

# Package ‘VISTA’

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**Type** Package

**Title** Visualization and Integrated System for Transcriptomic Analysis

**Version** 1.1.0

**Description** The VISTA (Visualization and Integrated System for Transcriptomic Analysis) platform streamlines differential expression workflows by wrapping DESeq2 and edgeR into a SummarizedExperiment-based container with consistent metadata. The package includes visualization utilities, MSigDB enrichment helpers, and optional deconvolution support to simplify interactive exploration of RNA-seq experiments.

**License** GPL-3

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**Imports** AnnotationDbi, cli, clusterProfiler, colorspace, DESeq2, dplyr, edgeR, forcats, ggplot2, ggrepel, GGally, ggpubr, grid, matrixStats, methods, msigdb, limma, purrr, rlang, S4Vectors, scales, stringr, SummarizedExperiment, tibble, tidyr, tidyselect, viridis

**Suggests** airway, BiocStyle, circlize, ComplexHeatmap, DT, EnhancedVolcano, ggpointdensity, ggridges, ggalluvial, ggcorrplot, ggrain, ggvenn, enrichplot, knitr, magrittr, patchwork, org.Hs.eg.db, org.Mm.eg.db, quarto, rmarkdown, yaml, writexl, testthat (>= 3.0.0), uwot, xCell2

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<https://cparsania.github.io/VISTA/>

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**Author** Chirag Parsania [aut, cre]  
**Maintainer** Chirag Parsania <chirag.parsania@gmail.com>

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---

```
.align_de_to_counts
```

*Align a DE table to reference gene order; add NA rows for missing genes. Keeps a real gene\_id column and returns a base data.frame. Canonical column order: gene\_id, baseMean, log2fc, lfcSE, stat, pvalue, padj, regulation, ...*

---

### Description

Align a DE table to reference gene order; add NA rows for missing genes. Keeps a real gene\_id column and returns a base data.frame. Canonical column order: gene\_id, baseMean, log2fc, lfcSE, stat, pvalue, padj, regulation, ...

### Usage

```
.align_de_to_counts(
  df,
  ref_rn,
  id_col = NULL,
  strict = FALSE,
  warn_missing = TRUE
)
```

---

```
.categorize_deg_results
```

*Categorize Differential Expression Results (DESeq2 or edgeR)*

---

### Description

This function classifies genes as "Up", "Down", or "Other" based on fold-change and p-value thresholds. It supports input from DESeq2 (DESeqResults), edgeR (e.g., topTags()), or a general tibble/data frame.

### Usage

```
.categorize_deg_results(
  de_results,
  log2fc_cutoff = 1,
  pval_cutoff = 0.05,
  p_value_type = c("padj", "pvalue", "FDR", "PValue")
)
```

### Arguments

de_results	A differential expression results object. Can be a DESeqResults object, an edgeR topTags() table, or a data frame/tibble containing fold changes and p-values.
log2fc_cutoff	Numeric; minimum absolute log2 fold change to classify a DEG. Default is 1.
pval_cutoff	Numeric; p-value or FDR threshold to define significance. Default is 0.05.
p_value_type	String; which column to use for filtering significance. One of "padj", "pvalue", "FDR", "PValue". Default is "padj".

**Value**

A tibble with gene IDs, fold changes, p-values, and a new regulation column, indicating the category of each gene:

- "Up": Genes with log2 fold change  $\geq$  log2fc\_cutoff and p-value  $\leq$  pval\_cutoff.
- "Down": Genes with log2 fold change  $\leq$  -log2fc\_cutoff and p-value  $\leq$  pval\_cutoff.
- "Other": Genes not meeting the above criteria.

---

`.cluster_log2fc_matrix`*Cluster genes by their log2FC profiles using k-means*

---

**Description**

Cluster genes by their log2FC profiles using k-means

**Usage**

```
.cluster_log2fc_matrix(df, gene_id_col = "display_gene", k = 3)
```

**Arguments**

<code>df</code>	A long data.frame with columns: <code>gene_id_col</code> , <code>comparison</code> , <code>log2fc</code> .
<code>gene_id_col</code>	Character string of column name for gene IDs (e.g. "gene_name" or "display_gene").
<code>k</code>	Number of clusters.

**Value**

A data.frame with gene IDs and cluster assignments.

---

`.EnhancedVolcano2`*Enhanced volcano plot with smart column detection & coloring*

---

**Description**

Internal helper that wraps `EnhancedVolcano` and colors points by regulation.

- If `regulation_col` is present (e.g., "Up"/"Down"/"Other"), it is used.
- Otherwise, regulation is derived from FC/P cutoffs.

**Usage**

```
.EnhancedVolcano2(
  toptable,
  lab,
  x = NULL,
  y = NULL,
  pCutoff = 1e-04,
  FCcutoff = 1.5,
  col_by_regul = TRUE,
  regulation_col = NULL,
  col_up = "#b2182b",
  col_down = "#2166ac",
  col_others = "#e0e0e0",
  return_keyvals = FALSE,
  ...
)
```

**Arguments**

toptable	data.frame with DE results.
lab	Character vector of labels (same length as nrow(toptable)).
x	FC column name (auto-detected if NULL).
y	P/P-adj column name (auto-detected if NULL).
pCutoff	Numeric; P-value cutoff. Default 1e-4.
FCcutoff	Numeric; symmetric scalar or c(down, up). Default 1.5.
col_by_regul	Logical; color by regulation. Default TRUE.
regulation_col	Optional column in toptable to use directly (expects levels Up/Down/Other).
col_up	col_down, col_others Colors.
return_keyvals	Logical; invisibly return the computed keyvals. Default FALSE.
...	Passed to EnhancedVolcano::EnhancedVolcano()

**Value**

ggplot object (and invisibly the keyvals if return\_keyvals=TRUE)

---

.filter\_genes

*Filter genes by user-specified IDs or variability*

---

**Description**

This internal function subsets the normalized expression matrix to retain only selected genes (by name) or top variable genes (by variance).

**Usage**

```
.filter_genes(mat, genes = NULL, top_n_genes = NULL)
```

### Arguments

mat                    A numeric matrix with genes as rows and samples as columns.  
genes                  Optional character vector of gene IDs to retain.  
top\_n\_genes           Optional integer; the number of top variable genes to keep.

### Value

A filtered matrix.

---

.plot\_corr\_heatmap     *Plot a correlation heatmap from a matrix*

---

### Description

Plot a correlation heatmap from a matrix

### Usage

```
.plot_corr_heatmap(  
  cor_mat,  
  vis_method = "square",  
  plot_type = "full",  
  show_diagonal = TRUE,  
  show_corr_values = TRUE,  
  col_corr_values = "black",  
  size_corr_values = 4,  
  cluster_samples = TRUE,  
  scale_range = NULL  
)
```

### Arguments

cor\_mat                A symmetric correlation matrix.  
vis\_method             Type of shape for visualization: "square" or "circle".  
plot\_type              Type of plot: "full", "lower", or "upper".  
show\_diagonal         Logical; whether to show diagonal values.  
show\_corr\_values       Logical; whether to label correlation values.  
col\_corr\_values        Color for text labels.  
size\_corr\_values       Numeric size of text labels.  
cluster\_samples        Logical; whether to cluster samples hierarchically.  
scale\_range            Optional numeric vector of length 2 to fix the color scale.

### Value

A ggplot2 heatmap.

---

`.plot_mds` *Plot MDS Coordinates*

---

### Description

Internal plotting function for rendering MDS results using ggplot2.

### Usage

```
.plot_mds(
  mds_df,
  group_col,
  circle_size,
  label_replicates,
  sample_colors,
  color_vals
)
```

### Arguments

<code>mds_df</code>	A data frame with MDS coordinates and sample metadata.
<code>group_col</code>	The grouping column used for coloring points.
<code>circle_size</code>	Size of the points.
<code>label_replicates</code>	Logical; whether to label each point with the sample name.
<code>sample_colors</code>	Logical; whether to color points by group.
<code>color_vals</code>	Named color vector for groups.

### Value

A ggplot object.

---

`.plot_pca` *Plot PCA results using ggplot2*

---

### Description

Internal function that creates a PCA plot using ggplot2 with optional coloring, labeling, clustering ellipses, and customizable color palettes.

### Usage

```
.plot_pca(
  pca_df,
  group_col,
  circle_size,
  label_replicates,
  sample_colors,
```

```
    show_clusters,  
    color_vals,  
    pca  
  )
```

### Arguments

<code>pca_df</code>	A data frame of PCA coordinates and metadata (from <code>.prepare_pca_dataframe()</code> ).
<code>group_col</code>	Column name used for grouping/coloring samples.
<code>circle_size</code>	Point size for the scatter plot.
<code>label_replicates</code>	Logical; whether to display sample labels.
<code>sample_colors</code>	Logical; whether to color by group.
<code>show_clusters</code>	Logical; whether to draw ellipses for group clusters.
<code>color_vals</code>	Named color vector for groups.
<code>pca</code>	Original PCA object used to compute variance explained for axis labels.

### Value

A `ggplot2` object.

---

`.prepare_corr_matrix` *Prepare correlation matrix from normalized expression*

---

### Description

Prepare correlation matrix from normalized expression

### Usage

```
.prepare_corr_matrix(mat, meta, corr_method = "pearson")
```

### Arguments

<code>mat</code>	A numeric matrix of log-normalized gene expression (genes $\times$ samples).
<code>corr_method</code>	Correlation method; one of "pearson", "kendall", or "spearman".

### Value

A correlation matrix.

---

`.prepare_mds_dataframe`*Prepare MDS Data Frame*

---

**Description**

Internal helper to convert MDS coordinates and sample metadata into a plottable data frame.

**Usage**

```
.prepare_mds_dataframe(mds, meta)
```

**Arguments**

<code>mds</code>	A matrix of MDS coordinates from <code>cmdscale()</code> .
<code>meta</code>	A data frame with sample metadata.

**Value**

A tidy data frame for MDS plotting.

---

`.prepare_pca_dataframe`*Prepare PCA result as a tidy data frame*

---

**Description**

Converts PCA output and metadata into a tidy format suitable for `ggplot2`. Includes PC1 and PC2 scores and merges with sample metadata.

**Usage**

```
.prepare_pca_dataframe(pca, meta)
```

**Arguments**

<code>pca</code>	A PCA object returned by <code>stats::prcomp()</code> .
<code>meta</code>	A sample metadata data frame, typically from <code>.prepare_sample_metadata()</code> .

**Value**

A data frame containing PCA components and sample metadata.

---

`.prepare_sample_metadata`*Prepare sample metadata with optional filtering and group ordering*

---

**Description**

This internal helper returns a sample metadata `data.frame` from a VISTA object, optionally filtered by specific sample groups. The function also ensures the grouping column is treated as a factor with appropriate level ordering, either based on user input (`sample_group`) or on original appearance.

**Usage**

```
.prepare_sample_metadata(x, sample_group = NULL, group_column = NULL)
```

**Arguments**

`x` A VISTA object.  
`sample_group` Optional character vector of groups to include, based on the `group_column`.

**Details**

This is a general-purpose metadata preparation function intended to support multiple downstream plotting or reporting utilities.

**Value**

A filtered `data.frame` containing sample metadata and a `sample` column.

---

`.run_deseq_comparisons`*Perform pairwise DE comparisons using DESeq2 results*

---

**Description**

Perform pairwise DE comparisons using DESeq2 results

**Usage**

```
.run_deseq_comparisons(  
  dds,  
  group_column,  
  group_numerator,  
  group_denominator,  
  log2fc_cutoff,  
  pval_cutoff,  
  p_value_type  
)
```

**Arguments**

<code>dds</code>	A DESeq2 object after running DESeq().
<code>group_column</code>	The column used for grouping in the design formula.
<code>group_numerator</code>	Vector of numerator group names.
<code>group_denominator</code>	Vector of denominator group names.
<code>log2fc_cutoff</code>	Absolute log2 fold-change cutoff for DEG classification.
<code>pval_cutoff</code>	P-value threshold for DEG classification.
<code>p_value_type</code>	Column to use for p-value filtering ("padj" or "pvalue").

