/.claude/skills/nadia",
    nadia_skill_path()
))
```

`nadia_tables` *List the contents of a* `.nadia` *file without loading it*

Description

List the contents of a `.nadia` file without loading it

Usage

```
nadia_tables(file)
```

Arguments

`file`	Path to a `.nadia` file.

Value

A data frame with `name`, `type` (`table` or `view`) and `rows`.

See Also

`read_nadia()`

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
    data(nadia_dia)
    f <- file.path(tempdir(), "tables.nadia")
    write_nadia(f, nadia_dia, verbose = FALSE)

    nadia_tables(f)

    unlink(f)
}
```

nm_prepare_se *Prepare a SummarizedExperiment from a proteomics_data object*

Description

Convenience wrapper that extracts metadata and protein data from a `proteomics_data` object (from any of the preprocess_*() functions), performs zero-to-NA conversion, protein filtering, and returns a SE with assays `"raw"` and `"log2"` – ready for `nm_run_normalizations()` or `normalization_metrics(..., methods = "all")`.

Usage

```
nm_prepare_se(
  preprocessing,
  min_reps = NULL,
  min_groups = 1,
  covariate_df = NULL,
  verbose = TRUE
)
```

Arguments

`preprocessing`	A `proteomics_data` object, from any of the `preprocess_*()` functions.
`min_reps`	Minimum replicates with non-NA values per group for protein filtering. If NULL, auto-computed as half the smallest group. Default `NULL`.
`min_groups`	Minimum groups meeting `min_reps` (default: 1).
`covariate_df`	Optional covariate data.frame for paired designs (must contain a `Column` column). Default `NULL`.
`verbose`	Logical. Print progress messages. Default `TRUE`.

Details

Internally calls `normalize_proteomics()` with `norm_method = "log2"` (no additional normalization).

Value

SummarizedExperiment with assays `"raw"` and `"log2"`.

Examples

```
data(nadia_dia)
se <- nm_prepare_se(nadia_dia, verbose = FALSE)
dim(se)
SummarizedExperiment::assayNames(se)
```

`nm_run_normalizations` *Run multiple normalization methods from a baseline assay*

Description

Takes a SummarizedExperiment with a log2-scale assay and applies each requested normalization method, returning a new SE with one assay per method.

Usage

```
nm_run_normalizations(
  se,
  assay_name = "log2",
  methods = "all",
  method_args = list(),
  include_baseline = TRUE,
  verbose = TRUE
)
```

Arguments

`se`	SummarizedExperiment with at least one log2-scale assay.
`assay_name`	Name of the baseline assay to normalize from. Default `"log2"`.
`methods`	Character vector of method names, or `"all"` for all 12 benchmark methods. Default `"all"`.
`method_args`	Named list of per-method arguments. E.g. `list(cycloess = list(method = "fast", span = 0.8))`.
`include_baseline`	Logical. Include the baseline assay in the output SE. Default `TRUE`.
`verbose`	Logical. Print progress messages. Default `TRUE`.

Value

SummarizedExperiment with one assay per successfully normalized method (plus baseline if `include_baseline = TRUE`).

Examples

```
data(nadia_dia)
se <- nm_prepare_se(nadia_dia, verbose = FALSE)
se_bench <- nm_run_normalizations(se, methods = c("cycloess", "quantile", "MAD"),
                                  verbose = FALSE)
SummarizedExperiment::assayNames(se_bench)
```

normalization_metrics *Generate quality metric plots for normalization comparison*

Description

Calls all (or selected) nm_plot_*() functions on a SummarizedExperiment produced by import_norm_matrices(). Each plot is wrapped in tryCatch() so that a failure in one plot does not abort the entire run.

Usage

```
normalization_metrics(
  se,
  assay_names = NULL,
  condition_col = "Condition",
  plots = "all",
  cor_method = "pearson",
  pca_scales = c("free", "fixed", "both"),
  mds_scales = c("free", "fixed", "both"),
  methods = NULL,
  method_args = list(),
  base_assay = "log2",
  verbose = TRUE,
  output_dir = NULL,
  export_plots = TRUE,
  export_tables = TRUE,
  plot_width = 12,
  plot_height = 8,
  plot_dpi = 150
)
```

Arguments

se	SummarizedExperiment from import_norm_matrices().
assay_names	Character vector of assay names to include. NULL (default) = all assays.
condition_col	Column name in colData(se) with condition labels. Default "Condition".
plots	Character vector of plot names to generate, or "all" (default). Valid names: "boxplot", "density", "pcv", "pmad", "pev", "pca", "correlation", "mds", "scatter", "qq", "metrics", "pc1_ranking", "mds1_ranking", "final_ranking". When pca_scales = "both", "pca" expands to "pca_free" + "pca_fixed". When mds_scales = "both", "mds" expands to "mds_free" + "mds_fixed".
cor_method	Correlation method for the "correlation" plot. Default "pearson".
pca_scales	Facet scaling for PCA plot: "free" (default), "fixed", or "both" to generate and export both variants (pca_free and pca_fixed in the returned list).
mds_scales	Facet scaling for MDS plot: "free" (default), "fixed", or "both" to generate and export both variants (mds_free and mds_fixed in the returned list).
methods	Character vector of normalization method names to auto-benchmark, "all" for the 12 benchmark methods ("log2" is the baseline and is excluded, so this is one fewer than the 13 that normalize_proteomics() accepts), or NULL (default) to skip auto-normalization and use existing assays.

method_args	Named list of per-method arguments forwarded to nm_run_normalizations(). E.g. list(cycloess = list(method = "fast", span = 0.8)).
base_assay	Name of the baseline assay to normalize from when using auto-normalization. Default "log2".
verbose	Logical. Print progress messages. Default TRUE.
output_dir	Character. Path to export directory. If NULL (default), no files are exported. When set, tables (TSV) and/or plots (PNG) are saved to this directory (created if needed).
export_plots	Logical. Export plots as PNG when output_dir is set. Default TRUE.
export_tables	Logical. Export tables as TSV when output_dir is set. Default TRUE.
plot_width	Numeric. Width in inches for exported plots. Default 12.
plot_height	Numeric. Height in inches for exported plots. Default 8.
plot_dpi	Numeric. Resolution for exported plots. Default 150.

Details

When methods is provided, the function first runs nm_run_normalizations() to automatically apply the requested normalization methods from the base_assay, then computes metrics and generates plots on the resulting multi-assay SE.

Value

Named list of ggplot objects (or NULL for failed plots), plus data.frames always computed regardless of plots selection: metrics_table (one row per method and metric), pc1_rank, mds1_rank, pcv_rank, pmad_rank, pev_rank, cor_rank, and final_rank (combined ranking as the mean of the five ranks Rank_PCV, Rank_PMAD, Rank_PEV, Rank_Cor and Rank_Sep; pc1_rank and mds1_rank are standalone diagnostics and do not enter it).

Reproducibility

Two columns use random numbers: Hopkins, which samples random reference points, and PERMANOVA_pval, which permutes the group labels. Both draw from the caller's RNG, so call set.seed() beforehand to reproduce them. Every other column is deterministic.

Examples

```
data(nadia_dia)
se <- nm_prepare_se(nadia_dia, verbose = FALSE)

# Auto-benchmark: normalize from the "log2" baseline, then score the methods
res <- normalization_metrics(se, methods = c("cycloess", "quantile", "MAD"),
                             plots = c("pcv", "final_ranking"), verbose = FALSE)
res$final_rank
res$pcv
```

`normalize_proteomics` *Normalize proteomics data*

Description

Complete normalization pipeline: zero-to-NA conversion, protein filtering by group presence, SummarizedExperiment creation, and normalization with the selected method. Output is always in log2 scale.

Usage

```
normalize_proteomics(
  data,
  metadata = NULL,
  min_reps = NULL,
  min_groups = 1,
  norm_method = "cycloess",
  cyclic_loess_method = c("fast", "pairs"),
  cyclic_loess_iterations = 3,
  cyclic_loess_span = 0.7,
  verbose = TRUE
)
```

Arguments

`data`	Either a `proteomics_data` object – the output of `preprocess_spectronaut()`, `preprocess_diann()`, `preprocess_tmt()` or `preprocess_lfq()` – in which case `metadata` is derived from it and must be left `NULL`, or a data frame with ProteinGroups, GeneNames, UniqPepts and the intensity columns.
`metadata`	Data frame with Column, Condition, Replicate. Only needed when `data` is a data frame.
`min_reps`	Minimum replicates for filtering. NULL = auto: floor(min_group_size / 2)
`min_groups`	Minimum groups meeting min_reps (default: 1)
`norm_method`	Normalization method (default: "cycloess"). One of: • Group A (input: raw intensities): "log2Norm", "GlobalMedian", "GlobalMean", "eqmedians", "vsn" • Group B (input: log2 assay): "log2" (no extra normalization), "quantile", "Rlr", "MAD", "cycloess", "medianNorm", "meanNorm", "quantile.robust"
`cyclic_loess_method`	Cyclic Loess method: "fast" or "pairs" (default: "fast")
`cyclic_loess_iterations`	Number of iterations for Cyclic Loess (default: 3)
`cyclic_loess_span`	Span parameter for Cyclic Loess (default: 0.7)
`verbose`	Print progress messages (default: TRUE)

Value

List with:

- se: SummarizedExperiment with assays raw, log2, and <norm_method> (assays raw + log2 only when norm_method = "log2")
- filter_summary: Filtering summary
- na_overview: NA statistics

Examples

```
data(nadia_dia)

# The object returned by preprocess_*() is accepted directly
norm <- normalize_proteomics(nadia_dia, norm_method = "cycloess",
                             verbose = FALSE)
SummarizedExperiment::assayNames(norm$se)

# Zeros become NA and low-coverage proteins are filtered out
norm$filter_summary

# Any of the 13 methods can be used
norm2 <- normalize_proteomics(nadia_dia, norm_method = "quantile",
                              verbose = FALSE)
SummarizedExperiment::assayNames(norm2$se)
```

---

pattern_profiler_analysis

Pattern Profiler Analysis

Description

Complete clustering pipeline starting from a SummarizedExperiment. Writes a parquet file in LONG format for visualisation.