**Value**

A list with:

- `comparisons`: List of DEG result tibbles (with gene ID and fold changes)
- `deg_summary`: Summary table of DEG counts by regulation

---

`.tidy_de_results`      *Standardize Differential Expression Results*

---

**Description**

Harmonize DE results (DESeq2/edgeR) to a common schema and ensure gene IDs are stored as rownames. Returns `S4Vectors::DataFrame`.

**Usage**

```
.tidy_de_results(tbl, rowname_col = NULL)
```

**Arguments**

<code>tbl</code>	data.frame/tibble or <code>S4Vectors::DataFrame</code> with DE results.
<code>rowname_col</code>	optional column to promote to rownames if missing.

**Value**

`S4Vectors::DataFrame` with rownames = gene IDs and columns like log2FC, pvalue, padj (if present), baseMean/AveExpr mapped to baseMean, etc.

as\_vista

*Coerce SummarizedExperiment to VISTA***Description**

Convert a pre-existing SummarizedExperiment into a valid VISTA object.

**Usage**

```
as_vista(
  se,
  assay_name = "norm_counts",
  group_column,
  comparisons = list(),
  deg_summary = list(),
  cutoffs = list(),
  group_palette = "Dark 3",
  validate = TRUE
)
```

**Arguments**

se	A SummarizedExperiment object.
assay_name	Assay in se to use as norm_counts (default: "norm_counts").
group_column	Grouping column in colData(se).
comparisons	Optional named list of differential expression tables.
deg_summary	Optional named list of DEG summary tables.
cutoffs	Optional named list of threshold metadata.
group_palette	Palette name for group colors.
validate	Logical; run object validation before returning.

**Value**

A VISTA object.

**Examples**

```
mat <- matrix(rnorm(60), nrow = 10)
rownames(mat) <- paste0("gene", seq_len(nrow(mat)))
colnames(mat) <- paste0("sample", seq_len(ncol(mat)))
se <- SummarizedExperiment::SummarizedExperiment(
  assays = list(norm_counts = mat),
  colData = S4Vectors::DataFrame(
    cond = rep(c("A", "B"), each = 3),
    row.names = colnames(mat)
  ),
  rowData = S4Vectors::DataFrame(
    gene_id = rownames(mat),
    row.names = rownames(mat)
  )
)
```

```
)
v <- as_vista(se, group_column = "cond")
v
```

---

benchmark\_vista\_equivalence

*Benchmark VISTA against standalone differential-expression backends*

---

## Description

Run VISTA and direct DESeq2, edgeR, and limma pipelines with matched preprocessing, contrast definitions, and DEG thresholds, then compare the resulting tables, DEG calls, normalized matrices, and critical plot inputs.

## Usage

```
benchmark_vista_equivalence(
  counts,
  sample_info,
  column_geneid,
  group_column,
  group_numerator,
  group_denominator,
  methods = c("deseq2", "edgeR", "limma"),
  min_counts = 10,
  min_replicates = 1,
  log2fc_cutoff = 1,
  pval_cutoff = 0.05,
  p_value_type = "padj",
  covariates = NULL,
  design_formula = NULL,
  tolerance = 1e-08,
  return_plots = FALSE
)
```

## Arguments

counts	Raw counts (matrix/data.frame) with a gene-id column and sample columns.
sample_info	Data frame with sample metadata.
column_geneid	Column name in counts that contains gene identifiers.
group_column	Column in sample_info used to group samples.
group_numerator	Character vector of numerator groups for pairwise comparisons.
group_denominator	Character vector of denominator groups.
methods	Character vector of backends to benchmark. Any subset of c("deseq2", "edgeR", "limma").
min_counts	Minimum total counts per gene to retain.

min_replicates	Minimum samples per group meeting filtering criteria.
log2fc_cutoff	Absolute log <sub>2</sub> fold-change threshold for DEG calling.
pval_cutoff	P-value (or adjusted p-value) threshold.
p_value_type	Either "padj" or "pvalue".
covariates	Optional character vector of additional sample_info columns.
design_formula	Optional model formula (or formula string) including group_column.
tolerance	Numeric tolerance used for floating-point comparisons.
return_plots	Logical; if TRUE, return paired VISTA/reference plots for MA, volcano, DEG count, and PCA views.

### Value

A list with fields valid, comparison\_summary, visual\_summary, and methods. Each element of methods contains the VISTA object, direct backend results, structural validation output, self-consistency checks, and optional plot objects.

### Examples

```
v <- example_vista()
si <- as.data.frame(sample_info(v))
data("count_data", package = "VISTA")
count_subset <- count_data[seq_len(500), c("gene_id", si$sample_names), drop = FALSE]

bm <- benchmark_vista_equivalence(
  counts = count_subset,
  sample_info = si,
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control",
  methods = "limma",
  min_counts = 5,
  min_replicates = 1
)

bm$comparison_summary

data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

target_groups <- c("control", "treatment1")
sample_subset <- sample_metadata[sample_metadata$cond_long %in% target_groups, ]
count_subset <- count_data[seq_len(150), c("gene_id", sample_subset$sample_names)]

bm <- benchmark_vista_equivalence(
  counts = count_subset,
  sample_info = sample_subset,
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control",
  methods = c("deseq2", "edger"),
  min_counts = 5,
```

```
  min_replicates = 1
)

bm$comparison_summary
bm$visual_summary
```

---

count\_data

*Example RNA-seq count matrix shipped with VISTA*

---

### Description

A count matrix derived from the Bioconductor airway dataset and formatted for VISTA examples. The first column stores Ensembl gene IDs; the remaining columns are sample-level counts.

### Usage

```
data(count_data)
```

### Format

A tibble with 63,677 rows and 9 columns.

**gene\_id** Character column storing Ensembl gene identifiers.

**SRR1039508** Numeric count values for airway sample SRR1039508.

**SRR1039509** Numeric count values for airway sample SRR1039509.

**SRR1039512** Numeric count values for airway sample SRR1039512.

**SRR1039513** Numeric count values for airway sample SRR1039513.

**SRR1039516** Numeric count values for airway sample SRR1039516.

**SRR1039517** Numeric count values for airway sample SRR1039517.

**SRR1039520** Numeric count values for airway sample SRR1039520.

**SRR1039521** Numeric count values for airway sample SRR1039521.

### Source

Derived from the airway Bioconductor dataset.

**Description**

This wrapper performs differential expression (DE) analysis (DESeq2, edgeR, limma, or both) and returns a fully initialized VISTA object. The object stores expression matrices and annotations in the SummarizedExperiment core, while all DE outputs and configuration live in `metadata(vista)`:

- `$de_results`: named SimpleList of per-contrast DE tables
- `$de_summary`: named SimpleList of summary tables
- `$de_cutoffs`: list of thresholds/method options
- `$group`: list with column, palette, colors

**Usage**

```
create_vista(
  counts,
  sample_info,
  column_geneid,
  group_column,
  group_numerator,
  group_denominator,
  method = c("deseq2", "edgeR", "limma", "both"),
  min_counts = 10,
  min_replicates = 1,
  log2fc_cutoff = 1,
  pval_cutoff = 0.05,
  p_value_type = "padj",
  covariates = NULL,
  design_formula = NULL,
  consensus_mode = c("intersection", "union"),
  consensus_log2fc = c("mean", "deseq2", "edgeR"),
  result_source = NULL,
  group_palette = "Dark 2",
  comparison_palette = "Dark 3",
  validate = TRUE
)
```

**Arguments**

<code>counts</code>	Raw counts (matrix/data.frame) with a gene-id column and sample columns.
<code>sample_info</code>	Data frame with sample metadata. Must contain <code>sample_names</code> (or have row-names equal to sample columns in <code>counts</code> ) and the <code>group_column</code> .
<code>column_geneid</code>	Column name in <code>counts</code> that contains gene identifiers.
<code>group_column</code>	Column in <code>sample_info</code> used to group samples.
<code>group_numerator</code>	Character vector of numerator groups for pairwise comparisons.

group_denominator	Character vector of denominator groups (same length/order as numerator).
method	"deseq2", "edger", "limma", or "both".
min_counts	Minimum total counts per gene to retain (default: 10).
min_replicates	Minimum samples per group meeting min_counts (default: 1).
log2fc_cutoff	Absolute LFC threshold for DEG calling (default: 1).
pval_cutoff	p-value (raw or adjusted) threshold (default: 0.05).
p_value_type	Which p-value column to use ("padj" or "pvalue"). Default: "padj".
covariates	Optional character vector of additional sample_info columns to adjust for. These are included as additive terms in the DE design.
design_formula	Optional model formula (or formula string) overriding automatic construction from group_column + covariates. Must include group_column.
consensus_mode	When method = "both", how to define consensus calls: "intersection" (both methods significant in same direction) or "union" (either method significant; discordant directions excluded).
consensus_log2fc	When method = "both", how to populate consensus log2fc: "mean", "deseq2", or "edger".
result_source	Active DE source used in metadata(v)\$de_results. For method = "both", one of "consensus", "deseq2", "edger". For single-method runs, this must match method.
group_palette	Qualitative palette name for colorspace::qualitative_hcl(). One of c("Pastel 1", "Dark 2", "Dark 3", "Set 2", "Set 3", "Warm", "Cold", "Harmonic", "Dynamic"). Default: "Dark 2".
comparison_palette	Qualitative palette name used to assign colors per comparison (stored in metadata(v)\$comparison). Defaults to "Dark 3".
validate	Logical; if TRUE (default), run full validate_vista() checks before returning the object.

## Details

Contrast names follow "numerator\_VS\_denominator". Each DE table must have rownames identical to the final norm\_counts rownames. When method = "both", method-specific and consensus DE tables are stored in metadata(v)\$de\_results\_by\_method and metadata(v)\$de\_summary\_by\_method, and the active source is tracked in metadata(v)\$de\_active\_source.

## Value

A VISTA object:

- **assays(v)**: norm\_counts (matrix)
- **colData(v)**: sample\_info (DataFrame)
- **rowData(v)**: row\_data (DataFrame)
- **metadata(v)**: de\_results, de\_summary, de\_cutoffs, group, comparison, provenance

## See Also

[as\\_vista](#), [VISTA-class](#), [qualitative\\_hcl](#)

**Examples**

```

# Load example data
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

# Create VISTA object with DESeq2 (default method)
vista <- create_vista(
  counts = count_data[seq_len(100), ],
  sample_info = sample_metadata[seq_len(6), ],
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control",
  log2fc_cutoff = 0.6,
  pval_cutoff = 0.05
)

# Examine the VISTA object
vista

# Access comparisons
names(comparisons(vista))

# View DEG summary
deg_summary(vista)

# View cutoffs used
cutoffs(vista)

# Multiple comparisons example

vista_multi <- create_vista(
  counts = count_data,
  sample_info = sample_metadata,
  column_geneid = "gene_id",
  group_column = "cell",
  group_numerator = c("N052611", "N080611"),
  group_denominator = c("N61311", "N61311"),
  method = "edger",
  log2fc_cutoff = 1.0,
  pval_cutoff = 0.01
)

```

---

derive\_vista\_metadata *Derive starter sample metadata from count sample names*

---

**Description**

derive\_vista\_metadata() creates a starter sample\_info table from count sample names. It is intended for projects where users have count columns but do not yet have a separate metadata sheet. The derived table can be edited, passed through read\_vista\_metadata(), and then aligned with match\_vista\_inputs().

**Usage**

```
derive_vista_metadata(
  counts,
  column_geneid = NULL,
  sample_names = NULL,
  parser = c("auto", "split", "regex", "none"),
  split = "_",
  fields = NULL,
  pattern = NULL,
  sample_column = "sample_names",
  repair_sample_names = c("auto", "none"),
  return_type = c("data.frame", "template"),
  verbose = TRUE
)
```

**Arguments**

counts	Count input accepted by read_vista_counts(), or the list returned by read_vista_counts().
column_geneid	Optional gene identifier column for raw tabular count inputs. Ignored when counts is the list output of read_vista_counts().
sample_names	Optional explicit sample names to derive metadata from. When supplied, these override names extracted from counts.
parser	Metadata parsing mode. "auto" tries a simple delimiter-based split when sample names have a consistent structure. "split" uses split explicitly. "regex" uses pattern. "none" returns only the sample_names column.
split	Delimiter used when parser = "split" or when "auto" chooses split-based parsing.
fields	Optional field names for parsed metadata columns. When omitted, VISTA uses part_1, part_2, etc.
pattern	Regular expression used when parser = "regex". Capture groups are mapped to fields in order.
sample_column	Name of the sample identifier column in the returned metadata. Default is "sample_names".
repair_sample_names	Strategy passed to read_vista_counts() when sample names are taken from counts. One of "auto" or "none".
return_type	Return "data.frame" (default) or "template". Both return a data frame; "template" adds empty placeholder columns for group and batch.
verbose	Logical; print an informational derivation summary.