Usage

```
pattern_profiler_analysis(
  se_proc,
  DEPs_results,
  assay_name = NULL,
  filter_mode = c("any", "all", "specific"),
  alpha = 0.05,
  comparison = NULL,
  condition_order = NULL,
  aggregate = c("median", "mean"),
  c_range = 2:10,
  auto_select_c = TRUE,
  c = NULL,
  selection_method = c("xb", "consensus", "elbow"),
  min_membership = 0.25,
```

```
  n_starts = 3L,
  output_file = NULL,
  verbose = TRUE
)
```

Arguments

se_proc	SummarizedExperiment with intensity data
DEPs_results	DataFrame with differential expression results (must have an 'Assay' column)
assay_name	Name of the assay to cluster. It is also the value used to filter DEPs_results by its Assay column, so the two must agree. With the default NULL it is taken from DEPs_results$Assay, which records the assay the differential abundance was computed on; supply it explicitly when those results cover more than one assay.
filter_mode	Filtering mode: "any" (significant in at least one comparison), "all" (ALL features, with no significance filtering), "specific" (significant in the comparison given by comparison)
alpha	Significance threshold (default: 0.05)
comparison	Specific comparison (for filter_mode="specific")
condition_order	Condition order for the profiles
aggregate	Aggregation method: "median" or "mean"
c_range	Range of cluster numbers to evaluate
auto_select_c	Automatic selection of the number of clusters (default: TRUE)
c	Fixed number of clusters (if auto_select_c=FALSE)
selection_method	Selection method: "xb", "consensus", "elbow"
min_membership	Minimum membership threshold for inclusion in the output
n_starts	Integer. Number of random starts used when auto_select_c = TRUE: each candidate number of clusters is fitted n_starts times and the metrics are averaged, so that the choice of c does not hang on a single partition. Default 3.
output_file	Path of the output parquet file. NULL by default, which writes nothing to disk; the long-format data is returned regardless in the long_output element of the result. Writing it needs the suggested package arrow, which is checked before the clustering starts.
verbose	Show progress messages

Value

List (invisible) with the clustering results: optimal_c, m, conditions, feature counts, selection_metrics, cluster_counts, the Mfuzz cl object, the standardised eset_std and long_output, the long-format data.frame that is written when output_file is given.

Reproducibility

Fuzzy c-means starts from a random partition, so the cluster labels, the memberships and, with auto_select_c = TRUE, the chosen number of clusters depend on the caller's RNG. Call set.seed() immediately before the function to make a run reproducible on its own, whatever ran before it.

Examples

```
if (requireNamespace("Mfuzz", quietly = TRUE) &&
    requireNamespace("e1071", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)

  # auto_select_c = TRUE would cluster once per value of c_range
  set.seed(42)
  pp <- pattern_profiler_analysis(
    res$se_proc,
    DEPs_results    = res$DEPs_results,
    assay_name      = "Impseqrob_min",
    filter_mode     = "any",
    condition_order = c("A", "B", "D"),
    auto_select_c   = FALSE,
    c               = 3,
    verbose         = FALSE
  )
  print(pp$cluster_counts)
  print(head(pp$long_output))
}
```

---

pca_covariates_plot *PCA Plots Colored by Covariates*

Description

Generates PCA scatter plots (PC1 vs PC2) from a SummarizedExperiment assay, coloring points by different covariates. Useful for visually identifying batch effects or confounding.

Usage

```
pca_covariates_plot(
  se,
  assay_name = NULL,
  covariates,
  na_action = "complete",
  fill_value = -1,
  center = TRUE,
  scale. = TRUE,
  de_results = NULL,
  comparison = "any",
  alpha = 0.05,
  filter_samples = FALSE,
  condition_column = "Condition",
  point_size = 3,
  verbose = TRUE
)
```

Arguments

se	SummarizedExperiment object.
assay_name	Character. Assay to analyze. NULL = second assay (normalized, pre-imputation).
covariates	Character vector. Column names in colData(se) to use for coloring (e.g., c("Injection", "Digestion", "Condition")).
na_action	Character: "complete" (default) or "fill".
fill_value	Numeric. NA replacement when na_action="fill" (default -1).
center	Logical. Center before PCA (default TRUE).
scale.	Logical. Scale before PCA (default TRUE).
de_results	Data.frame with differential expression results (e.g., result$DEPs_results). Must contain columns "Protein.IDs", "adj.P.Val", and "Comparison". When provided, PCA is computed using only significant proteins. Default NULL (all proteins).
comparison	Character. Which comparison to filter by. Use "any" (default) to keep proteins significant in any comparison, or specify a comparison name (e.g., "Post_vs_Pre") to filter to that one only. Ignored if de_results is NULL.
alpha	Numeric. Significance threshold for adj.P.Val when filtering by de_results (default 0.05). Ignored if de_results is NULL.
filter_samples	Logical. If TRUE and a specific comparison is given (not "any"), subset samples to only those belonging to the comparison conditions. Mirrors pca_highchart_list(filter_samples_to_c Default FALSE (use all samples).
condition_column	Character. Column name in colData(se) containing condition labels, used when filter_samples=TRUE. Default "Condition".
point_size	Numeric. Size of scatter points (default 3).
verbose	Logical (default TRUE).

Details

Categorical covariates use a discrete color scale; numeric covariates use a continuous viridis gradient.

Value

Named list:

grid ggplot2 facet_wrap with one panel per covariate

plots Named list of individual ggplot2 objects per covariate

pca_summary data.frame with PC1/PC2 variance explained

assay_name Assay used

n_proteins Number of proteins used

Examples

```
data(nadia_dia)

# nadia_dia has no batch information, so the example builds a plausible one:
# two digestion batches crossed with the three conditions.
cov <- data.frame(Column = nadia_dia$metadata$Coding,
```

```
                  Batch = rep(c("b1", "b2"),
                              length.out = nrow(nadia_dia$metadata)),
                  stringsAsFactors = FALSE)
res <- process_proteomics(nadia_dia, covariate_df = cov, verbose = FALSE)

# How the samples lay out in PCA space against each covariate
p <- pca_covariates_plot(res$se_proc, assay_name = "Impseqrob_min",
                         covariates = c("Condition", "Batch"))
names(p)
```

`pca_highchart_list` *Build a List of PCA Plots for Multiple Subsets*

Description

Automatically builds PCA plots for "all", "any" and/or specific comparisons. Similar to factoextra::fviz_pca_ind with ellipse options.

Usage

```
pca_highchart_list(
  pca_input,
  modes = c("all", "any"),
  alpha = 0.05,
  color_by = "Condition",
  group_order = NULL,
  palette = NULL,
  addEllipses = TRUE,
  ellipse_type = c("convex", "confidence"),
  ellipse_level = 0.95,
  ellipse_fill_opacity = 0.12,
  ellipse_line_width = 1,
  ellipse_npoints = 100,
  point_size = 5,
  show_labels = FALSE,
  label_size = 10,
  center = TRUE,
  scale. = TRUE,
  filter_samples_to_comparison = FALSE
)
```

Arguments

`pca_input`	Data frame in long format (see build_pca_scores for the structure)
`modes`	Vector of modes to generate: "all", "any", and/or comparison names (default: c("all", "any"))
`alpha`	Significance threshold for DEPs (default: 0.05)
`color_by`	Column used to colour the points (default: "Condition")
`group_order`	Order of the groups/conditions (optional)

palette — Colour palette: NULL for the default; "pkg::name" for a palette from paletteer; "brewer:Name", or the bare name, for an RColorBrewer palette; or a vector of colours, unnamed or named after the groups. A palette with fewer colours than groups is interpolated.

addEllipses — Show ellipses/hulls around the groups (default: TRUE)

ellipse_type — Ellipse type: "convex" or "confidence" (default: "convex")

ellipse_level — Confidence level for ellipse_type = "confidence" (default: 0.95)

ellipse_fill_opacity — Ellipse fill opacity (0-1, default: 0.12)

ellipse_line_width — Outline line width (default: 1)

ellipse_npoints — Number of points for the confidence ellipse (default: 100)

point_size — Point radius (default: 5)

show_labels — Show the point labels (SampleID) (default: FALSE)

label_size — Label font size in px (default: 10)

center — Center the data before PCA (default: TRUE)

scale. — Scale the data before PCA (default: TRUE)

filter_samples_to_comparison — For specific comparisons, restrict the samples to the conditions involved (default: FALSE)

Value

Named list of highchart objects

Examples

```
if (requireNamespace("highcharter", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)

  # One PCA over all proteins and one over the significant ones
  hc_pcas <- pca_highchart_list(
    res$PCA_Input,
    modes         = c("all", "any"),
    group_order   = c("A", "B", "D"),
    ellipse_type  = "confidence",
    ellipse_level = 0.95
  )
  names(hc_pcas)
}
```

`prepare_heatmap_data` *Prepare Long-Format Data for tidyHeatmap*

Description

Prepare Long-Format Data for tidyHeatmap

Usage

```
prepare_heatmap_data(
  data,
  mode = c("all", "any", "target"),
  alpha = 0.05,
  comparison = NULL,
  feature_ids = NULL,
  scale_data = c("row", "none", "column"),
  sample_order = c("clustering", "condition", "custom"),
  condition_order = NULL
)
```

Arguments

`data`	Data frame in long format with columns: • SampleID: sample identifier • FeatureID: protein/feature identifier • Intensity: intensity value (log2) • Condition: experimental condition • Replicate: replicate number • sig_any: logical flagging significance (for mode="any") • adjP_*: adjusted p-value columns (for mode="target")
`mode`	Filtering mode: "all", "any", or "target"
`alpha`	Significance threshold for mode "target" (default: 0.05)
`comparison`	Name of the comparison for mode "target" (e.g. "B-A")
`feature_ids`	Vector of specific FeatureIDs (when supplied, mode/alpha are ignored)
`scale_data`	Scaling type: "none", "row", "column" (default: "row")
`sample_order`	Sample order: "clustering", "condition", or a custom vector
`condition_order`	Condition order when sample_order = "condition"

Value

Data frame in long format, ready for tidyHeatmap

preprocess_diann *Preprocess DIA-NN protein-group matrices*

Description

Converts a DIA-NN protein-group matrix (report.pg_matrix.tsv, wide TSV format) into the same output structure as preprocess_spectronaut(): three data.frames (metadata, protein_id, protein_quant) ready for the downstream pipeline (process_proteomics() and the associated modules).

DIA-NN names its intensity columns after the raw file, which says nothing about the experimental design, so the design has to be declared. There are two ways: rename the columns to Abundance: <Condition>_<Replicate> as Proteome Discoverer writes them, or pass a sample sheet through annot_path. The design is never inferred from the raw-file name – a guess that happened to be right for one export would be wrong and silent for the next.

A protein-group matrix carries only intensities. The identification metrics the wide contract expects are filled from what DIA-NN does report (N.Sequences, N.Proteotypic.Sequences), left as NA where it reports nothing (the precursor counts), or omitted where nothing downstream needs them (coverage and the Spectronaut C-score).

Usage

```
preprocess_diann(
  file_path,
  condition_order,
  annot_path = NULL,
  export_dir = NULL,
  timestamp_suffix = TRUE,
  verbose = TRUE
)
```

Arguments

file_path	Path to the report.pg_matrix.tsv exported by DIA-NN.
condition_order	Character vector with the order of the experimental conditions (e.g. c("A", "B", "D")). Only the runs whose condition is in this vector are kept, so it doubles as a filter. Conditions listed but absent from the report are dropped, with a warning, so that no empty factor level reaches the metadata.
annot_path	Path to a sample sheet with columns Column and Condition, used to read the report exactly as DIA-NN wrote it: Column holds the run headers, raw-file names and all. If NULL (default), the columns are expected to follow the Abundance: convention. Any other column in the sheet is ignored – batch structure belongs in covariate_df of process_proteomics(), see vignette("batch-correction"). The sheet is a file rather than a vector of labels because a vector would be positional, and nothing guarantees the column order of an export: a re-export that reordered them would relabel every run without any way to notice. Matching by name either matches or fails.
export_dir	Directory to export the TSV files to. If NULL (default), no files are exported.

timestamp_suffix
: Logical. If TRUE (default), appends a timestamp to the names of the exported files.

verbose
: Logical. If TRUE (default), shows progress messages.

Value

A list with class c("diann_data", "proteomics_data", "list") containing:

metadata Data frame with one record per run, including the number of protein groups quantified in each

protein_id Data frame with the identification metrics per protein (wide format, the global metrics replicated per run)

protein_quant Data frame with the quantification metrics per protein (includes PG.Quantity_<Coding>)

The call that produced the object and a fingerprint of the file it was read from (path, size, modification time and MD5) travel with it as the attributes nadia_call and nadia_source. They are attributes rather than list elements so that the three-element structure above is unchanged; write_nadia() records them as the provenance of an analysis.

Examples

```
# A trimmed DIA-NN protein-group matrix ships with the package. Its run
# columns have been renamed to the "Abundance: <Condition>_<Replicate>"
# convention, so no further argument is needed.
report <- system.file("extdata", "nadia_diann_report.tsv.gz",
                      package = "NADIA")

diann <- preprocess_diann(report, condition_order = c("A", "B", "D"),
                          verbose = FALSE)
diann
table(diann$metadata$R.Condition)

# Straight from DIA-NN, where the columns are still raw-file paths, the
# design is given instead by a sheet whose 'Column' holds those paths:
# preprocess_diann("report.pg_matrix.tsv",
#                  condition_order = c("A", "B", "D"),
#                  annot_path = "design.tsv")
```

---

preprocess_lfq *Preprocess Proteome Discoverer LFQ exports*

Description

Converts a Proteome Discoverer LFQ protein export (wide TSV format) into the same output structure as preprocess_spectronaut() / preprocess_tmt(): three data.frames (metadata, protein_id, protein_quant) ready for the downstream pipeline (process_proteomics()).

The experimental design comes from the Abundance: <Condition>_<Replicate> column suffixes, exactly as in preprocess_tmt() and preprocess_diann(). For a report whose columns are not named that way, annot_path takes a sample sheet instead.

The intensities (Abundance: <sample>) and the three per-sample metric families (Score Mascot, # PSMs (by Search Engine), # Peptides (by Search Engine)) are mapped BY SAMPLE NAME, never by position: Proteome Discoverer writes the four families in different orders.

Usage

```
preprocess_lfq(
  file_path,
  annot_path = NULL,
  condition_order = NULL,
  export_dir = NULL,
  timestamp_suffix = TRUE,
  verbose = TRUE
)
```

Arguments

file_path	Path to the data TSV exported from Proteome Discoverer.
annot_path	Path to a sample sheet with columns Column and Condition, where Column holds the text after Abundance: . If NULL (default), the design comes from the suffixes. Any other column in the sheet is ignored – batch structure belongs in covariate_df of process_proteomics(), see vignette("batch-correction").
condition_order	Character vector with the order of the conditions. If NULL (default), it is derived from the data (order of appearance). If supplied, it fixes the factor levels and discards samples whose condition is not in the list; conditions listed but absent are dropped too, with a warning, so that no empty factor level reaches the metadata.
export_dir	Directory to export the TSVs to. NULL (default) = no export.
timestamp_suffix	Logical. If TRUE (default), appends a timestamp to the exported files.
verbose	Logical. If TRUE (default), shows progress messages.

Value

A list with class c("lfq_data", "proteomics_data", "list") containing metadata, protein_id and protein_quant.

The call that produced the object and a fingerprint of the files it was read from – the report, and the sample sheet when there is one – (path, size, modification time and MD5) travel with it as the attributes nadia_call and nadia_source. They are attributes rather than list elements so that the three-element structure above is unchanged; write_nadia() records them as the provenance of an analysis.

Examples

```
# A trimmed Proteome Discoverer LFQ report ships with the package. Its columns
# follow the "Abundance: <Condition>_<Replicate>" convention, so the design
# needs no further argument.
report <- system.file("extdata", "nadia_lfq_report.tsv.gz", package = "NADIA")

lfq <- preprocess_lfq(report, verbose = FALSE)
lfq
lfq$metadata[, c("Coding", "R.Condition", "R.Replicate")]

# The same design, declared in a sheet instead. Use this route when the
# columns are not named by the convention; here it is the same experiment, so
# it produces the same sample table.
annot <- system.file("extdata", "nadia_lfq_annotation.tsv", package = "NADIA")
```

```
from_sheet <- preprocess_lfq(report, annot_path = annot, verbose = FALSE)
identical(from_sheet$metadata, lfq$metadata)
```

`preprocess_se` *Import Protein Intensities from a SummarizedExperiment*

Description

Converts a `SummarizedExperiment` of protein intensities into the `proteomics_data` object that every NADIA reader returns. It is the way in for data imported with other Bioconductor tools, for instance one of the assays of a `QFeatures` object. `process_proteomics()` also accepts the `SummarizedExperiment` directly and calls this function; call it yourself to keep the object, for example to store it with `write_nadia()`.

Usage

```
preprocess_se(
  se,
  condition_order = NULL,
  assay_name = NULL,
  log2_input = FALSE,
  condition_column = "Condition",
  replicate_column = "Replicate",
  verbose = TRUE
)
```

Arguments

`se`	A `SummarizedExperiment` with protein intensities.
`condition_order`	Optional character vector with the conditions to keep, in the order they should appear. `NULL` (default) keeps them all, in the order of the factor levels or, for text, of first appearance.
`assay_name`	Name or index of the assay with the intensities. `NULL` (default) takes the first one.
`log2_input`	`TRUE` if the intensities are on the log2 scale. Default `FALSE`, linear intensities.
`condition_column`	Column of `colData(se)` with the condition of each sample. Default `"Condition"`.
`replicate_column`	Column of `colData(se)` with the replicate number. Default `"Replicate"`; if the column is absent, the replicates are numbered.
`verbose`	Print progress messages. Default `TRUE`.

Details

What is read from the object:

- **Intensities**: the assay `assay_name`, proteins in rows and samples in columns. With `log2_input = TRUE` the values are taken back to the linear scale, because NADIA applies the log2 transformation when it normalises. Zeros are treated as missing values, as for the other readers.

- **Proteins**: the row names, which must be present and unique. The gene names come from `rowData()$Genes` and the descriptions from `rowData()$Description`, when those columns exist.
- **Design**: the condition from `colData()[[condition_column]]` and the replicate from `colData()[[replicate_co` without a replicate column the samples are numbered within each condition, in column order.

The samples are renamed `<condition>_<replicate>`, the convention the rest of NADIA relies on, and the original column names are kept in `metadata$R.FileName`. Identification metrics (precursor or peptide counts, scores) are not read from `rowData()`, so those columns of the tables are left empty.

Value

An object of class `c("se_data", "proteomics_data", "list")` with the elements `metadata`, `protein_id` and `protein_quant`, like the other readers.

See Also

`process_proteomics()`, which accepts the `SummarizedExperiment` directly.

Examples

```
data(nadia_dia)
# A SummarizedExperiment built from the example data
quant <- as.matrix(nadia_dia$protein_quant[, grep("^PG\\.Quantity_",
                                                  names(nadia_dia$protein_quant))])
rownames(quant) <- nadia_dia$protein_quant$PG.ProteinGroups
se <- SummarizedExperiment::SummarizedExperiment(
  assays  = list(intensity = quant),
  colData = data.frame(Condition = nadia_dia$metadata$R.Condition,
                       Replicate = nadia_dia$metadata$R.Replicate),
  rowData = data.frame(Genes = nadia_dia$protein_quant$PG.Genes))

pre <- preprocess_se(se, verbose = FALSE)
pre

# The same values on the log2 scale
SummarizedExperiment::assay(se, "intensity") <- log2(quant)
pre_log2 <- preprocess_se(se, log2_input = TRUE, verbose = FALSE)
```

`preprocess_spectronaut` *Preprocess Spectronaut reports*

Description

Converts a Spectronaut report (long TSV format) into three structured tables: run metadata, protein identification and protein quantification.

The report has to carry the right columns, and rather than leave that to be reconstructed by hand the package ships the Spectronaut export schema that produces them:

```
system.file("extdata", "NADIA_Report.rs", package = "NADIA")
```

Import that file into Spectronaut as a report schema and export with it. The result has the shape of `nadia_dia_report.tsv.gz`, the example that ships alongside it.