**Value**

A data frame containing sample\_names plus any parsed metadata columns.

**Examples**

```
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

counts_in <- count_data[seq_len(8), c("gene_id", sample_metadata$sample_names[seq_len(6)]), drop = FALSE]
```

```

meta <- derive_vista_metadata(
  counts_in,
  column_geneid = "gene_id",
  parser = "regex",
  pattern = "SRR(\\d+)",
  fields = "run_id"
)
head(meta)

```

---

enrichMsigDB

*Perform MSigDB over-representation analysis on a VISTA object*


---

### Description

This function performs ORA on a set of genes from a VISTA object. Gene identifiers stored as “ENSG00000187634:SAMD11” will be split at the colon and the appropriate part extracted based on `from_type`. Genes are then optionally converted via `orgdb` to match the identifier type required by the MSigDB gene sets.

### Usage

```

enrichMsigDB(
  x,
  gene_list,
  from_type = "SYMBOL",
  orgdb,
  msigdb_category = "H",
  msigdb_subcategory = NULL,
  species = "Mus musculus",
  background = NULL,
  col_genetype = "GENETYPE",
  feature_type = "protein-coding",
  ...
)

```

### Arguments

<code>x</code>	A VISTA object.
<code>gene_list</code>	A non-empty character vector of gene identifiers. This argument is required and must not be NULL.
<code>from_type</code>	Identifier type of the genes in <code>gene_list</code> . One of "SYMBOL", "ENSEMBL", or "ENTREZID" (default "SYMBOL"). Ensembl IDs have version suffixes stripped automatically.
<code>orgdb</code>	An <code>OrgDb</code> object used for ID conversion. If omitted, a default is chosen based on species: <code>org.Mm.eg.db</code> for mouse, <code>org.Hs.eg.db</code> for human.
<code>msigdb_category</code>	MSigDB category (e.g. "H", "C2", "C5"). Default "H".
<code>msigdb_subcategory</code>	Optional MSigDB sub-collection (e.g. "BP" for C5). Default NULL.
<code>species</code>	Species name for MSigDB (default "Mus musculus").

background	Optional character vector of background gene IDs. If NULL, all features in the VISTA object (optionally filtered by feature_type) are used.
col_genetype	Column name in rowData(x) used to filter the background by gene type (default "GENETYPE").
feature_type	Gene type to retain in the background when background is NULL (default "protein-coding").
...	Additional arguments to pass to clusterProfiler::enricher().

**Value**

A list containing a single enrichResult object named "enrich".

**Examples**

```
v <- example_vista()
genes <- head(as.character(row_data(v)$gene_id), 20)
if (requireNamespace('msigdb', quietly = TRUE)) {
  out <- try(enrichMsigDB(v, gene_list = genes, from_type = 'ENSEMBL', msigdb_category = 'H'), silent = TRUE)
  if (!inherits(out, 'try-error')) out
}
```

---

example\_vista

*Build a small example VISTA object*


---

**Description**

Creates a lightweight VISTA object from built-in package datasets (count\_data and sample\_metadata) for use in examples and tutorials. The default call returns a precomputed object to keep examples and package checks fast. Non-default argument combinations fall back to rebuilding the object from the packaged example inputs.

**Usage**

```
example_vista(n_genes = 150, n_per_group = 3, method = "deseq2")
```

**Arguments**

n_genes	Number of genes to include (default 150).
n_per_group	Number of samples per group (control and treatment1) to include (default 3).
method	Differential expression backend passed to <a href="#">create_vista()</a> .

**Value**

A VISTA object.

**Examples**

```
v <- example_vista()
v
```

---

export\_vista\_assets     *Export a complete VISTA asset bundle*

---

## Description

Generates a standardized folder with selected VISTA plots, tabular outputs, and a manifest describing all saved files.

## Usage

```
export_vista_assets(
  x,
  out_dir = "vista_assets",
  sample_comparison = NULL,
  display_id = NULL,
  include_plots = c("pca", "mds", "corr_heatmap", "deg_bar", "volcano", "ma",
    "expression_heatmap"),
  include_data = c("comparison", "norm_counts", "sample_info", "row_data", "deg_summary",
    "cutoffs"),
  plot_format = "png",
  width = 8,
  height = 6,
  heatmap_height = 10,
  units = "in",
  dpi = 300,
  top_n_labels = 50,
  heatmap_n_genes = 60,
  write_excel = FALSE,
  overwrite = TRUE
)
```

## Arguments

x	A VISTA object.
out_dir	Output directory for exported assets.
sample_comparison	Optional comparison to use for comparison-specific outputs. Defaults to the first available comparison.
display_id	Optional gene identifier column used in labeling for volcano/MA/heatmap plots.
include_plots	Character vector of plot keys to export. Supported: "pca", "mds", "corr_heatmap", "deg_bar", "deg_pie", "deg_donut", "volcano", "ma", "expression_heatmap".
include_data	Character vector of data keys passed to <a href="#">save_vista_data()</a> .
plot_format	Plot format (e.g. "png" or "pdf").
width	Base plot width.
height	Base plot height.
heatmap_height	Height used specifically for expression heatmap export.
units	Plot dimension units.
dpi	Raster resolution for plots.

**top\_n\_labels**    Number of top genes to annotate in MA plots.  
**heatmap\_n\_genes**    Number of top genes used in exported expression heatmaps.  
**write\_excel**    Logical; if TRUE, also writes a combined XLSX workbook for all requested include\_data tables (requires **writexl**).  
**overwrite**    Logical; if FALSE, aborts when out\_dir already contains files.

### Value

Invisibly, a list with out\_dir, sample\_comparison, manifest, plot\_files, and data\_files.

### Examples

```

v <- example_vista()
out_dir <- file.path(tempdir(), "vista_assets_example")
res <- export_vista_assets(
  v,
  out_dir = out_dir,
  include_plots = "pca",
  include_data = "comparison"
)
names(res)
  
```

---

get\_celltype\_barplot    *Plot cell-type composition as stacked bars*

---

### Description

Plot cell-type composition as stacked bars

### Usage

```

get_celltype_barplot(
  x,
  group_column = NULL,
  sample_names = NULL,
  base_size = 12,
  cell_types = NULL,
  top_n = NULL,
  collapse_other = TRUE,
  normalize = c("sample", "none"),
  facet_by = c("group", "none")
)
  
```

### Arguments

**x**    A VISTA object.  
**group\_column**    Optional column in sample\_info(x) used to facet/order samples. If NULL, uses the active VISTA group column when available.  
**sample\_names**    Optional character vector of sample names to include.  
**base\_size**    Base font size.

cell_types	Optional character vector of cell types to keep.
top_n	Optional top-N cell types by mean score (ignored when cell_types is provided).
collapse_other	Logical; collapse non-selected cell types into "Other".
normalize	One of "sample" (default; per-sample relative scores) or "none".
facet_by	Faceting mode: "group" (default) or "none".

**Value**

A ggplot object.

**Examples**

```
mat <- matrix(rpois(20, lambda = 20), nrow = 5)
rownames(mat) <- paste0("gene", seq_len(5))
colnames(mat) <- paste0("sample", seq_len(4))
se <- SummarizedExperiment::SummarizedExperiment(
  assays = list(norm_counts = mat),
  colData = S4Vectors::DataFrame(
    cond = c("A", "A", "B", "B"),
    row.names = colnames(mat)
  ),
  rowData = S4Vectors::DataFrame(
    gene_id = rownames(mat),
    row.names = rownames(mat)
  )
)
v <- as_vista(se, group_column = "cond")
md <- S4Vectors::metadata(v)
md$cell_fractions <- data.frame(
  fibroblast = c(0.2, 0.3, 0.4, 0.5),
  epithelial = c(0.8, 0.7, 0.6, 0.5),
  row.names = colnames(mat)
)
S4Vectors::metadata(v) <- md
get_celltype_barplot(v, group_column = "cond")
```

---

get\_celltype\_group\_dotplot

*Plot group-level deconvolution scores as dot plot*

---

**Description**

Plot group-level deconvolution scores as dot plot

**Usage**

```
get_celltype_group_dotplot(
  x,
  group_column = NULL,
  cell_types = NULL,
  top_n = 12,
```

```

summary_fun = c("mean", "median"),
error = c("se", "sd", "none"),
add_points = TRUE,
point_size = 2.5,
base_size = 12
)

```

### Arguments

x	A VISTA object.
group_column	Column in <code>sample_info(x)</code> that defines groups. If NULL, uses the active VISTA group column when available.
cell_types	Optional character vector of cell types to include.
top_n	Number of top cell types by mean score when <code>cell_types</code> is NULL.
summary_fun	One of "mean" or "median" for group summary.
error	Error-bar type: "se", "sd", or "none".
add_points	Logical; overlay sample-level jittered points.
point_size	Point size for summary points.
base_size	Base font size.

### Value

A ggplot object.

### Examples

```

mat <- matrix(rpois(20, lambda = 20), nrow = 5)
rownames(mat) <- paste0("gene", seq_len(5))
colnames(mat) <- paste0("sample", seq_len(4))
se <- SummarizedExperiment::SummarizedExperiment(
  assays = list(norm_counts = mat),
  colData = S4Vectors::DataFrame(
    cond = c("A", "A", "B", "B"),
    row.names = colnames(mat)
  ),
  rowData = S4Vectors::DataFrame(
    gene_id = rownames(mat),
    row.names = rownames(mat)
  )
)
v <- as_vista(se, group_column = "cond")
md <- S4Vectors::metadata(v)
md$cell_fractions <- data.frame(
  fibroblast = c(0.2, 0.3, 0.4, 0.5),
  epithelial = c(0.8, 0.7, 0.6, 0.5),
  row.names = colnames(mat)
)
S4Vectors::metadata(v) <- md
get_celltype_group_dotplot(v, group_column = "cond")

```

---

get\_celltype\_heatmap *Plot cell-type deconvolution heatmap*

---

## Description

Plot cell-type deconvolution heatmap

## Usage

```
get_celltype_heatmap(  
  x,  
  group_column = NULL,  
  sample_names = NULL,  
  cell_types = NULL,  
  top_n = 20,  
  transform = c("none", "zscore", "log1p"),  
  cluster_rows = TRUE,  
  cluster_columns = TRUE,  
  label = FALSE,  
  base_size = 11,  
  return_type = c("plot", "matrix", "both")  
)
```

## Arguments

x	A VISTA object.
group_column	Optional grouping column from sample_info(x). If provided and cluster_columns = FALSE, samples are ordered by this group.
sample_names	Optional character vector of sample names to include.
cell_types	Optional character vector of cell types to include.
top_n	Number of top cell types by mean score when cell_types is NULL.
transform	One of "none", "zscore", or "log1p".
cluster_rows	Logical; hierarchical cluster cell types.
cluster_columns	Logical; hierarchical cluster samples.
label	Logical; overlay numeric values on tiles.
base_size	Base font size.
return_type	One of "plot", "matrix", or "both".

## Value

A ggplot object, matrix, or list depending on return\_type.

**Examples**

```

mat <- matrix(rpois(20, lambda = 20), nrow = 5)
rownames(mat) <- paste0("gene", seq_len(5))
colnames(mat) <- paste0("sample", seq_len(4))
se <- SummarizedExperiment::SummarizedExperiment(
  assays = list(norm_counts = mat),
  colData = S4Vectors::DataFrame(
    cond = c("A", "A", "B", "B"),
    row.names = colnames(mat)
  ),
),
rowData = S4Vectors::DataFrame(
  gene_id = rownames(mat),
  row.names = rownames(mat)
)
)
v <- as_vista(se, group_column = "cond")
md <- S4Vectors::metadata(v)
md$cell_fractions <- data.frame(
  fibroblast = c(0.2, 0.3, 0.4, 0.5),
  epithelial = c(0.8, 0.7, 0.6, 0.5),
  row.names = colnames(mat)
)
S4Vectors::metadata(v) <- md
get_celltype_heatmap(v, group_column = "cond")

```

---

get\_cell\_fractions      *Retrieve stored cell fraction estimates*

---

**Description**

Retrieve stored cell fraction estimates

**Usage**

```
get_cell_fractions(x)
```

**Arguments**

x                      A VISTA object.