Usage

```
preprocess_spectronaut(
  file_path,
  condition_order,
  export_dir = NULL,
  agg_coverage_run = c("max", "mean", "median", "min"),
  agg_coverage_global = c("max", "mean", "median", "min"),
  agg_mw = c("max", "mean", "median", "min"),
  agg_cscore_runwise = c("mean", "max", "median", "min"),
  timestamp_suffix = TRUE,
  verbose = TRUE
)
```

Arguments

`file_path`	Path to the Spectronaut TSV file.
`condition_order`	Character vector that selects the experimental conditions to retain and sets their order in subsequent analysis stages (e.g. `c("Control", "Treated")`). Runs whose condition is not listed are dropped; conditions listed but absent from the report are dropped too, with a warning, so that no empty factor level reaches the metadata.
`export_dir`	Directory to export the TSV files to. If `NULL` (default), no files are exported.
`agg_coverage_run`	Aggregation method for the per-sample PG.Coverage. Options: "max" (default), "mean", "median", "min".
`agg_coverage_global`	Aggregation method for PG.Coverage.Global. Options: "max" (default), "mean", "median", "min".
`agg_mw`	Aggregation method for PG.MolecularWeight. Options: "max" (default), "mean", "median", "min".
`agg_cscore_runwise`	Aggregation method for the run-wise C-score, stored as `PG.Score.RunWise`. Options: "mean" (default), "max", "median", "min".
`timestamp_suffix`	Logical. If `TRUE` (default), appends a timestamp to the names of the exported files.
`verbose`	Logical. If `TRUE` (default), shows progress messages.

Value

A list with class `spectronaut_data` containing:

metadata Data frame with the run information (1 row per sample)

protein_id Data frame with the identification metrics per protein

protein_quant Data frame with the quantification metrics per protein

The call that produced the object and a fingerprint of the file it was read from (path, size, modification time and MD5) travel with it as the attributes `nadia_call` and `nadia_source`. They are attributes rather than list elements so that the three-element structure above is unchanged; `write_nadia()` records them as the provenance of an analysis.

Examples

```
# A trimmed Spectronaut report ships with the package
report <- system.file("extdata", "nadia_dia_report.tsv.gz", package = "NADIA")

prep <- preprocess_spectronaut(report,
                               condition_order = c("A", "B", "D"),
                               verbose = FALSE)
prep
dim(prep$protein_quant)

# Nothing is written to disk unless export_dir is given
prep <- preprocess_spectronaut(report,
                               condition_order = c("A", "B", "D"),
                               export_dir = tempdir(),
                               verbose = FALSE)
```

---

preprocess_tmt *Preprocess Proteome Discoverer TMT exports*

Description

Converts a Proteome Discoverer protein export (wide TSV format, with `Abundance: <Condition>_<Replicate>` columns) into the same output structure as `preprocess_spectronaut()`: three data.frames (`metadata`, `protein_id`, `protein_quant`) ready for the downstream pipeline (`process_proteomics()` and the associated modules).

The global PD identification metrics (`# PSMs`, `# Peptides`, `# Unique Peptides`, `Coverage [%]`) are replicated into per-channel columns to fit the wide Spectronaut contract.

Usage

```
preprocess_tmt(
  file_path,
  condition_order,
  annot_path = NULL,
  export_dir = NULL,
  timestamp_suffix = TRUE,
  verbose = TRUE
)
```

Arguments

`file_path`	Path to the TSV exported from Proteome Discoverer.

`condition_order`
: Character vector with the order of the experimental conditions (e.g. `c("A","B","D","IS")`). Only the channels whose condition is in this vector are kept – handy for excluding Internal Standards by omitting `"IS"`. Conditions listed but absent from the report are dropped, with a warning, so that no empty factor level reaches the metadata.

`annot_path`
: Path to a sample sheet with columns `Column` and `Condition`, for reports whose channels are not named `<Condition>_<Replicate>` – an export left with the TMT tags, `126`, `127N` and so on. `Column` holds the text after `Abundance:` . If `NULL` (default), the design comes from the suffixes. Any other column in the sheet is ignored – batch structure belongs in `covariate_df` of `process_proteomics()`, see `vignette("batch-correction")`.

`export_dir`
: Directory to export the TSV files to. If `NULL` (default), no files are exported.

`timestamp_suffix`
: Logical. If `TRUE` (default), appends a timestamp to the names of the exported files.

`verbose`
: Logical. If `TRUE` (default), shows progress messages.

Value

A list with class `c("tmt_data", "proteomics_data", "list")` containing:

metadata Data frame with one record per channel/sample

protein_id Data frame with the identification metrics per protein (wide format, global metrics replicated per channel)

protein_quant Data frame with the quantification metrics per protein (includes `PG.Quantity_<Coding>`)

The call that produced the object and a fingerprint of the file it was read from (path, size, modification time and MD5) travel with it as the attributes `nadia_call` and `nadia_source`. They are attributes rather than list elements so that the three-element structure above is unchanged; `write_nadia()` records them as the provenance of an analysis.

Examples

```
# A trimmed Proteome Discoverer TMTpro report ships with the package: three
# conditions of eight replicates, split across two TMT mixes (replicates 1-4
# are the first mix, 5-8 the second) and bridged by four "IS" channels.
report <- system.file("extdata", "nadia_tmt_report.tsv.gz", package = "NADIA")

# condition_order is required, and doubles as a filter: the report also holds
# an "IS" channel (internal standards) that is left out by not listing it
tmt <- preprocess_tmt(report,
                      condition_order = c("A", "B", "D"),
                      verbose = FALSE)
tmt
table(tmt$metadata$R.Condition)
```

print.diann_data *Print a summary of a DIA-NN preprocessing result*

Description

Reports the number of runs, protein groups and conditions, so that the shape of the experiment can be checked at a glance before processing it.

Usage

```
## S3 method for class 'diann_data'
print(x, ...)
```

Arguments

x	A diann_data object, as returned by preprocess_diann().
...	Ignored, present for compatibility with the print generic.

Value

x, invisibly. Called for the summary it prints.

Examples

```
diann <- preprocess_diann(
  system.file("extdata", "nadia_diann_report.tsv.gz", package = "NADIA"),
  condition_order = c("A", "B", "D"),
  verbose = FALSE)
print(diann)
```

print.lfq_data *Print a summary of an LFQ preprocessing result*

Description

Reports the number of samples, protein groups and conditions, so that the shape of the experiment can be checked at a glance before processing it.

Usage

```
## S3 method for class 'lfq_data'
print(x, ...)
```

Arguments

x	An lfq_data object, as returned by preprocess_lfq().
...	Ignored, present for compatibility with the print generic.

Value

x, invisibly. Called for the summary it prints.

Examples

```
lfq <- preprocess_lfq(
  system.file("extdata", "nadia_lfq_report.tsv.gz", package = "NADIA"),
  annot_path = system.file("extdata", "nadia_lfq_annotation.tsv",
                           package = "NADIA"),
  verbose = FALSE)
print(lfq)
```

---

print.nadia_db *Print a summary of a* .nadia *file*

Description

Print a summary of a .nadia file

Usage

```
## S3 method for class 'nadia_db'
print(x, ...)
```

Arguments

x	A nadia_db object.
...	Ignored.

Value

x, invisibly.

---

print.proteomics_heatmap *Draw a proteomics heatmap*

Description

Renders the object built by proteomics_heatmap() on the current graphics device, adding the title stored in the object. Printing is what actually draws the heatmap: building it does not.

Usage

```
## S3 method for class 'proteomics_heatmap'
print(x, ...)
```

Arguments

x	A proteomics_heatmap object, as returned by proteomics_heatmap().
...	Further arguments passed to ComplexHeatmap::draw().

Value

The drawn HeatmapList, invisibly. Called for its side effect.

Examples

```
if (requireNamespace("ComplexHeatmap", quietly = TRUE) &&
    requireNamespace("tidyHeatmap", quietly = TRUE) &&
    requireNamespace("circlize", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)
  hm <- proteomics_heatmap(res$PCA_Input, mode = "any")

  # Drawing needs a graphics device; send it to a temporary file
  f <- tempfile(fileext = ".png")
  grDevices::png(f)
  print(hm)
  grDevices::dev.off()
  file.remove(f)
}
```

---

print.proteomics_result

Print method for proteomics_result

Description

Print method for proteomics_result

Usage

```
## S3 method for class 'proteomics_result'
print(x, ...)
```

Arguments

x	proteomics_result object
...	Additional arguments (ignored)

Value

x, invisibly. Called for the summary it prints: the assays of the SummarizedExperiment, the comparisons performed, the number of differential proteins and the parameters used.

Examples

```
data(nadia_dia)
res <- process_proteomics(nadia_dia, verbose = FALSE)
print(res)
```

---

print.se_data *Print a Summary of Data Imported from a SummarizedExperiment*

Description

Print a Summary of Data Imported from a SummarizedExperiment

Usage

```
## S3 method for class 'se_data'
print(x, ...)
```

Arguments

x	An se_data object, as returned by preprocess_se().
...	Ignored, present for compatibility with the print generic.

Value

x, invisibly. Called for the summary it prints.

Examples

```
data(nadia_dia)
quant <- as.matrix(nadia_dia$protein_quant[, grep("^PG\\.Quantity_",
                                                  names(nadia_dia$protein_quant))])
rownames(quant) <- nadia_dia$protein_quant$PG.ProteinGroups
se <- SummarizedExperiment::SummarizedExperiment(
  assays  = list(intensity = quant),
  colData = data.frame(Condition = nadia_dia$metadata$R.Condition))
print(preprocess_se(se, verbose = FALSE))
```

---

print.spectronaut_data *Print a summary of a Spectronaut preprocessing result*

Description

Reports the number of runs, protein groups and conditions, so that the shape of the experiment can be checked at a glance before processing it.

Usage

```
## S3 method for class 'spectronaut_data'
print(x, ...)
```

Arguments

x	A spectronaut_data object, as returned by preprocess_spectronaut().
...	Ignored, present for compatibility with the print generic.

Value

x, invisibly. Called for the summary it prints.

Examples

```
data(nadia_dia)
print(nadia_dia)
```

---

print.tmt_data *Print a summary of a TMT preprocessing result*

Description

Reports the number of channels, protein groups and conditions, so that the shape of the experiment can be checked at a glance before processing it.

Usage

```
## S3 method for class 'tmt_data'
print(x, ...)
```

Arguments

x	A tmt_data object, as returned by preprocess_tmt().
...	Ignored, present for compatibility with the print generic.

Value

x, invisibly. Called for the summary it prints.

Examples

```
tmt <- preprocess_tmt(
  system.file("extdata", "nadia_tmt_report.tsv.gz", package = "NADIA"),
  condition_order = c("A", "B", "D"),
  verbose = FALSE)
print(tmt)
```

process_proteomics *Process proteomics data*

Description

Complete processing pipeline: filtering, normalization, imputation and differential expression analysis. Coordinates sub-modules Normalization.R, Imputation.R, and DEAnalysis.R.

Usage

```
process_proteomics(
  preprocessing,
  export_dir = NULL,
  min_reps_filter = NULL,
  min_groups_filter = 1,
  norm_method = "cycloess",
  cyclic_loess_method = "fast",
  cyclic_loess_iterations = 3,
  cyclic_loess_span = 0.7,
  batch_correct = FALSE,
  batch_column = "Batch",
  batch_algorithm = "ComBat",
  batch_ComBat_mode = 1,
  batch_covariates = NULL,
  batch_qualitycontrol = FALSE,
  imp_method = "combo",
  mar_method = "Impseqrob",
  mnar_method = "min",
  prop_na_mnar = 0.51,
  prop_present_mar = 0.5,
  min_present_mar = 1,
  require_n_conditions = 1,
  max_na_prop = NULL,
  method_args = list(),
  with_value = NA_real_,
  comparisons = NULL,
  control = NULL,
  logFC_threshold = 0,
  alpha = 0.05,
  eBayes_trend = NULL,
  eBayes_robust = NULL,
  de_method = "limma",
  covariate_df = NULL,
  covariate_column = NULL,
  bio_replicate_column = NULL,
  export_normalized = TRUE,
  export_imputed = TRUE,
  export_format = "tsv",
  export_volcano = TRUE,
  export_boxplot = TRUE,
  export_pca = TRUE,
```

```
  assay_name = NULL,
  log2_input = FALSE,
  verbose = TRUE
)
```

Arguments

preprocessing	A proteomics_data object, as returned by preprocess_spectronaut(), preprocess_diann(), preprocess_tmt(), preprocess_lfq() or preprocess_se(); or a SummarizedExperiment of protein intensities with the condition in colData()$Condition (see preprocess_se()).
export_dir	Output directory for exported files. Defaults to NULL, which writes nothing to disk; pass a path to enable the exports controlled by export_normalized, export_imputed, export_volcano, export_boxplot and export_pca.
min_reps_filter	Minimum replicates for filtering. If NULL, auto-computed
min_groups_filter	Minimum groups for filtering (default: 1)
norm_method	Normalization method passed to normalize_proteomics() (default: "cycloess"). See normalize_proteomics() for all 13 options.
cyclic_loess_method	Cyclic Loess method: "fast" or "pairs" (default: "fast")
cyclic_loess_iterations	Number of iterations for Cyclic Loess (default: 3)
cyclic_loess_span	Span parameter for Cyclic Loess (default: 0.7)
batch_correct	Logical. Apply BERT batch correction after normalization (default: FALSE). Requires covariate_df with batch_column.
batch_column	Column in covariate_df containing batch assignments (default: "Batch"). Must have >= 2 unique values.
batch_algorithm	Batch correction algorithm: "ComBat" (default), "limma", or "ref"
batch_ComBat_mode	Integer 1-4 for ComBat parametric/mean-only settings (default: 1)
batch_covariates	Character vector of colData column names to protect during BERT batch correction (default: NULL). Categorical columns are encoded as indicator variables automatically; numeric columns are passed through unchanged and therefore act as continuous covariates.
batch_qualitycontrol	Logical. Compute ASW quality metrics (default: FALSE)
imp_method	Imputation method (default: "combo"). See impute_proteomics() for all options.
mar_method	MAR method for combo mode (default: "Impseqrob")
mnar_method	MNAR method for combo mode (default: "min")
prop_na_mnar	NA proportion for MNAR classification (default: 0.51)
prop_present_mar	Present proportion for MAR (default: 0.5)
min_present_mar	Minimum present values for MAR (default: 1)

require_n_conditions
: Required conditions with presence (default: 1)

max_na_prop
: Maximum NA proportion above which a protein is removed before imputation. NULL (the default) disables the filter.

method_args
: Named list of per-method argument lists

with_value
: Constant value for imp_method="with"

comparisons
: Comparisons for DE. If NULL, generates all pairwise

control
: Control condition. If NULL, compares all

logFC_threshold
: LogFC threshold for significance (default: 0)

alpha
: Adjusted p-value threshold (default: 0.05)

eBayes_trend
: Use trend estimation in eBayes. If NULL (default), it is resolved from de_method: TRUE for "limma", FALSE for "limpa".

eBayes_robust
: Use robust estimation in eBayes. If NULL (default), it is resolved from de_method: TRUE for "limma", FALSE for "limpa".

de_method
: DE method: "limma" (default) or "limpa" (probabilistic, requires imp_method="limpa")

covariate_df
: Data frame with Column + covariate column(s) for paired/blocked design (default: NULL)

covariate_column
: Name(s) of the covariate column(s) for the DE model. Single string (e.g., "Subject") or character vector (e.g., c("Subject", "Batch")). Default: NULL

bio_replicate_column
: Column name in covariate_df identifying biological replicates (e.g., "Patient", "Subject"). Used with limma::duplicateCorrelation() to account for technical replicates or paired designs via random effect blocking. Default: NULL

export_normalized
: Export normalized matrix (default: TRUE)

export_imputed
: Export imputed matrix (default: TRUE)

export_format
: Export format: "tsv", "parquet", or "both" (default: "tsv"). It applies to every file written, the matrices and the plot inputs alike. Parquet needs the suggested package arrow, which is checked before the analysis starts.

export_volcano
: Export VolcanoPlot_Input (default: TRUE)

export_boxplot
: Export BoxPlot_Input (default: TRUE)

export_pca
: Export PCA_Input (default: TRUE)

assay_name
: For a SummarizedExperiment input, the assay with the intensities (default: the first). See preprocess_se().

log2_input
: For a SummarizedExperiment input, TRUE if the intensities are on the log2 scale (default FALSE, linear).

verbose
: Print progress messages (default: TRUE)

Details

The input is a proteomics_data object, which every preprocessing function returns with the same three elements, so the pipeline is indifferent to the acquisition and the search engine the data came from. A SummarizedExperiment is also accepted, for data imported with other tools: it is converted by preprocess_se(), with assay_name and log2_input.

Value

List of class proteomics_result with:

- se_proc: Processed SummarizedExperiment with all assays
- DEPs_results: Data frame with differential expression results
- BoxPlot_Input: Long-format data frame with one row per protein, sample and assay (columns Column, Assay, Intensity, Condition, Replicate, Protein.IDs). Feed it to `boxplot_highchart_list()`.
- PCA_Input: Long-format data frame with the imputed intensities plus one adjP_* column per comparison and a sig_any flag. Feed it to `pca_highchart_list()`, `proteomics_heatmap()` or `proteomics_heatmap_list()`.
- comparisons: Comparisons performed
- parameters: Parameters used

`BoxPlot_Input` and `PCA_Input` are always returned, whether or not `export_dir` is given: the plotting layer needs them, and requiring a round trip through disk to obtain them would be gratuitous.

Examples

```
data(nadia_dia)

# Normalization, imputation and differential expression in one call
res <- process_proteomics(nadia_dia, verbose = FALSE)
res

SummarizedExperiment::assayNames(res$se_proc)
table(res$DEPs_results$Comparison, res$DEPs_results$Change)

# The plotting layer is fed straight from the result, no files involved
names(res$BoxPlot_Input)
names(res$PCA_Input)

# Another combination: quantile normalization and a single imputation method
res2 <- process_proteomics(nadia_dia, norm_method = "quantile",
                           imp_method = "QRILC", verbose = FALSE)
SummarizedExperiment::assayNames(res2$se_proc)
```

---

protein_list_reactable

Interactive Reactable Table for Protein_ID Data (post-Spectronaut)

Description

Builds a reactable table with 2-level grouped headers, static columns pinned (sticky) to the left and data bars coloured by condition inside each numeric cell. It reproduces the usual Excel layout and improves on it.

Usage

```
protein_list_reactable(
  data,
  metadata = NULL,
  page_size = 15,
  height = 720,
  element_id = NULL,
  selection = NULL,
  searchable = TRUE
)
```

Arguments

data	Data frame or path to a Protein_ID TSV/CSV/Parquet file (output of any preprocess_*() function -> protein_id).
metadata	Optional: metadata data frame (run_summary) with a Coding column that fixes the order of the sample columns.
page_size	Rows per page (default 15).
height	Table height in px (default 720).
element_id	Reactable element ID (default NULL).
selection	"single" | "multiple" | NULL.
searchable	Enable the search box (default TRUE).

Value

A reactable object.

Examples

```
if (requireNamespace("reactable", quietly = TRUE)) {
  data(nadia_dia)

  # metadata$Coding fixes the order of the sample columns
  tbl <- protein_list_reactable(nadia_dia$protein_id,
                                metadata = nadia_dia$metadata)
  class(tbl)
}
```

---

protein_list_widget *Full Widget for the Protein_ID Table with Filters, Search and Excel Export*

Description

Wraps protein_list_reactable() with:

- A search bar and buttons (toggle filters, clear, export to Excel).
- Per-condition chips that hide/show the 16 associated columns.
- A numeric filter on MW in Da with AND/OR operators.
- Excel export with 2-level headers (merged groups + sub-labels) and a per-condition tint, reproducing the manual layout.

Usage

```
protein_list_widget(
  data,
  metadata = NULL,
  page_size = 15,
  height = 720,
  element_id = "protein_id_table",
  selection = NULL,
  searchable = TRUE
)
```

Arguments

data	Data frame or path to a Protein_ID TSV/CSV/Parquet file (output of any preprocess_*() function -> protein_id).
metadata	Optional: metadata data frame (run_summary) with a Coding column that fixes the order of the sample columns.
page_size	Rows per page (default 15).
height	Table height in px (default 720).
element_id	Element ID (default "protein_id_table").
selection	"single" | "multiple" | NULL.
searchable	Enable the search box (default TRUE).

Value

A browsable htmltools object.