**Value**

A data.frame of cell fraction estimates with samples in rows.

**Examples**

```

v <- example_vista()
if (requireNamespace('xCell2', quietly = TRUE)) {
  vx <- try(run_cell_deconvolution(v, method = 'xCell2'), silent = TRUE)
  if (!inherits(vx, 'try-error')) head(get_cell_fractions(vx))
}

```

---

get\_chromosome\_plot *Plot gene positions along chromosomes using a TxDb*

---

### Description

Retrieves gene coordinates on the fly from a user-supplied TxDb and plots selected genes along chromosomes, optionally colouring by a numeric value and labeling the most variable genes.

### Usage

```
get_chromosome_plot(
  x,
  txdb,
  keytype = "GENEID",
  id_column = NULL,
  genes = NULL,
  value_column = NULL,
  comparison = NULL,
  group_value = NULL,
  label_top_n = 20,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  line_length = 0.02,
  line_width = 0.6,
  filter_chrom = NULL,
  value_label = NULL,
  use_data_range = FALSE,
  force_fc_limits = FALSE,
  scale_mode = c("diverging", "sequential"),
  scale_low = NULL,
  scale_mid = NULL,
  scale_high = NULL,
  scale_midpoint = 0
)
```

### Arguments

x	A VISTA object.
txdb	A TxDb object (e.g., from <b>GenomicFeatures</b> ).
keytype	Key type in the TxDb matching id_column (default "GENEID").
id_column	Optional column in rowData(x) used to match to TxDb keys. When NULL, rownames(x) are used as keys.
genes	Optional character vector of gene IDs to label (alternative to label_top_n). When provided, all genes are plotted but only these are labeled. Defaults to NULL (no explicit label set).
value_column	Optional column in rowData(x) used for colouring.
comparison	Optional comparison name; when supplied, uses log2fc from metadata(x)\$de_results[[comparison]] for colouring. If multiple comparisons are provided, one panel per comparison is shown (log2FC clipped to +/-2).

group_value	Optional group label (from group_column); when supplied, uses mean expression for that group for colouring (assay norm_counts).
label_top_n	Integer; number of genes with largest lvalue (or random if no value) to label. Ignored when genes is provided. Set to 0 to disable labels.
display_id	Optional column in rowData(x) to use for point labels (fallback to gene_id/rownames).
display_from	Optional source ID type for mapping when display_id is not present in rowData(x).
display_orgdb	Optional OrgDb object used for identifier mapping when display_id is not present in rowData(x).
line_length	Horizontal half-length (in megabases) of the tick used to mark each gene position. Default 0.02. Increase for longer ticks.
line_width	Line width of the tick marks. Default 0.6.
filter_chrom	Optional character vector of chromosomes to keep (e.g., c("chr1", "chr2")). When NULL, all chromosomes returned by the TxDb are shown.
value_label	Optional legend title override for the colour scale.
scale_mode	Colour scale mode: "diverging" (default) or "sequential".
scale_low	Optional low-end colour override.
scale_mid	Optional midpoint colour override (used with diverging scale).
scale_high	Optional high-end colour override.
scale_midpoint	Numeric midpoint passed to ggplot2::scale_color_gradient2() when scale_mode = "diverging".

### Details

The genes argument is only used as an explicit label set (all genes are still plotted). Values in genes must match either the rownames of x or the values in id\_column when that is supplied. For example, if id\_column = "ENTREZID", then genes should contain Entrez IDs to be labeled. When multiple comparisons are supplied, value\_column and group\_value are ignored and the plot is faceted by comparison with a fixed +/-2 log2FC scale.

### Value

A ggplot2 object.

---

get_corr_heatmap	<i>Draw a sample correlation heatmap</i>
------------------	--

---

### Description

Plots sample-sample correlation matrix derived from normalized counts with optional clustering and annotations.

**Usage**

```

get_corr_heatmap(
  x,
  sample_group = NULL,
  group_column = NULL,
  genes = NULL,
  corr_method = "pearson",
  triangle = c("full", "lower", "upper"),
  cluster_by = c("correlation", "group", "input", "none"),
  show_diagonal = TRUE,
  label = TRUE,
  show_corr_values = NULL,
  label_color = "black",
  col_corr_values = NULL,
  label_size = 4,
  limits = NULL,
  base_size = 12,
  viridis_option = "viridis",
  viridis_direction = 1,
  viridis_begin = 0,
  viridis_end = 1
)

```

**Arguments**

<code>x</code>	A VISTA object.
<code>sample_group</code>	Optional character vector of groups (referencing <code>group_column</code> ) to include.
<code>group_column</code>	Optional column name in <code>sample_info</code> defining the grouping used for filtering.
<code>genes</code>	Optional character vector of gene IDs to limit the matrix.
<code>corr_method</code>	Correlation method passed to <code>stats::cor()</code> (e.g., "pearson").
<code>triangle</code>	Either "full", "lower", or "upper" to control which triangle is drawn.
<code>cluster_by</code>	Ordering strategy for samples: "correlation" (default), "group", "input", or "none".
<code>show_diagonal</code>	Logical; include the correlation diagonal when TRUE.
<code>label</code>	Logical; overlay correlation coefficients as text.
<code>show_corr_values</code>	Deprecated alias for <code>label</code> . When supplied, it overrides <code>label</code> .
<code>label_color</code>	Color for the text labels.
<code>col_corr_values</code>	Deprecated alias for <code>label_color</code> . When supplied, it overrides <code>label_color</code> .
<code>label_size</code>	Numeric text size multiplier.
<code>limits</code>	Optional numeric vector of length two giving limits for the color scale.
<code>base_size</code>	Base theme size.
<code>viridis_option</code>	Character viridis palette name.
<code>viridis_direction</code>	Integer (1 or -1) controlling palette direction.
<code>viridis_begin, viridis_end</code>	Palette endpoints between 0 and 1.

**Value**

An object returned by this function.

**Examples**

```
v <- example_vista()
p <- get_corr_heatmap(v)
print(p)
```

---

get_deg_alluvial	<i>Plot alluvial diagram showing gene regulation transitions across comparisons</i>
------------------	---

---

**Description**

Plot alluvial diagram showing gene regulation transitions across comparisons

**Usage**

```
get_deg_alluvial(x, sample_comparisons, show_other = FALSE)
```

**Arguments**

`x` A VISTA object (DE results in comparisons(`x`)).

`sample_comparisons` Character vector of comparison names to include ( $\geq 2$ ).

`show_other` Logical; include "Other" genes. Default FALSE.

**Value**

A ggplot object.

**Examples**

```
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")
si <- as.data.frame(sample_metadata[seq_len(8), ], stringsAsFactors = FALSE)
trt_idx <- which(si$cond_long == "treatment1")
si$cond_long[trt_idx] <- rep(c("treatment1", "treatment2"), length.out = length(trt_idx))
si$groups <- si$cond_long
v <- create_vista(
  counts = count_data[seq_len(120), c("gene_id", si$sample_names)],
  sample_info = si,
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = c("treatment1", "treatment2"),
  group_denominator = c("control", "control"),
  min_counts = 5,
  min_replicates = 1
)
if (requireNamespace('ggalluvial', quietly = TRUE)) {
  p <- get_deg_alluvial(v, sample_comparisons = names(comparisons(v)))
  print(p)
}
```

---

get\_deg\_count\_barplot *Barplot of DEG counts (Up/Down) across comparisons*

---

### Description

Barplot of DEG counts (Up/Down) across comparisons

### Usage

```
get_deg_count_barplot(  
  x,  
  sample_comparisons = NULL,  
  label = TRUE,  
  base_size = 12,  
  colors = c(Up = "red4", Down = "blue4"),  
  facet_by = c("none", "regulation", "comparison"),  
  facet_scales = "fixed"  
)
```

### Arguments

x	A VISTA object containing DEG summaries.
sample_comparisons	Optional character vector of comparison names to display.
label	Logical; overlay numeric counts above bars when TRUE.
base_size	Numeric base font size for the plot.
colors	Named vector giving fill colors for "Up" and "Down" bars.
facet_by	Either "none", "regulation", or "comparison" describing the facet variable. Use "none" for a single panel.
facet_scales	Scale option passed to facet_wrap() when faceting.

### Value

An object returned by this function.

### Examples

```
v <- example_vista()  
p <- get_deg_count_barplot(v)  
print(p)
```

---

```
get_deg_count_donutplot
```

*Donut chart of DEG counts (Up/Down) across comparisons*

---

### Description

Donut chart of DEG counts (Up/Down) across comparisons

### Usage

```
get_deg_count_donutplot(
  x,
  sample_comparisons = NULL,
  label = c("both", "count", "percent", "none"),
  label_digits = 1,
  base_size = 12,
  colors = c(Up = "red4", Down = "blue4"),
  show_other = FALSE,
  other_color = "grey70",
  text_color = "black",
  facet_by = c("comparison", "none"),
  ncol = NULL
)
```

### Arguments

<code>x</code>	A VISTA object containing DEG summaries.
<code>sample_comparisons</code>	Optional character vector of comparison names to display.
<code>label</code>	Label mode: "both" (default), "count", "percent", or "none".
<code>label_digits</code>	Integer number of decimals used for percentage labels.
<code>base_size</code>	Numeric base font size for the plot.
<code>colors</code>	Named vector giving fill colors for "Up" and "Down" slices. When <code>show_other = TRUE</code> , an "Other" entry may also be supplied.
<code>show_other</code>	Logical; when TRUE, include non-DE genes as an "Other" slice using <code>other_color</code> unless overridden in <code>colors</code> .
<code>other_color</code>	Fill colour used for the "Other" slice when <code>show_other = TRUE</code> and <code>colors</code> does not include "Other".
<code>text_color</code>	Colour used for donut label text.
<code>facet_by</code>	Either "comparison" (default) to draw one donut per comparison, or "none" for a single donut.
<code>ncol</code>	Optional number of columns when faceting.

### Value

An object returned by this function.

**Examples**

```
v <- example_vista()
p <- get_deg_count_donutplot(v)
print(p)
```

---

get\_deg\_count\_pieplot *Pie chart of DEG counts (Up/Down) across comparisons*

---

**Description**

Pie chart of DEG counts (Up/Down) across comparisons

**Usage**

```
get_deg_count_pieplot(
  x,
  sample_comparisons = NULL,
  label = c("both", "count", "percent", "none"),
  label_digits = 1,
  base_size = 12,
  colors = c(Up = "red4", Down = "blue4"),
  show_other = FALSE,
  other_color = "grey70",
  text_color = "black",
  facet_by = c("comparison", "none"),
  ncol = NULL
)
```

**Arguments**

x	A VISTA object containing DEG summaries.
sample_comparisons	Optional character vector of comparison names to display.
label	Label mode: "both" (default), "count", "percent", or "none".
label_digits	Integer number of decimals used for percentage labels.
base_size	Numeric base font size for the plot.
colors	Named vector giving fill colors for "Up" and "Down" slices. When show_other = TRUE, an "Other" entry may also be supplied.
show_other	Logical; when TRUE, include non-DE genes as an "Other" slice using other_color unless overridden in colors.
other_color	Fill colour used for the "Other" slice when show_other = TRUE and colors does not include "Other".
text_color	Colour used for pie label text.
facet_by	Either "comparison" (default) to draw one pie per comparison, or "none" for a single pie.
ncol	Optional number of columns when faceting.

**Value**

An object returned by this function.

**Examples**

```
v <- example_vista()
p <- get_deg_count_pieplot(v)
print(p)
```

---

get\_deg\_venn\_diagram *DEG Venn diagram*

---

**Description**

Visualizes overlaps between DEG sets for two to four comparisons.