Examples

```
if (requireNamespace("reactable", quietly = TRUE)) {
  data(nadia_dia)

  w <- protein_list_widget(nadia_dia$protein_id,
                           metadata = nadia_dia$metadata)
  print(class(w))   # print(w) itself opens it in the Viewer / browser
}
```

---

proteomics_heatmap *Create a tidyHeatmap Heatmap for Proteomics*

Description

Create a tidyHeatmap Heatmap for Proteomics

Usage

```
proteomics_heatmap(
  data,
  mode = c("all", "any", "target"),
  alpha = 0.05,
  comparison = NULL,
  feature_ids = NULL,
  row_annotation = NULL,
  row_annotation_cols = NULL,
  row_annotation_palette = NULL,
  row_annotation_size = NULL,
  row_annotation_name_size = 8,
  row_order_by = NULL,
  split_rows_by = NULL,
  scale_data = c("row", "none", "column"),
  sample_order = "clustering",
  condition_order = NULL,
  cluster_rows = FALSE,
  cluster_columns = TRUE,
  show_row_names = NULL,
  show_column_names = TRUE,
  palette_value = NULL,
  palette_annotation = NULL,
  reverse_palette = FALSE,
  row_title = "Proteins",
  column_title = "Samples",
  row_title_size = 10,
  column_title_size = 10,
  show_row_title = TRUE,
  show_column_title = TRUE,
  show_annotation = TRUE,
  split_by_condition = FALSE,
  show_adjp_annotation = TRUE,
  palette_adjp = NULL,
  row_names_size = 7,
  column_names_size = 9,
  column_names_rotation = 45,
  column_dend_height = NULL,
  row_dend_width = NULL,
  show_heatmap_legend = TRUE,
  show_annotation_legend = TRUE,
  border_color = NULL,
  heatmap_title = NULL,
  heatmap_title_size = 14,
  heatmap_title_face = c("bold", "plain", "italic", "bold.italic"),
  export_path = NULL,
  export_file = NULL,
  plot_width = 10,
  plot_height = 8,
  export_dpi = 300
)
```

Arguments

`data`	Data frame in long format (see prepare_heatmap_data for the structure)
`mode`	Protein filtering mode: "all", "any", or "target"
`alpha`	Significance threshold for DEP proteins (default: 0.05)
`comparison`	Name of the comparison for mode "target" (e.g. "B-A")
`feature_ids`	Vector of specific FeatureIDs to show (default: NULL, uses the mode-based filtering). When supplied, only these proteins are shown and the mode/alpha filtering is ignored.
`row_annotation`	Row annotations (FeatureIDs). It can be: • Path to a TSV file with a "FeatureID" column plus additional categorical columns • Data frame with the same structure • NULL: no row annotations (default) Empty values, and proteins the annotation does not list, are shown as "NA" in white and placed last when ordering or splitting by it.
`row_annotation_cols`	Vector of column names to display as annotations. Default: NULL (uses every column except FeatureID)
`row_annotation_palette`	Named list of palettes, one per annotation. Example: list(Pathway = "brewer:Set1", Function = c("red", "blue", "green"))
`row_annotation_size`	Width of the row annotation bars. It can be: • Number: interpreted as centimetres (e.g. 0.3 = 0.3cm) • A unit object: grid::unit(0.3, "cm") • NULL: use tidyHeatmap's default value
`row_annotation_name_size`	Font size of the row annotation names (default: 8)
`row_order_by`	Row order. It can be: • NULL: no particular ordering (default) • "clustering": order by hierarchical clustering • A column name: order by that annotation (e.g. "Specie") • A vector of columns: order sequentially (e.g. c("Specie", "Process", "Function")) • Include "adjP" when mode = "target" to order by adjusted p-value
`split_rows_by`	Name of the annotation column used to split the rows into groups (default: NULL)
`scale_data`	Scaling type: "none", "row", "column" (default: "row")
`sample_order`	Sample order: "clustering", "condition", or a custom vector
`condition_order`	Condition order when sample_order = "condition"
`cluster_rows`	Cluster the rows (default: FALSE)
`cluster_columns`	Cluster the columns (default: TRUE)
`show_row_names`	Show the row names (default: TRUE when <= 50 proteins)

`show_column_names`
: Show the column names (default: TRUE)

`palette_value`
: Palette for the heatmap values (see get_heatmap_palette)

`palette_annotation`
: Palette for the Condition annotation

`reverse_palette`
: Reverse the value palette (default: FALSE)

`row_title`
: Title for the rows

`column_title`
: Title for the columns

`row_title_size`
: Font size of the row title (default: 10)

`column_title_size`
: Font size of the column title (default: 10)

`show_row_title`
: Show the row title (default: TRUE)

`show_column_title`
: Show the column title (default: TRUE)

`show_annotation`
: Show the Condition annotation (default: TRUE)

`split_by_condition`
: Split the heatmap by condition (default: FALSE)

`show_adjp_annotation`
: Show the adjP row annotation when mode="target" (default: TRUE)

`palette_adjp`
: Palette for the adjP annotation, three colours for adjP = 0, 0.01 and 0.05: `NULL` for the default (red-orange-white), `"pkg::name"` (paletteer), `"brewer:Name"` (RColorBrewer) or a vector of colours.

`row_names_size`
: Font size of the row names (default: 7)

`column_names_size`
: Font size of the column names (default: 9)

`column_names_rotation`
: Rotation of the column names in degrees (default: 45)

`column_dend_height`
: Height of the column dendrogram. It can be:
  - Number: interpreted as millimetres (e.g. 30 = 30mm)
  - A unit object: grid::unit(2, "cm")
  - NULL: use ComplexHeatmap's default value

`row_dend_width`
: Width of the row dendrogram. Same format as column_dend_height

`show_heatmap_legend`
: Show the heatmap legend (default: TRUE)

`show_annotation_legend`
: Show the annotation legends (default: TRUE)

`border_color`
: Border colour of the heatmap cells. It can be:
  - NULL or FALSE: no border (default)
  - TRUE: black border
  - A colour string: that specific colour (e.g. "black", "grey", "#CCCCCC")

`heatmap_title`
: Main heatmap title (default: NULL, no title)

`heatmap_title_size`
: Font size of the main title (default: 14)

heatmap_title_face
: Font face of the title: "plain", "bold", "italic", "bold.italic" (default: "bold")

export_path
: Path used to export the heatmap data to TSV (default: NULL, nothing is exported). The file contains FeatureID, the per-sample intensity values, and the metadata (adjP where applicable).

export_file
: Path used to export the plot. The format is taken from the extension:

- .png: PNG image (raster)
- .svg: SVG image (vector)
- .pdf: PDF document (vector)

plot_width
: Plot width in inches (default: 10). To get pixels: pixels = inches x dpi (e.g. 10" x 300dpi = 3000px)

plot_height
: Plot height in inches (default: 8). To get pixels: pixels = inches x dpi (e.g. 8" x 300dpi = 2400px)

export_dpi
: Resolution for PNG output in dots per inch (default: 300). Higher dpi = more detail. Common values: 72 (web), 150 (draft), 300 (publication)

Value

tidyHeatmap/ComplexHeatmap object

Examples

```
if (requireNamespace("ComplexHeatmap", quietly = TRUE) &&
    requireNamespace("tidyHeatmap", quietly = TRUE) &&
    requireNamespace("circlize", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)

  # Proteins significant in the B-A comparison, samples grouped by condition
  hm <- proteomics_heatmap(
    res$PCA_Input,
    mode            = "target",
    comparison      = "B-A",
    scale_data      = "row",
    sample_order    = "condition",
    condition_order = c("A", "B", "D")
  )
  print(class(hm))   # print(hm) itself draws it on the current device
}
```

---

proteomics_heatmap_list

Build a List of Heatmaps for Several Subsets

Description

Automatically builds heatmaps for "all", "any" and/or specific comparisons.

Usage

```
proteomics_heatmap_list(
  data,
  modes = c("all", "any"),
  alpha = 0.05,
  feature_ids = NULL,
  row_annotation = NULL,
  row_annotation_cols = NULL,
  row_annotation_palette = NULL,
  row_annotation_size = NULL,
  row_annotation_name_size = 8,
  row_order_by = NULL,
  split_rows_by = NULL,
  scale_data = c("row", "none", "column"),
  sample_order = "clustering",
  condition_order = NULL,
  cluster_rows = FALSE,
  cluster_columns = TRUE,
  show_row_names = NULL,
  show_column_names = TRUE,
  palette_value = NULL,
  palette_annotation = NULL,
  reverse_palette = FALSE,
  row_title_size = 10,
  column_title_size = 10,
  show_row_title = TRUE,
  show_column_title = TRUE,
  show_annotation = TRUE,
  split_by_condition = FALSE,
  show_adjp_annotation = TRUE,
  palette_adjp = NULL,
  row_names_size = 7,
  column_names_size = 9,
  column_names_rotation = 45,
  column_dend_height = NULL,
  row_dend_width = NULL,
  show_heatmap_legend = TRUE,
  show_annotation_legend = TRUE,
  border_color = NULL,
  heatmap_title = NULL,
  heatmap_title_size = 14,
  heatmap_title_face = "bold",
  export_path = NULL,
  export_modes = NULL,
  export_file = NULL,
  plot_width = 10,
  plot_height = 8,
  export_dpi = 300
)
```

Arguments

data	Data frame in long format (see prepare_heatmap_data for the structure)
modes	Vector of modes to generate: "all", "any", and/or comparison names (default: c("all", "any"))
alpha	Significance threshold for DEP proteins (default: 0.05)
feature_ids	Vector of specific FeatureIDs to show (default: NULL)
row_annotation	Row annotations (TSV path or data.frame)
row_annotation_cols	Columns to use as row annotations
row_annotation_palette	List of palettes for the row annotations
row_annotation_size	Width of the row annotation bars (a number in cm, or a unit)
row_annotation_name_size	Font size of the row annotation names (default: 8)
row_order_by	Row order: "clustering", annotation column(s), or include "adjP" for mode="target"
split_rows_by	Annotation column used to split the rows into groups
scale_data	Scaling type: "none", "row", "column" (default: "row")
sample_order	Sample order: "clustering", "condition", or a custom vector
condition_order	Condition order when sample_order = "condition"
cluster_rows	Cluster the rows (default: FALSE)
cluster_columns	Cluster the columns (default: TRUE)
show_row_names	Show the row names (default: auto)
show_column_names	Show the column names (default: TRUE)
palette_value	Palette for the heatmap values
palette_annotation	Palette for the Condition annotation
reverse_palette	Reverse the value palette (default: FALSE)
row_title_size	Font size of the row title (default: 10)
column_title_size	Font size of the column title (default: 10)
show_row_title	Show the row title (default: TRUE)
show_column_title	Show the column title (default: TRUE)
show_annotation	Show the Condition annotation (default: TRUE)
split_by_condition	Split the heatmap by condition (default: FALSE)
show_adjp_annotation	Show the adjP row annotation for comparisons (default: TRUE)
palette_adjp	Palette for the adjP annotation (see proteomics_heatmap)