**Usage**

```
get_deg_venn_diagram(
  x,
  sample_comparisons,
  regulation = "Up",
  palette = "Set 2",
  auto_scale = FALSE,
  show_percentage = TRUE,
  ...
)
```

**Arguments**

<code>x</code>	A VISTA object.
<code>sample_comparisons</code>	Character vector of 2–4 comparison names to include in the Venn diagram.
<code>regulation</code>	One of "Up", "Down", "Both", or "All" selecting which genes to include.
<code>palette</code>	Qualitative palette name passed to <code>colorspace::qualitative_hcl()</code> for fill colors.
<code>auto_scale</code>	Logical; pass through to <code>ggvenn::ggvenn()</code> to scale circles by size.
<code>show_percentage</code>	Logical; request percentage labels from <code>ggvenn::ggvenn()</code> .
<code>...</code>	Additional arguments forwarded to <code>ggvenn::ggvenn()</code> .

**Value**

An object returned by this function.

**Examples**

```
v <- example_vista()
comps <- names(comparisons(v))
if (length(comps) >= 2) {
  p <- get_deg_venn_diagram(v, sample_comparisons = comps[seq_len(2)])
  print(p)
}
```

---

get\_enrichment\_chord *Chord diagram of enrichment gene–pathway relationships*

---

**Description**

Draws a chord diagram linking genes to the enriched pathways they belong to. Chords can be coloured by fold-change, regulation direction, or source pathway.

**Usage**

```
get_enrichment_chord(
  x,
  vista = NULL,
  sample_comparison = NULL,
  pathways = NULL,
  top_n = 8,
  pathway_column = c("Description", "ID"),
  gene_column = c("auto", "geneID", "core_enrichment"),
  gene_sep = "/",
  min_pathways = 1,
  max_genes = 50,
  gene_order_by = c("none", "foldchange", "abs_foldchange"),
  gene_id_column = NULL,
  display_id = NULL,
  color_by = c("foldchange", "regulation", "pathway"),
  up_color = "#D73027",
  down_color = "#1A9850",
  other_color = "grey70",
  pathway_colors = NULL,
  transparency = 0.4,
  gap_degree = 2,
  label_cex = 0.7,
  title = NULL
)
```

**Arguments**

x	An enrichResult, gseaResult, or compareClusterResult from clusterProfiler, or a list containing an enrich element (e.g. output of <a href="#">get_msigdb_enrichment()</a> ).
vista	Optional VISTA object. Required when color_by is "foldchange" or "regulation".
sample_comparison	Character scalar naming the DE comparison in vista to pull log2FC values from. Required when vista is supplied.

pathways	Optional character vector of pathway names to include. Matches against pathway_column.
top_n	Number of top pathways to display when pathways is NULL (default 8).
pathway_column	Column in the enrichment result to match pathway names: "Description" (default) or "ID".
gene_column	Column storing gene members: "auto" (default), "geneID", or "core_enrichment".
gene_sep	Delimiter separating genes in gene_column (default "/").
min_pathways	Minimum number of pathways a gene must appear in to be shown. Set to 2 to display only hub genes shared across terms. Default 1 (show all genes).
max_genes	Maximum number of genes to display (default 50). A safety cap for readability.
gene_order_by	Order of gene sectors in the chord plot: "none" (default), "foldchange" (descending log2FC), or "abs_foldchange" (descending absolute log2FC). Fold-change based ordering requires vista + sample_comparison.
gene_id_column	Column in rowData(vista) used to map enrichment gene IDs to vista row-names (for FC lookup).
display_id	Column in rowData(vista) providing display-friendly gene names.
color_by	How to colour chords: "foldchange" (continuous gradient), "regulation" (Up / Down / Other), or "pathway" (source pathway). Falls back to "pathway" when vista is NULL.
up_color	Colour for up-regulated genes (default "#D73027").
down_color	Colour for down-regulated genes (default "#1A9850").
other_color	Colour for non-significant genes (default "grey70").
pathway_colors	Optional named vector of colours for pathway sectors. When NULL, colours are generated from an HCL palette.
transparency	Chord transparency, 0–1 (default 0.4).
gap_degree	Gap between sectors in degrees (default 2).
label_cex	Text size for sector labels (default 0.7).
title	Optional plot title.

## Details

The plot reveals **hub genes** (those driving multiple enriched terms) and pathway redundancy (terms sharing many genes). This complements [get\\_enrichment\\_plot\(\)](#) (which shows significance) and [get\\_pathway\\_heatmap\(\)](#) (which shows expression patterns).

## Value

Invisibly returns a list with:

**gene\_data** Tibble of genes with pathway membership and (optionally) fold-change values.

**hub\_genes** Character vector of genes appearing in two or more pathways.

The chord diagram is drawn as a side effect.

**Examples**

```

v <- example_vista()
msig <- get_msigdb_enrichment(
  v,
  sample_comparison = names(comparisons(v))[1],
  regulation = "Both",
  msigdb_category = "H",
  from_type = "ENSEMBL"
)
get_enrichment_chord(msig, top_n = 5)

data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

vista <- create_vista(
  counts = count_data[seq_len(200), ],
  sample_info = sample_metadata[seq_len(6), ],
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control"
)

msig <- get_msigdb_enrichment(
  vista,
  sample_comparison = names(comparisons(vista))[1],
  regulation = "Up", from_type = "ENSEMBL"
)

# Simple: pathway-coloured chords
get_enrichment_chord(msig)

# With fold-change colouring
get_enrichment_chord(
  msig, vista = vista,
  sample_comparison = names(comparisons(vista))[1],
  color_by = "foldchange"
)

# Hub genes only (shared across 2+ pathways)
pw_long <- get_pathway_genes(msig, return_type = "long")
if (any(table(pw_long$gene) >= 2)) {
  get_enrichment_chord(msig, min_pathways = 2)
}

```

---

get\_enrichment\_plot    *Plot enrichment results using  $-\log_{10}(FDR)$*

---

**Description**

Generates a dot plot of enrichment results for `enrichResult`, `gseaResult`, or `compareClusterResult` objects (including those returned by `enrichMsigDB()`). Points are sized by gene/set count and

coloured by  $-\log_{10}(\text{FDR})$ . For compareCluster results, the plot is faceted by cluster with top terms selected per cluster.

### Usage

```
get_enrichment_plot(x, top_n = 10, title = NULL)
```

### Arguments

**x** An object of class enrichResult, gseaResult, or compareClusterResult.  
**top\_n** Integer; number of top terms to plot (per cluster for compareCluster).  
**title** Optional plot title.

### Value

A ggplot2 object.

### Examples

```
## Not run:
v <- example_vista()
com <- names(comparisons(v))[1]
if (requireNamespace('msigdb', quietly = TRUE)) {
  ms <- try(get_msigdb_enrichment(v, sample_comparison = com, regulation = 'Up', from_type = 'ENSEMBL'), silent = TRUE)
  if (!inherits(ms, 'try-error') && !is.null(ms$enrich)) print(get_enrichment_plot(ms$enrich))
}

## End(Not run)
```

---

get\_expression\_barplot

*Plot gene expression as barplots*

---

### Description

Displays selected genes as grouped summary bars or individual sample-level bars. By default, expression is summarized per group with mean  $\pm$  SD bars. With by = "sample", each sample is drawn separately.

### Usage

```
get_expression_barplot(
  x,
  genes,
  sample_group = NULL,
  group_column = NULL,
  log_transform = TRUE,
  stats_group = FALSE,
  facet_scale = "free_y",
  facet_scales = facet_scale,
  facet_nrow = NULL,
  facet_ncol = NULL,
```

```

  p.label = "p.signif",
  comparisons = NULL,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  by = c("group", "sample"),
  sample_order = c("input", "group", "expression"),
  fill_by = NULL,
  facet_by = c("auto", "gene", "none")
)

```

### Arguments

x	A VISTA object.
genes	Character vector (<=25 genes) to plot.
sample_group	Optional character vector of groups (from group_column) to include.
group_column	Optional column name in sample_info to use for grouping samples.
log_transform	Logical; log2-transform expression before plotting.
stats_group	Logical; add statistical comparisons between groups when TRUE.
facet_scale	Scaling option passed to facet_wrap() (deprecated; use facet_scales).
facet_scales	Facet scales argument passed to facet_wrap() when faceting by gene.
facet_nrow, facet_ncol	Optional layout passed to facet_wrap() when faceting.
p.label	Label format for ggpubr::stat_compare_means().
comparisons	Optional list of specific group comparisons for stat_compare_means().
display_id	Optional ID/column name to use for labels/facets. If supplied and present in rowData(x), those values are used; otherwise falls back to ID mapping.
display_from	Optional source ID type for mapping (used when display_id is not found in rowData).
display_orgdb	Optional OrgDb object used for ID mapping when display_id is set but not found in rowData.
by	One of "group" (default; summarize replicates by group) or "sample" (show one bar per sample).
sample_order	Ordering used when by = "sample": "input" preserves the current sample order, "group" groups samples by group_column, and "expression" ranks samples by mean expression across the selected genes.
fill_by	Fill mapping for by = "sample" barplots. Use "group" (default) or any discrete column from the joined plotting data, such as a sample metadata column or "sample". Group-summary barplots (by = "group") only support group-based fill because each bar already represents an aggregated group mean.
facet_by	Faceting mode: "auto" (default; facet by gene when more than one gene is requested), "gene", or "none". For multiple genes, "none" falls back to "gene" to preserve readability.

### Value

A ggplot2 object.

**Examples**

```

# Create VISTA object
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

vista <- create_vista(
  counts = count_data[seq_len(200), ],
  sample_info = sample_metadata[seq_len(6), ],
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control"
)

# Plot expression for select genes
genes <- rownames(vista)[seq_len(3)]
get_expression_barplot(vista, genes = genes)

# With statistics
get_expression_barplot(vista, genes = genes, stats_group = TRUE)

# Without log transformation
get_expression_barplot(vista, genes = genes, log_transform = FALSE)

```

---

```
get_expression_boxplot
```

*Plot gene expression distributions as boxplots*

---

**Description**

Displays per-sample or per-group distributions for selected genes using normalized counts. The x-axis unit is controlled by `by`, and faceting is controlled explicitly by `facet_by`.

**Usage**

```

get_expression_boxplot(
  x,
  genes = NULL,
  sample_group = NULL,
  group_column = NULL,
  log_transform = TRUE,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  facet_scales = "free_y",
  facet_nrow = NULL,
  facet_ncol = NULL,
  stats_group = FALSE,
  p.label = "p.signif",
  comparisons = NULL,
  pool_genes = FALSE,

```

```

  by = "group",
  facet_by = "auto",
  fill_by = NULL,
  sample_order = c("input", "group", "expression")
)

```

### Arguments

x	A VISTA object.
genes	Optional character vector of genes to display ( $\leq 20$ ). Defaults to all genes.
sample_group	Optional character vector specifying which groups (as defined by group_column) to include.
group_column	Optional column name in sample_info used as the grouping variable.
log_transform	Logical; apply $\log_2(x + 1)$ transform before plotting.
display_id	Optional column in rowData(x) to use for gene labels (facets).
display_from	Optional source ID type for mapping (used when display_id is not found in rowData).
display_orgdb	Optional OrgDb object used for ID mapping when display_id is set but not found in rowData.
facet_scales	Facet scales argument passed to facet_wrap() (default "free_y").
facet_nrow, facet_ncol	Optional layout passed to facet_wrap() when faceting.
stats_group	Logical; add statistical comparisons between groups when TRUE. Only supported when by = "group".
p.label	Label format for ggpubr::stat_compare_means().
comparisons	Optional list of specific group comparisons for stat_compare_means().
pool_genes	Logical; when TRUE, pool selected genes into one distribution per x-axis category (scenario 1).
by	When pool_genes = TRUE, either "group" or "sample" (x-axis and optional fill). When pool_genes = FALSE, either "group" or "gene" (x-axis for per-gene distributions).
facet_by	Faceting control: for pooled genes, "group" or "none"; for per-gene, "none" (default) or "gene". "auto" selects the most readable layout.
fill_by	Fill mapping. Special values are "group", "gene", and "x" (the plotted x-axis variable, when available). You may also supply a discrete column from the joined plotting data, such as a sample metadata column or "sample".
sample_order	Ordering used when sample names are shown on the x-axis: "input", "group", or "expression".

### Value

An object returned by this function.

### Examples

```

v <- example_vista()
genes <- head(rownames(v), 3)
p <- get_expression_boxplot(v, genes = genes)
print(p)

```

---

```
get_expression_chromosome_plot
```

*Chromosome plot for expression*

---

### Description

Convenience wrapper around `get_chromosome_plot()` for expression-based colouring (optional group mean, rowData columns, or assay columns).

### Usage

```
get_expression_chromosome_plot(
  x,
  txdb,
  keytype = "GENEID",
  id_column = NULL,
  genes = NULL,
  sample_group = NULL,
  group_column = NULL,
  value_column = NULL,
  value_from = c("rowData", "assay"),
  value_assay = "norm_counts",
  facet_value_columns = FALSE,
  side_by_side_groups = FALSE,
  paginate = TRUE,
  panels_per_page = 24,
  summarise_replicates = FALSE,
  summarise_method = c("mean", "median"),
  group_value = NULL,
  label_n = 20,
  label_genes = c("top", "all", "none"),
  display_id = NULL,
  line_length = 0.02,
  line_width = 0.6,
  filter_chrom = NULL,
  log_transform = TRUE,
  value_label = "log2(mean expr)"
)
```

### Arguments

<code>x</code>	A VISTA object.
<code>txdb</code>	A TxDb object (e.g., from <b>GenomicFeatures</b> ).
<code>keytype</code>	Key type in the TxDb matching <code>id_column</code> (default "GENEID").
<code>id_column</code>	Optional column in <code>rowData(x)</code> used to match to TxDb keys. When NULL, <code>rownames(x)</code> are used as keys.
<code>genes</code>	Optional character vector of gene IDs to label (alternative to <code>label_top_n</code> ). When provided, all genes are plotted but only these are labeled. Defaults to NULL (no explicit label set).

sample_group	Optional character vector of groups (from group_column) used to subset assay columns when value_from = "assay".
group_column	Optional column name in sample_info used for sample_group selection and replicate summarisation.
value_column	Optional column in rowData(x) used for colouring.
value_from	Source for value_column data: "rowdata" (default) or "assay". When "assay", the selected assay column is copied into rowData temporarily for colouring.
value_assay	Assay name to pull values from when value_from = "assay". Default "norm_counts".
facet_value_columns	Ignored (kept for compatibility); multiple value_columns are always arranged in a chromosome-by-column grid.
side_by_side_groups	Logical; when plotting multiple value_columns, arrange one row per chromosome with one panel per selected sample/group. This is useful for direct side-by-side group comparison.
paginate	Logical; when TRUE, split large multi-panel chromosome plots into pages to avoid patchwork viewport-size errors.
panels_per_page	Maximum number of panels per page when paginate = TRUE. Set to NULL to disable automatic paging.
summarise_replicates	Logical; when TRUE and value_from = "assay", aggregate replicates by group_column before plotting.
summarise_method	"mean" or "median" summarisation used when summarise_replicates = TRUE.
group_value	Optional group label (from group_column); when supplied, uses mean expression for that group for colouring (assay norm_counts).
label_n	Integer; number of genes with the largest absolute values to label when genes is not supplied. Set to 0 to disable automatic labels.
label_genes	One of "top" (default), "all", or "none" controlling chromosome text labels when genes is not supplied.
display_id	Optional column in rowData(x) to use for point labels (fallback to gene_id/rownames).
line_length	Horizontal half-length (in megabases) of the tick used to mark each gene position. Default 0.02. Increase for longer ticks.
line_width	Line width of the tick marks. Default 0.6.
filter_chrom	Optional character vector of chromosomes to keep (e.g., c("chr1", "chr2")). When NULL, all chromosomes returned by the TxDb are shown.
log_transform	Logical; when group_value is used (and value_column is NULL) or when value_from = "assay", apply $\log_2(x + 1)$ before coloring.
value_label	Optional legend title override for the colour scale.

## Details

- If multiple value\_columns are supplied, one plot is produced per column with its own colour legend titled by that column. Chromosomes are laid out top-down in a single column: for each chromosome, plots for all value\_columns appear sequentially. Legends for each column are shown only on the first occurrence (at the bottom) to avoid overlap. Requires **patchwork**; otherwise a list of plots is returned.

- Set `side_by_side_groups = TRUE` to place selected groups/samples in separate columns for each chromosome (same-row comparison).
- `paginate = TRUE` automatically splits large panel collections into a list of patchwork pages, which prevents "viewport too small" rendering errors in IDE plot panes.
- For `value_from = "assay"`, colours follow the VISTA ecosystem: group colours are used when `summarise_replicates = TRUE`, while sample colours are derived from group colours when plotting individual replicates.
- For `value_from = "assay"` with `value_column = NULL`, all selected assay columns are used (samples after `sample_group` filtering, or groups after replicate summarisation).
- Labels are kept consistent across `value_columns`: if `genes` is provided it is used for all panels; otherwise the top `label_n` (by absolute value in the first `value_column`) are used for all panels.
- When `value_from = "assay"`, the specified assay column is copied into `rowData` on the fly so it can be used for colouring.
- When `group_value` is provided (and no `value_column`), colouring is based on log2 mean expression for that group (assay `norm_counts`), using a data-driven colour scale. Ignored when `value_column` is supplied.

### Value

A `ggplot2` object or a list of `ggplot2` objects when multiple `value_columns` are provided and `patchwork` is unavailable.

### Examples

```
v <- example_vista()
p <- try(get_expression_chromosome_plot(v), silent = TRUE)
if (!inherits(p, 'try-error')) print(p)
```

---

get\_expression\_density

*Plot expression distributions as density curves*

---

### Description

Shows expression distributions pooled across the selected genes, coloured by group (or sample), with optional faceting by group or sample.

### Usage

```
get_expression_density(
  x,
  genes = NULL,
  sample_group = NULL,
  group_column = NULL,
  log_transform = TRUE,
  facet_scales = "free",
  facet_nrow = NULL,
  facet_ncol = NULL,
  alpha = 0.4,
```

```

adjust = 1,
color_by = c("group", "sample"),
facet_by = c("none", "group", "sample"),
sample_order = c("input", "group", "expression"),
palette = NULL,
colors = NULL
)

```

### Arguments

x	A VISTA object.
genes	Optional character vector of genes to display. Defaults to all genes.
sample_group	Optional character vector specifying which groups (as defined by group_column) to include.
group_column	Optional column name in sample_info used as the grouping variable.
log_transform	Logical; apply $\log_2(x + 1)$ transform before plotting.
facet_scales	Facet scales argument passed to facet_wrap() (default "free").
facet_nrow, facet_ncol	Optional layout passed to facet_wrap() when faceting.
alpha	Numeric transparency for density fill.
adjust	Bandwidth adjustment factor passed to geom_density().
color_by	Either "group" (default) or "sample" to choose fill/color variable.
facet_by	One of "none" (default), "group", or "sample" to facet densities.
sample_order	Ordering for sample-level display: "input", "group", or "expression".
palette	Optional qualitative palette name used when generating colours.
colors	Optional named character vector of manual colours overriding palette.

### Value

A ggplot2 object.

### Examples

```

v <- example_vista()
genes <- head(rownames(v), 3)
p <- get_expression_density(v, genes = genes)
print(p)

```

---

get\_expression\_heatmap

*Expression heatmap*

---

### Description

Summarizes expression for selected genes/groups via ComplexHeatmap with optional transformations and annotations. With only a VISTA object, the function will plot the top variable genes across all samples.

**Usage**

```

get_expression_heatmap(
  x,
  genes = NULL,
  top_n = 50,
  sample_group = NULL,
  group_column = NULL,
  value_transform = c("zscore", "log2", "raw"),
  summarise_replicates = TRUE,
  summarise_method = c("mean", "median"),
  convert_rowmeans = FALSE,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  repair_genes = FALSE,
  show_row_names = NULL,
  label_size = 10,
  label_specific_rows = NULL,
  label_specific_rows_gp = grid::gpar(fontsize = 5),
  show_column_names = TRUE,
  cluster_rows = TRUE,
  show_row_dend = TRUE,
  cluster_columns = TRUE,
  kmeans_k = NULL,
  annotate_columns = FALSE,
  cluster_by = NULL,
  column_anno_palette = "Dark 3",
  column_anno_colors = NULL,
  color_default = TRUE,
  col = NULL,
  heatmap_name = NULL,
  show_heatmap_legend = TRUE,
  return_type = c("heatmap", "clusters", "both"),
  ...
)

```

**Arguments**

x	A VISTA object.
genes	Optional character vector of gene identifiers to display. When omitted, VISTA selects the top variable genes across the included samples.
top_n	Integer number of genes to select automatically when genes = NULL. Defaults to 50.
sample_group	Character vector of group labels specifying which samples to include (based on the selected grouping column).
group_column	Optional column name in sample_info used to interpret sample_group.
value_transform	One of "zscore", "log2", or "raw" controlling how expression values are transformed.
summarise_replicates	Logical; average replicates per group before plotting when TRUE.

summarise_method	"mean" or "median" summarization used when summarise_replicates = TRUE.
convert_rowmeans	Logical; subtract row means prior to plotting.
display_id	Optional ID/column name to use for row labels. If supplied
display_from	Optional source ID type for mapping (used when display_id
display_orgdb	Optional OrgDb object used for ID mapping when
repair_genes	Logical; if TRUE, split gene_id strings such as ID: SYMBOL to display the symbol.
show_row_names	Logical; display row names (genes) beside the heatmap. When NULL, VISTA turns labels on automatically for auto-selected genes.
label_size	Numeric font size for row names.
label_specific_rows	Optional character vector of row names to highlight via anno_mark().
label_specific_rows_gp	grid::gpar() object controlling the highlighted row labels.
show_column_names	Logical; draw column names when TRUE.
cluster_rows	Logical; cluster rows when drawing the heatmap.
show_row_dend	Logical; display the row dendrogram.
cluster_columns	Logical; cluster columns.
kmeans_k	Optional integer specifying the number of k-means clusters to compute for rows.
annotate_columns	Logical or character vector. TRUE adds the group_column annotation and also includes cluster_by when supplied; a character vector adds multiple annotations from sample_info.
cluster_by	Optional annotation column used to split/cluster columns. Defaults to the first annotation column when annotate_columns is enabled.
column_anno_palette	Qualitative palette name used for the column annotation.
column_anno_colors	Optional named list of annotation color vectors. Each element should be a named character vector keyed by the levels of one annotation column.
color_default	Logical; use the default blue-white-red palette when TRUE. Set to FALSE to supply col.
col	Optional circlize::colorRamp2 function used when color_default = FALSE.
heatmap_name	Optional legend title.
show_heatmap_legend	Logical; display the heatmap legend.
return_type	"heatmap", "clusters", or "both" selecting the returned object.
...	Additional arguments passed to ComplexHeatmap::Heatmap().

**Value**

An object returned by this function.

A ComplexHeatmap object, a cluster data frame, or a list containing both depending on return\_type.

**Examples**

```

v <- example_vista()
genes <- head(rownames(v), 20)
if (requireNamespace('ComplexHeatmap', quietly = TRUE) &&
    requireNamespace('circlize', quietly = TRUE)) {
  hm <- get_expression_heatmap(
    v,
    genes = genes,
    sample_group = unique(as.character(sample_info(v)$cond_long)),
    return_type = 'heatmap'
  )
  ComplexHeatmap::draw(hm)
}
v <- example_vista()
if (requireNamespace("ComplexHeatmap", quietly = TRUE) &&
    requireNamespace("circlize", quietly = TRUE)) {
  hm <- get_expression_heatmap(v, return_type = "heatmap")
  ComplexHeatmap::draw(hm)
}

```

---

get\_expression\_joyplot

*Plot expression distributions as ridgelines*

---

**Description**

Shows per-group (or per-sample) expression distributions pooled across the selected genes using ridge (joy) plots. Genes are pooled; no faceting to keep shapes comparable.