`row_names_size` Font size of the row names (default: 7)

`column_names_size`
: Font size of the column names (default: 9)

`column_names_rotation`
: Rotation of the column names (default: 45)

`column_dend_height`
: Height of the column dendrogram (a number in mm, or a unit)

`row_dend_width` Width of the row dendrogram (a number in mm, or a unit)

`show_heatmap_legend`
: Show the heatmap legend (default: TRUE)

`show_annotation_legend`
: Show the annotation legends (default: TRUE)

`border_color` Border colour of the cells (NULL, TRUE, or a colour)

`heatmap_title` Main heatmap title (default: NULL, no title). "{mode}" can be used as a placeholder, and is replaced by the mode name

`heatmap_title_size`
: Font size of the main title (default: 14)

`heatmap_title_face`
: Font face of the title (default: "bold")

`export_path` Base path used to export the data to TSV (default: NULL). The mode name is appended to the file name (e.g. "export_all.tsv", "export_B-A.tsv")

`export_modes` Vector of modes to export (default: NULL, exports all of them). Only relevant when export_path is set. Example: c("all", "B-A")

`export_file` Base path used to export the plots. The mode is appended to the name. The format is taken from the extension (.png, .svg, .pdf)

`plot_width` Plot width in inches (default: 10)

`plot_height` Plot height in inches (default: 8)

`export_dpi` Resolution for PNG output in dots per inch (default: 300)

Value

Named list of tidyHeatmap objects

Examples

```
if (requireNamespace("ComplexHeatmap", quietly = TRUE) &&
    requireNamespace("tidyHeatmap", quietly = TRUE) &&
    requireNamespace("circlize", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)

  # "any" plus one heatmap per named comparison
  hm_list <- proteomics_heatmap_list(
    res$PCA_Input,
    modes           = c("any", "B-A"),
    sample_order    = "condition",
    condition_order = c("A", "B", "D"),
    palette_value   = "brewer:RdYlBu"
  )
  print(names(hm_list))   # print(hm_list[["B-A"]]) draws one of them
}
```

`pvca_analysis` *PVCA Analysis – Orchestrator*

Description

Runs the full PVCA workflow: compute variance components, generate plot, and optionally export results.

Usage

```
pvca_analysis(
  se,
  assay_name = NULL,
  technical_factors = character(0),
  biological_factors = character(0),
  pca_covariates = NULL,
  pca_threshold = 0.6,
  variance_threshold = 0.01,
  na_action = "complete",
  fill_value = -1,
  colors = NULL,
  verbose = TRUE,
  output_dir = NULL,
  export_plots = TRUE,
  export_tables = TRUE,
  plot_width = 10,
  plot_height = 6,
  plot_dpi = 150
)
```

Arguments

`se`	SummarizedExperiment object.
`assay_name`	Character. Assay to analyze. NULL = second assay (normalized, pre-imputation).
`technical_factors`	Character vector. Factors representing technical variation (e.g., "Injection", "Digestion").
`biological_factors`	Character vector. Factors representing biological variation (e.g., "Condition", "Gender", "Age").
`pca_covariates`	Character vector or NULL. If provided, generates PCA plots colored by each covariate (grid + individual plots). These are included in the returned list and exported as PNGs. Default NULL (skip).
`pca_threshold`	Numeric (0-1). Cumulative variance threshold for PCA (default 0.6).
`variance_threshold`	Numeric (0-1). Minimum weight for individual display (default 0.01).
`na_action`	Character: "complete", "fill", or "none" (default "complete").
`fill_value`	Numeric. NA replacement when na_action = "fill" (default -1).
`colors`	Named character vector for category colors (default NULL = built-in palette).

verbose	Logical (default TRUE).
output_dir	Character. Directory for exports. NULL = no export.
export_plots	Logical (default TRUE).
export_tables	Logical (default TRUE).
plot_width	Numeric in inches (default 10).
plot_height	Numeric in inches (default 6).
plot_dpi	Numeric (default 150).

Value

Named list:

variance_components data.frame with label, weights, category

plot ggplot2 object

n_proteins Number of proteins used in the analysis

assay_name Assay analyzed

parameters List of parameters used

Examples

```
data(nadia_dia)

# nadia_dia has no batch information, so the example builds a plausible one:
# two digestion batches crossed with the three conditions.
cov <- data.frame(Column = nadia_dia$metadata$Coding,
                  Batch = rep(c("b1", "b2"),
                              length.out = nrow(nadia_dia$metadata)),
                  stringsAsFactors = FALSE)
res <- process_proteomics(nadia_dia, covariate_df = cov, verbose = FALSE)

# Variance decomposition: how much of the signal each factor explains
pv <- pvca_analysis(res$se_proc, assay_name = "Impseqrob_min",
                    technical_factors = "Batch",
                    biological_factors = "Condition",
                    verbose = FALSE)
pv$pvca_table
```

---

quant_list_widget *Full Widget for the Protein_QUANT Table with the log2 Matrix Appended*

Description

Reactable table that reproduces the layout of the Protein-List_QUANT Excel sheet, with 2-level headers, sticky columns, a blue palette, aggregated filters and Excel export. It appends to Protein_QUANT the 16 columns of the normalized/imputed log2 matrix, matching by Protein Groups.

Usage

```
quant_list_widget(
  data = NULL,
  matrix_data = NULL,
  metadata = NULL,
  page_size = 15,
  height = 720,
  element_id = "quant_id_table",
  selection = NULL,
  searchable = TRUE
)
```

Arguments

data	Data frame or path to a Protein_QUANT TSV/CSV/Parquet file. Required; there is no default.
matrix_data	Data frame or path to a TSV/CSV/Parquet file with the normalized/imputed log2 matrix (a ProteinGroups column + _ samples).
metadata	Optional: metadata data frame with a Coding column that fixes the sample order.
page_size	Rows per page (default 15).
height	Table height in px (default 720).
element_id	Reactable element ID.
selection	"single" | "multiple" | NULL.
searchable	Enable the search box (default TRUE).

Value

A browsable object.

Examples

```
if (requireNamespace("reactable", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)

  # The log2 matrix: a ProteinGroups column plus one column per sample
  mat <- SummarizedExperiment::assay(res$se_proc, "Impseqrob_min")
  mat_df <- data.frame(ProteinGroups = rownames(mat), mat,
                       check.names = FALSE)

  w <- quant_list_widget(nadia_dia$protein_quant, matrix_data = mat_df,
                         metadata = nadia_dia$metadata)
  print(class(w))
}
```

read_nadia *Read a* .nadia *file*

Description

Loads the whole analysis: the preprocessing tables, the processing results, the intensity matrices, the parameters and the provenance. The canonical tables come out of the SQL views stored in the file, with their R classes and column order restored.

Usage

```
read_nadia(file)
```

Arguments

file	Path to a .nadia file.

Details

To get objects the rest of the package can use directly, pass the result to nadia_preprocessing() or nadia_result().

Value

An object of class nadia_db: a list with file, meta, parameters, calls, packages, source_files, the canonical tables (metadata, protein_id, protein_quant and, when present, DEPs_results, BoxPlot_Input, PCA_Input, pattern_profiler), the matrices and the imputed_values mask.

See Also

write_nadia(), nadia_result(), nadia_preprocessing()

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
    data(nadia_dia)
    res <- process_proteomics(nadia_dia, verbose = FALSE)
    f <- file.path(tempdir(), "read.nadia")
    write_nadia(f, nadia_dia, res, verbose = FALSE)

    db <- read_nadia(f)
    db
    identical(db$protein_quant, nadia_dia$protein_quant)

    unlink(f)
}
```

read_pattern_profiler_data

Read Pattern Profiler data from a parquet file

Description

Read Pattern Profiler data from a parquet file

Usage

```
read_pattern_profiler_data(file_path, min_membership = NULL)
```

Arguments

file_path	Path to the parquet file
min_membership	Optional filter by minimum membership

Value

DataFrame with the clustering data

Examples

```
if (requireNamespace("arrow", quietly = TRUE) &&
    requireNamespace("Mfuzz", quietly = TRUE) &&
    requireNamespace("e1071", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)

  # Write the clustering to parquet, then read it back
  f <- file.path(tempdir(), "pattern_profiler.parquet")
  pattern_profiler_analysis(res$se_proc, res$DEPs_results,
                            assay_name = "Impseqrob_min",
                            auto_select_c = FALSE, c = 3,
                            output_file = f, verbose = FALSE)

  pp_data <- read_pattern_profiler_data(f, min_membership = 0.5)
  unlink(f)
  print(head(pp_data))
}
```

results_list_reactable

Interactive Reactable Table for Differential Expression Results

Description

Builds a professionally formatted reactable table to display protein differential expression results. Works both in Shiny (it returns a reactable object) and standalone via `results_list_widget()`.

Usage

```
results_list_reactable(
  data,
  protein_quant = NULL,
  comparisons = NULL,
  ain = NULL,
  alpha = 0.05,
  lfc_thr = 0,
  page_size = 15,
  height = 720,
  show_missing = TRUE,
  element_id = NULL,
  selection = NULL,
  searchable = TRUE
)
```

Arguments

data	Data frame or path to a TSV/CSV/Parquet file with DE results. Required columns: Protein.IDs, Gene.Names, logFC, P.Value, adj.P.Val, Change, Comparison. Optional: Assay, and the four missingness columns MissGlobal, MissComp, MissCND1 and MissCND2, which are shown only if all four are present
protein_quant	Data frame (preprocessing$protein_quant) or path to a Protein_QUANT_*.tsv file. If not NULL, the Description and Quant_Pepts columns are added.
comparisons	Vector of comparisons to include (NULL = all of them)
ain	Vector of assays to keep (NULL = all of them)
alpha	Significance threshold used to highlight the FDR (default: 0.05)
lfc_thr	log2 fold-change threshold (default: 0, reserved for future use)
page_size	Rows per page (default: 15)
height	Table height in pixels (default: 720)
show_missing	Show the missingness percentage columns (default: TRUE)
element_id	Element ID for the Reactable JS API (default: NULL)
selection	Selection type: "single", "multiple", or NULL (default: NULL)
searchable	Enable the internal search box (default: TRUE)

Value

A reactable object

Examples

```
if (requireNamespace("reactable", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)

  # protein_quant adds the Description and Quant_Pepts columns
  tbl <- results_list_reactable(
    res$DEPs_results,
    protein_quant = nadia_dia$protein_quant,
    comparisons   = "B-A"
```