**Usage**

```

get_expression_joyplot(
  x,
  genes = NULL,
  sample_group = NULL,
  group_column = NULL,
  log_transform = TRUE,
  alpha = 0.7,
  scale = 1.2,
  y_by = c("group", "sample"),
  color_by = c("group", "sample"),
  sample_order = c("input", "group", "expression"),
  palette = NULL,
  colors = NULL
)

```

**Arguments**

x	A VISTA object.
genes	Optional character vector of genes to display. Defaults to all genes.
sample_group	Optional character vector specifying which groups (as defined by group_column) to include.

group_column	Optional column name in sample_info used as the grouping variable.
log_transform	Logical; apply $\log_2(x + 1)$ transform before plotting.
alpha	Numeric transparency for fills.
scale	Numeric scaling factor for ridges (passed to geom_density_ridges()).
y_by	Either "group" (default) or "sample" to choose the y-axis (ridge) grouping.
color_by	Either "group" (default) or "sample" to choose fill colors.
sample_order	Ordering for sample-level display: "input", "group", or "expression".
palette	Optional qualitative palette name used when generating colours.
colors	Optional named character vector of manual colours overriding palette.

**Value**

A ggplot2 object.

**Examples**

```
v <- example_vista()
genes <- head(rownames(v), 3)
p <- get_expression_joyplot(v, genes = genes)
print(p)
```

---

get\_expression\_lineplot

*Gene expression line plot*

---

**Description**

Plots normalized expression for selected genes across samples or summarized groups with optional transformations and group faceting.

**Usage**

```
get_expression_lineplot(
  x,
  genes = NULL,
  sample_group = NULL,
  group_column = NULL,
  log_transform = TRUE,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  facet_scales = "free_y",
  facet_nrow = NULL,
  facet_ncol = NULL,
  stats_group = FALSE,
  p.label = "p.signif",
  comparisons = NULL,
  pool_genes = FALSE,
  by = c("sample", "group"),
```

```

facet_by = c("auto", "group", "gene", "none"),
fill_by = NULL,
sample_order = c("input", "group", "expression"),
value_transform = NULL,
palette = NULL,
colors = NULL,
line_width = 1,
point_size = 2,
base_size = 12
)

```

### Arguments

x	A VISTA object.
genes	Character vector of gene identifiers to plot.
sample_group	Optional character vector specifying which groups (values taken from group_column) to include.
group_column	Optional column name in sample_info defining the grouping/faceting variable.
log_transform	Logical; log2-transform expression values before plotting.
display_id	Optional ID/column name to use for gene labels. If supplied and present in rowData(x), those values are used.
display_from	Optional source ID type for mapping (reserved for compatibility with other expression plotting APIs).
display_orgdb	Optional OrgDb object used for ID mapping when display_id is set but not found in rowData.
facet_scales	Scaling option passed to facet_wrap().
facet_nrow, facet_ncol	Optional layout passed to facet_wrap() when faceting.
stats_group	Logical retained for API consistency. Statistical overlays are not currently added by get_expression_lineplot().
p.label	Label format retained for API consistency with other expression plots.
comparisons	Optional list of comparisons retained for API consistency.
pool_genes	Logical; when TRUE, average the selected genes into a single trajectory.
by	Plot unit: "sample" (default) or "group" to average replicates before plotting.
facet_by	Faceting mode: "auto" (default), "none", "group", or "gene".
fill_by	Argument retained for API consistency; ignored because line plots use colour rather than fill.
sample_order	Ordering used for sample-level plots: "input", "group", or "expression".
value_transform	Deprecated compatibility alias for transformation choice; one of "log2", "zscore", or "none".
palette	Optional qualitative palette name used for gene colours.
colors	Optional named character vector of manual gene colours.
line_width	Line width.
point_size	Point size.
base_size	Base theme size.

**Value**

An object returned by this function.

**Examples**

```
v <- example_vista()
genes <- head(rownames(v), 3)
p <- get_expression_lineplot(v, genes = genes)
print(p)
```

---

```
get_expression_lollipop
```

*Plot expression as a lollipop chart*

---

**Description**

Displays selected genes as stem-and-dot (lollipop) plots. By default, expression is summarized per group (mean across replicates). With `by = "sample"`, the plot shows individual samples.

**Usage**

```
get_expression_lollipop(
  x,
  genes,
  sample_group = NULL,
  group_column = NULL,
  by = c("group", "sample"),
  sample_order = c("input", "group", "expression"),
  facet_by = c("auto", "gene", "none"),
  log_transform = TRUE,
  facet_scale = "free_y",
  facet_nrow = NULL,
  facet_ncol = NULL,
  point_size = 6,
  line_size = 1.2,
  label = TRUE,
  label_digits = 1,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL
)
```

**Arguments**

<code>x</code>	A VISTA object.
<code>genes</code>	Character vector (<=15 genes) to plot.
<code>sample_group</code>	Optional character vector of groups (from <code>group_column</code> ) to include.
<code>group_column</code>	Optional column name in <code>sample_info</code> to use for grouping samples.
<code>by</code>	One of "group" (default; summarize replicates by group) or "sample" (show individual samples).

<code>sample_order</code>	Ordering used when <code>by = "sample"</code> : "input" preserves the current sample order, "group" groups samples by <code>group_column</code> , and "expression" ranks samples by mean expression across the selected genes.
<code>facet_by</code>	Faceting mode: "auto" (default; facet by gene when more than one gene is requested), "gene", or "none". For multiple genes, "none" falls back to "gene" to avoid unreadable combined panels.
<code>log_transform</code>	Logical; log2-transform expression before plotting.
<code>facet_scale</code>	Scaling option passed to <code>facet_wrap()</code> when plotting multiple genes.
<code>facet_nrow, facet_ncol</code>	Optional layout passed to <code>facet_wrap()</code> when faceting.
<code>point_size</code>	Numeric size of the dots.
<code>line_size</code>	Numeric size of the stems.
<code>label</code>	Logical; draw numeric labels above the dots.
<code>label_digits</code>	Integer; digits to show in labels when <code>label = TRUE</code> .
<code>display_id</code>	Optional ID/column name to use for labels/facets. If supplied and present in <code>rowData(x)</code> , those values are used; otherwise falls back to ID mapping.
<code>display_from</code>	Optional source ID type for mapping (used when <code>display_id</code> is not found in <code>rowData</code> ).
<code>display_orgdb</code>	Optional <code>OrgDb</code> object used for ID mapping when <code>display_id</code> is set but not found in <code>rowData</code> .

### Value

An object returned by this function.

A `ggplot2` object.

### Examples

```
v <- example_vista()
genes <- head(rownames(v), 5)
p <- get_expression_lollipop(v, genes = genes)
print(p)
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

vista <- create_vista(
  counts = count_data[seq_len(200), ],
  sample_info = sample_metadata[seq_len(6), ],
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control"
)

genes <- rownames(vista)[seq_len(3)]
get_expression_lollipop(vista, genes = genes)
get_expression_lollipop(vista, genes = genes[seq_len(2)], by = "sample")
```

---

get\_expression\_matrix *Retrieve an expression matrix from a VISTA object*

---

### Description

Returns the specified assay (default "norm\_counts") with optional gene/sample subsetting, replicate summarization by group, and simple transformations.

### Usage

```
get_expression_matrix(  
  x,  
  assay_name = "norm_counts",  
  genes = NULL,  
  sample_names = NULL,  
  group_column = NULL,  
  summarise = FALSE,  
  transform = c("none", "log2", "zscore")  
)
```

### Arguments

x	A VISTA object.
assay_name	Assay to extract (default: "norm_counts").
genes	Optional character vector of gene IDs to keep.
sample_names	Optional character vector of sample IDs (or group labels when summarise = TRUE) to keep.
group_column	Optional column in sample_info used when summarising replicates. Defaults to the stored group_column.
summarise	Logical; if TRUE, averages replicates per group_column.
transform	One of "none", "log2", or "zscore" applied after subsetting and optional summarisation. Z-scores are computed within the selected samples/columns.

### Value

A numeric matrix with genes in rows and samples (or groups) in columns.

### Examples

```
v <- example_vista()  
m <- get_expression_matrix(v)  
dim(m)
```

---

```
get_expression_raincloud
```

*Raincloud plot of expression values*

---

### Description

Uses `ggplot::geom_rain()` to combine a half-violin, boxplot, and jittered points per sample/group to show distribution, summary, and individual values.

### Usage

```
get_expression_raincloud(
  x,
  genes = NULL,
  sample_group = NULL,
  group_column = NULL,
  by = "group",
  value_transform = c("log2", "zscore", "none"),
  summarise = FALSE,
  facet_by = c("auto", "gene", "none"),
  fill_by = NULL,
  facet_nrow = NULL,
  facet_ncol = NULL,
  sample_order = c("input", "group", "expression"),
  rain_side = c("r", "l", "f", "f1x1", "f2x2"),
  id.long.var = NULL,
  alpha = 0.5,
  point_size = 1.5,
  p.label = "p.signif",
  stats_group = FALSE,
  stats_method = "t.test",
  label = FALSE,
  label_column = "gene",
  label_size = 3,
  label_max_overlaps = 50,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL
)
```

### Arguments

<code>x</code>	A VISTA object.
<code>genes</code>	Optional character vector of gene IDs to include; defaults to all genes selected by the plotting mode.
<code>sample_group</code>	Optional subset of groups (values of <code>group_column</code> ) to keep.
<code>group_column</code>	Grouping column in <code>sample_info</code> ; defaults to the stored grouping.
<code>by</code>	Plot unit. Violin plots currently support only "group".

value_transform	Deprecated compatibility alias. "log2" maps to log_transform = TRUE, "none" maps to FALSE, and "zscore" applies a per-gene z-score transform.
summarise	Logical; when TRUE, collapse replicates within each group for each gene (one value per gene per group). This is useful for pooled multi-gene raincloud plots where each dot represents one gene-level summary in a group.
facet_by	Faceting mode. Uses the same argument pattern as <code>get_expression_boxplot()</code> , but <code>pool_genes = TRUE</code> falls back to "none" because pooled violins already aggregate across genes.
fill_by	Fill mapping. Uses the same values as <code>get_expression_boxplot()</code> , including discrete sample metadata columns.
facet_nrow, facet_ncol	Optional layout passed to <code>facet_wrap()</code> when faceting.
sample_order	Ordering for sample-level display before values are grouped into violins.
rain_side	Side specification passed to <code>ggrain::geom_rain()</code> ; one of "r", "l", "f", "f1x1", or "f2x2".
id.long.var	Optional column name passed to <code>ggrain::geom_rain()</code> as <code>id.long.var</code> to identify repeated measurements.
alpha	Alpha for jittered points.
point_size	Point size for jittered points.
p.label	Label type passed to <code>ggpubr::stat_compare_means()</code> .
stats_group	Logical; add pairwise statistical tests when TRUE.
stats_method	Statistical method passed to <code>ggpubr::stat_compare_means()</code> .
label	Logical; add text labels to points using <code>ggrepel</code> .
label_column	Column name in the plotting data used for labels. Defaults to "gene" for expression raincloud plots.
label_size	Text size for point labels.
label_max_overlaps	Maximum overlaps passed to <code>ggrepel::geom_text_repel()</code> .
display_id	Optional ID/column name to use for labels. If supplied and present in <code>rowData(x)</code> , those values are used; otherwise falls back to ID mapping.
display_from	Optional source ID type for mapping (used when <code>display_id</code> is not found in <code>rowData</code> ).
display_orgdb	Optional <code>OrgDb</code> object used for ID mapping when <code>display_id</code> is set but not found in <code>rowData</code> .

## Details

`id.long.var` controls which repeated unit is connected by lines in `ggrain::geom_rain()`.

Recommended usage for expression raincloud plots:

- `id.long.var = NULL` (default): best for clean distribution summaries.
- `id.long.var = "gene"`: best when plotting a small number of genes and showing gene-level trajectories across x levels.
- `id.long.var = "<subject_id_column>"`: best for paired/repeated-measure designs when a subject ID exists in `sample_info`.

- `id.long.var = "sample"` or the grouping variable is usually less informative and can over-connect points.
- Point labels (`label = TRUE`) work best with `facet_by = "none"` or a small number of genes.

For identifier display consistency with other VISTA plotting functions, set `display_id` (for example, "SYMBOL"). When provided, genes can be given in that ID space, and default point labels use the mapped display IDs.

### Value

A `ggplot2` object.