```
  )
  class(tbl)
}
```

`results_list_widget` *Full Widget with Filters, Search, Export and CSS*

Description

Wraps `results_list_reactable()` with interactive crosstalk filters (Comparison, Change, Method), a search box, an export-to-Excel button and embedded CSS. The result is browsable: printing it at the console opens it automatically in the RStudio Viewer or in the browser.

Usage

```
results_list_widget(
  data,
  protein_quant = NULL,
  comparisons = NULL,
  ain = NULL,
  alpha = 0.05,
  lfc_thr = 0,
  page_size = 15,
  height = 720,
  show_missing = TRUE,
  element_id = "deps_table",
  selection = NULL,
  searchable = TRUE
)
```

Arguments

`data`	Data frame or path to a TSV/CSV/Parquet file with DE results. Required columns: Protein.IDs, Gene.Names, logFC, P.Value, adj.P.Val, Change, Comparison. Optional: Assay, and the four missingness columns MissGlobal, MissComp, MissCND1 and MissCND2, which are shown only if all four are present
`protein_quant`	Data frame (preprocessing$protein_quant) or path to a Protein_QUANT_*.tsv file. If not NULL, the Description and Quant_Pepts columns are added.
`comparisons`	Vector of comparisons to include (NULL = all of them)
`ain`	Vector of assays to keep (NULL = all of them)
`alpha`	Significance threshold used to highlight the FDR (default: 0.05)
`lfc_thr`	log2 fold-change threshold (default: 0, reserved for future use)
`page_size`	Rows per page (default: 15)
`height`	Table height in pixels (default: 720)
`show_missing`	Show the missingness percentage columns (default: TRUE)
`element_id`	Element ID (default: "deps_table")
`selection`	Selection type: "single", "multiple", or NULL (default: NULL)
`searchable`	Enable the internal search box (default: TRUE)

Value

A browsable htmltools object

Examples

```
if (requireNamespace("reactable", quietly = TRUE) &&
    requireNamespace("crosstalk", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)

  # Printing the widget opens it in the Viewer / browser
  w <- results_list_widget(res$DEPs_results,
                           protein_quant = nadia_dia$protein_quant)
  print(class(w))
}
```

---

run_mfuzz_clustering *Run Mfuzz clustering*

Description

Run Mfuzz clustering

Usage

```
run_mfuzz_clustering(eset_std, c, m)
```

Arguments

eset_std	Standardised ExpressionSet
c	Number of clusters
m	Fuzziness parameter

Details

The initial partition is drawn from the caller's RNG.

Value

Mfuzz clustering object

select_optimal_clusters *Select the optimal number of clusters*

Description

Select the optimal number of clusters

Usage

```
select_optimal_clusters(
  eset_std,
  c_range = 2:10,
  m = NULL,
  method = c("xb", "consensus", "elbow"),
  n_starts = 3L,
  verbose = TRUE
)
```

Arguments

eset_std	Standardised ExpressionSet
c_range	Range of cluster numbers to evaluate
m	Fuzziness parameter
method	Method: "xb", "consensus", "elbow"
n_starts	Random starts per candidate, passed on to `evaluate_cluster_range()`
verbose	Show progress

Value

List with optimal_c, metrics, m

standardize_eset *Standardise an ExpressionSet (row-wise z-score)*

Description

Standardise an ExpressionSet (row-wise z-score)

Usage

```
standardize_eset(eset, verbose = TRUE)
```

Arguments

eset	ExpressionSet object
verbose	Print progress messages (default: TRUE)

Value

Standardised ExpressionSet

summarize_pattern_profiler *Summary of the Pattern Profiler data*

Description

Summary of the Pattern Profiler data

Usage

```
summarize_pattern_profiler(data)
```

Arguments

data	Pattern Profiler DataFrame

Value

List with summary statistics

Examples

```
if (requireNamespace("Mfuzz", quietly = TRUE) &&
    requireNamespace("e1071", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)
  pp <- pattern_profiler_analysis(res$se_proc, res$DEPs_results,
                                  assay_name = "Impseqrob_min",
                                  auto_select_c = FALSE, c = 3,
                                  verbose = FALSE)

  info <- summarize_pattern_profiler(pp$long_output)
  print(info$cluster_summary)
}
```

summary_list_widget *Interactive Reactable Table for the Sample Metadata*

Description

Builds a reactable table that reproduces the layout of the metadata Excel sheet (FileName, Condition, Replicate, Coding, # Unique PSMs, # Unique Peptides, # Protein Groups). Black header, rows tinted by condition in light shades and Condition/Coding cells with a strong colour chip (the same scheme used by protein_list_widget() / quant_list_widget()).

Usage

```
summary_list_widget(
  data = NULL,
  page_size = 16,
  height = 540,
  element_id = "summary_table",
  selection = NULL,
  searchable = FALSE
)
```

Arguments

data	Data frame or path to a metadata TSV/CSV file. Required; there is no default. It must have the columns R.FileName, R.Condition, R.Replicate, Coding, R.PrecursorsIdentified, R.StrippedSequencesIdentified, R.ProteinGroupsIdentified.
page_size	Page size (default 16, i.e. all the rows).
height	Height in px of the table container (default 540).
element_id	Widget id in the DOM (default "summary_table").
selection	Selection type ("multiple" or NULL).
searchable	Enable the global search box (default FALSE).

Value

An htmltools object (browsable tagList) ready to be rendered.

Examples

```
if (requireNamespace("reactable", quietly = TRUE)) {
  data(nadia_dia)

  # LFQ/TMT metadata lack the identification counts; the widget then shows
  # only FileName/Condition/Replicate/Coding
  w <- summary_list_widget(nadia_dia$metadata)
  print(class(w))
}
```

---

volcano_highchart_list

Interactive Volcano Plot with Highcharter

Description

Interactive Volcano Plot with Highcharter

Usage

```
volcano_highchart_list(
  de_res,
  ain = NULL,
  comparisons = NULL,
  lfc_thr = 0,
  alpha = 0.05,
  p_col = "adj.P.Val",
  point_size = 4,
  colors = NULL,
  palette = NULL,
  show_top_genes = 0,
  highlight_genes = NULL,
  title = NULL
)
```

Arguments

de_res	Data frame with differential expression results
ain	Vector of assays to filter on (optional)
comparisons	Vector of comparisons to include (optional)
lfc_thr	log2 fold-change threshold (default: 0)
alpha	Significance threshold (default: 0.05)
p_col	Column of p-values to use
point_size	Point size (default: 4)
colors	List of colours for "up", "down", "ns" (ignored when palette is used)
palette	Colour palette for up, down and non-significant proteins, in that order: `"pkg::name"` for a palette from paletteer, `"brewer:Name"` (or the bare name) for an RColorBrewer palette, or a vector of colours. Its first three colours are used. `NULL` (default) uses `colors`.
show_top_genes	Number of top genes to label by significance (default: 0)
highlight_genes	Vector of gene names to highlight manually (default: NULL)
title	Custom chart title (default: NULL, uses "Comparison (Assay)"). Use `{comparison}` as a placeholder (e.g. "Volcano Plot: {comparison}" -> "Volcano Plot: B-A")

Value

List of highchart objects

Examples

```
if (requireNamespace("highcharter", quietly = TRUE)) {
  data(nadia_dia)
  res <- process_proteomics(nadia_dia, verbose = FALSE)

  # One volcano per comparison, labelling the 10 most significant proteins
  hc_list <- volcano_highchart_list(
    res$DEPs_results,
    comparisons     = c("B-A", "D-A"),
```

```
    lfc_thr         = 1,
    alpha           = 0.05,
    show_top_genes  = 10
  )
  names(hc_list)
}
```

`wrap_heatmap_with_title` *Wrap a Heatmap Together With Its Title*

Description

Wrap a Heatmap Together With Its Title

Usage

```
wrap_heatmap_with_title(hm, title, title_size = 14, title_face = "bold")
```

Arguments

`hm`	tidyHeatmap object (InputHeatmap)
`title`	Heatmap title
`title_size`	Font size of the title
`title_face`	Font face of the title

Value

proteomics_heatmap object (S3 list)

`write_nadia` *Write a complete analysis to a single* `.nadia` *file*

Description

Stores the preprocessing tables, the processing results and, optionally, the Pattern Profiler output in one DuckDB database, together with the parameters and the provenance of the run. Nothing is duplicated: everything that can be derived is left out and rebuilt on reading, through SQL views stored in the file itself.

Usage

```
write_nadia(
  file,
  preprocessing,
  result = NULL,
  pattern_profiler = NULL,
  overwrite = FALSE,
  verbose = TRUE
)
```

Arguments

file	Path to write to. The .nadia extension is a convention; the file is a DuckDB database whatever it is called.
preprocessing	A proteomics_data object, from any of the preprocess_*() functions. Required: it is the base of the file.
result	Object from process_proteomics(), or NULL to store only the preprocessing.
pattern_profiler	Object from pattern_profiler_analysis(), or NULL. Can also be added later with nadia_add_pattern_profiler().
overwrite	Replace file if it already exists.
verbose	Print progress.

Details

Use read_nadia() to read it back, and nadia_result() to get an object the rest of the package can plot directly.

Value

The path, invisibly.

What goes in

Twelve tables. samples and proteins are the dimensions; protein_sample_metrics, intensities, imputed_values and de_results the facts; pp_membership and pp_profile the optional clustering; and nadia_meta, nadia_packages, nadia_source_files, nadia_calls, parameters and nadia_schema the provenance.

Three things are deliberately *not* stored, because they are exactly derivable: the log2 assay (log2 of the raw one), the PCA_Input table (the imputed assay joined to the DE results) and the observed cells of the imputed assay (identical to the normalized ones). The last of these is checked rather than assumed, since a model-based method such as limpa can revise observed values; when it does, the full assay is stored instead.

Where not to put it

Not inside a synchronised folder such as iCloud Drive, Dropbox or OneDrive while you are working. DuckDB keeps the file open with locks and partial writes, and a synchronising client can corrupt it. Write it locally and copy it afterwards.

See Also

read_nadia(), nadia_result(), nadia_add_pattern_profiler()

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
    data(nadia_dia)
    res <- process_proteomics(nadia_dia, verbose = FALSE)

    f <- file.path(tempdir(), "example.nadia")
    write_nadia(f, nadia_dia, res, verbose = FALSE)
```

```
    db <- read_nadia(f)
    db

    unlink(f)
}
```

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