### Examples

```
v <- example_vista()
genes <- head(rownames(v), 5)
p <- get_expression_raincloud(v, genes = genes, summarise = TRUE)
print(p)
```

---

get\_expression\_scatter

*Compare normalized expression between two samples or groups*

---

### Description

Plots gene-level expression for two selected samples or group means, colours points by local density (*viridis*), labels the most divergent genes, and reports Pearson/Spearman correlation.

### Usage

```
get_expression_scatter(
  x,
  sample_x,
  sample_y,
  by = c("sample", "group"),
  group_column = NULL,
  genes = NULL,
  log_transform = TRUE,
  label_n = 20,
  label_size = 3,
  method = c("pearson", "spearman"),
  display_id = NULL
)
```

### Arguments

<code>x</code>	A VISTA object.
<code>sample_x</code>	First sample or group to plot (character scalar).
<code>sample_y</code>	Second sample or group to plot (character scalar).
<code>by</code>	One of "sample" (use individual samples) or "group" (average replicates within group_column before plotting). Default "sample".

group_column	Column in sample_info used when by = "group" (defaults to stored grouping column).
genes	Optional character vector of genes to include; defaults to all.
log_transform	Logical; apply $\log_2(x + 1)$ transform. Default TRUE.
label_n	Integer; number of most divergent genes to label (ranked by $ x - y $ ). Set to 0 to disable labels.
label_size	Numeric size for labeled genes.
method	Correlation method for the subtitle; "pearson" (default) or "spearman".
display_id	Optional column in rowData(x) to use for point labels (fallback to gene_id/rownames when not available).

**Value**

A ggplot2 object.

**Examples**

```
v <- example_vista()
si <- as.data.frame(sample_info(v))
genes <- head(rownames(v), 50)
p <- get_expression_scatter(
  v,
  sample_x = si$sample_names[1],
  sample_y = si$sample_names[2],
  genes = genes
)
print(p)
```

---

get\_expression\_violinplot

*Violin plot of expression values*

---

**Description**

Mirrors the main user-facing arguments of `get_expression_boxplot()` so the two geoms can be swapped with minimal code changes. Violin plots currently keep group-based semantics (by = "group") because a violin requires replicate-level distributions within groups rather than one value per sample.

**Usage**

```
get_expression_violinplot(
  x,
  genes = NULL,
  sample_group = NULL,
  group_column = NULL,
  log_transform = TRUE,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
```

```

facet_scales = "free_y",
facet_nrow = NULL,
facet_ncol = NULL,
stats_group = FALSE,
p.label = "p.signif",
comparisons = NULL,
pool_genes = FALSE,
by = "group",
facet_by = c("auto", "gene", "none"),
fill_by = NULL,
sample_order = c("input", "group", "expression"),
value_transform = NULL,
summarise = FALSE
)

```

### Arguments

x	A VISTA object.
genes	Optional character vector of gene IDs to include; defaults to all genes selected by the plotting mode.
sample_group	Optional subset of groups (values of group_column) to keep.
group_column	Grouping column in sample_info; defaults to the stored grouping.
log_transform	Logical; log2-transform expression values before plotting.
display_id	Optional ID/column name to use for labels/facets. If supplied and present in rowData(x), those values are used.
display_from	Optional source ID type for mapping (reserved for compatibility with <a href="#">get_expression_boxplot()</a> ).
display_orgdb	Optional OrgDb object used for ID mapping when display_id is set but not found in rowData (reserved for compatibility with <a href="#">get_expression_boxplot()</a> ).
facet_scales	Scaling option passed to facet_wrap().
facet_nrow, facet_ncol	Optional layout passed to facet_wrap() when faceting.
stats_group	Logical; add statistical comparisons between groups when TRUE.
p.label	Label format for ggpubr::stat_compare_means().
comparisons	Optional list of specific group comparisons for stat_compare_means().
pool_genes	Logical; pool all selected genes into one violin per group.
by	Plot unit. Violin plots currently support only "group".
facet_by	Faceting mode. Uses the same argument pattern as <a href="#">get_expression_boxplot()</a> , but pool_genes = TRUE falls back to "none" because pooled violins already aggregate across genes.
fill_by	Fill mapping. Uses the same values as <a href="#">get_expression_boxplot()</a> , including discrete sample metadata columns.
sample_order	Ordering for sample-level display before values are grouped into violins.
value_transform	Deprecated compatibility alias. "log2" maps to log_transform = TRUE, "none" maps to FALSE, and "zscore" applies a per-gene z-score transform.
summarise	Logical retained for compatibility. Violin plots always use replicate-level values, so summarise = TRUE is ignored with a warning.

**Value**

A ggplot2 object.

**Examples**

```
v <- example_vista()
genes <- head(rownames(v), 4)
p <- get_expression_violinplot(v, genes = genes)
print(p)
```

---

get\_foldchange\_barplot

*Plot fold-change barplots across comparisons for selected genes*

---

**Description**

Plots log<sub>2</sub> fold changes for selected genes across one or more comparisons. `facet_by` controls per-gene or per-comparison layout explicitly.

**Usage**

```
get_foldchange_barplot(
  x,
  genes,
  sample_comparisons = NULL,
  coord_flip = FALSE,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  sort_by = c("input", "log2fc", "abs_log2fc"),
  facet_scales = "free_y",
  facet_nrow = NULL,
  facet_ncol = NULL,
  facet_by = c("auto", "gene", "comparison", "none")
)
```

**Arguments**

<code>x</code>	A VISTA object containing differential expression results.
<code>genes</code>	Character vector of gene IDs to plot.
<code>sample_comparisons</code>	Optional character vector of comparison names to include; defaults to all available.
<code>coord_flip</code>	Logical; flip axes when TRUE.
<code>display_id</code>	Optional column in <code>rowData(x)</code> to use for gene labels. Input gene matching still uses <code>gene_id</code> .
<code>display_from</code>	Optional source ID type for mapping when <code>display_id</code> is not present in <code>rowData(x)</code> .
<code>display_orgdb</code>	Optional <code>OrgDb</code> object used for identifier mapping when <code>display_id</code> is not present in <code>rowData(x)</code> .

**sort\_by**            How to order genes when faceting: "input" (use supplied order), "log2fc" (descending log2FC of the first comparison), or "abs\_log2fc" (descending max absolute log2FC across comparisons).

**facet\_scales**     Facet scales argument passed to facet\_wrap() when faceting (default "free\_y").

**facet\_nrow, facet\_ncol**     Optional layout passed to facet\_wrap() when faceting.

**facet\_by**            Faceting mode: "auto" (default), "gene", "comparison", or "none".

### Value

An object returned by this function.

A ggplot2 object.

### Examples

```

v <- example_vista()
comp <- names(comparisons(v))[1]
genes <- head(as.character(comparisons(v)[[comp]]$gene_id), 10)
p <- get_foldchange_barplot(v, sample_comparison = comp, genes = genes)
print(p)
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

vista <- create_vista(
  counts = count_data[seq_len(200), ],
  sample_info = sample_metadata[seq_len(6), ],
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control"
)

genes <- rownames(vista)[seq_len(3)]
get_foldchange_barplot(vista, genes = genes)
get_foldchange_barplot(vista, genes = genes, facet_by = "gene")

```

---

get\_foldchange\_boxplot

*Plot fold-change distributions across comparisons*

---

### Description

Builds boxplots of log2 fold changes for selected genes and comparisons, optionally adding statistics.

### Usage

```

get_foldchange_boxplot(
  x,
  genes = NULL,
  sample_comparisons = NULL,

```

```

display_id = NULL,
display_from = NULL,
display_orgdb = NULL,
facet_scales = "free_x",
facet_nrow = NULL,
facet_ncol = NULL,
facet_by = c("auto", "comparison", "none"),
p.label = "p.signif",
stats_group = FALSE,
stats_method = "t.test"
)

```

### Arguments

<code>x</code>	A VISTA object containing differential expression results.
<code>genes</code>	Optional character vector of gene IDs to include.
<code>sample_comparisons</code>	Optional character vector of comparison names to plot.
<code>display_id</code>	Optional ID/column name used to interpret genes and, when possible, map fold-change gene identifiers to display-friendly labels.
<code>display_from</code>	Optional source ID type for mapping when <code>display_id</code> is not present in <code>rowData(x)</code> .
<code>display_orgdb</code>	Optional <code>OrgDb</code> object used for identifier mapping when <code>display_id</code> is not present in <code>rowData(x)</code> .
<code>facet_scales</code>	Facet scales argument passed to <code>facet_wrap()</code> when <code>facet_by</code> != "none" (default "free_x").
<code>facet_nrow, facet_ncol</code>	Optional layout passed to <code>facet_wrap()</code> when faceting.
<code>facet_by</code>	Faceting mode: "auto" (default), "comparison", or "none".
<code>p.label</code>	Label type passed to <code>ggpubr::stat_compare_means()</code> .
<code>stats_group</code>	Logical; add pairwise statistical tests when TRUE.
<code>stats_method</code>	Statistical method passed to <code>ggpubr::stat_compare_means()</code> .

### Value

An object returned by this function.

### Examples

```

v <- example_vista()
comp <- names(comparisons(v))[1]
genes <- head(as.character(comparisons(v)[[comp]]$gene_id), 10)
p <- get_foldchange_boxplot(v, sample_comparison = comp, genes = genes)
print(p)

```

---

```
get_foldchange_chromosome_plot
```

*Chromosome plot for fold change*

---

### Description

Convenience wrapper around `get_chromosome_plot()` for fold-change colouring. When multiple comparisons are supplied, panels are faceted by comparison with  $\log_2FC$  clipped to  $\pm 2$ .

### Usage

```
get_foldchange_chromosome_plot(
  x,
  txdb,
  keytype = "GENEID",
  id_column = NULL,
  genes = NULL,
  sample_comparison = NULL,
  value_column = NULL,
  label_n = 20,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  line_length = 0.02,
  line_width = 0.6,
  filter_chrom = NULL
)
```

### Arguments

<code>x</code>	A VISTA object.
<code>txdb</code>	A TxDb object (e.g., from <b>GenomicFeatures</b> ).
<code>keytype</code>	Key type in the TxDb matching <code>id_column</code> (default "GENEID").
<code>id_column</code>	Optional column in <code>rowData(x)</code> used to match to TxDb keys. When NULL, <code>rownames(x)</code> are used as keys.
<code>genes</code>	Optional character vector of gene IDs to label (alternative to <code>label_top_n</code> ). When provided, all genes are plotted but only these are labeled. Defaults to NULL (no explicit label set).
<code>sample_comparison</code>	Optional comparison name (or vector of names) used for fold-change colouring.
<code>value_column</code>	Optional column in <code>rowData(x)</code> used for colouring.
<code>label_n</code>	Integer; number of genes with the largest absolute fold-change to label when genes is not supplied. Set to 0 to disable labels.
<code>display_id</code>	Optional column in <code>rowData(x)</code> to use for point labels (fallback to <code>gene_id/rownames</code> ).
<code>display_from</code>	Optional source ID type for mapping when <code>display_id</code> is not present in <code>rowData(x)</code> .
<code>display_orgdb</code>	Optional OrgDb object used for identifier mapping when <code>display_id</code> is not present in <code>rowData(x)</code> .

line_length	Horizontal half-length (in megabases) of the tick used to mark each gene position. Default 0.02. Increase for longer ticks.
line_width	Line width of the tick marks. Default 0.6.
filter_chrom	Optional character vector of chromosomes to keep (e.g., c("chr1", "chr2")). When NULL, all chromosomes returned by the TxDb are shown.

**Value**

A ggplot2 object.

**Examples**

```
v <- example_vista()
p <- try(get_foldchange_chromosome_plot(v, sample_comparison = names(comparisons(v))[1]), silent = TRUE)
if (!inherits(p, 'try-error')) print(p)
```

---

get\_foldchange\_heatmap

*Fold-change heatmap*

---

**Description**

Visualizes log<sub>2</sub> fold-change matrices across comparisons with ComplexHeatmap, supporting clustering and annotations. With only a VISTA object, the function will plot the top DE genes across the stored comparisons.

**Usage**

```
get_foldchange_heatmap(
  x,
  sample_comparisons = NULL,
  genes = NULL,
  top_n = 10,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  repair_genes = FALSE,
  show_row_names = NULL,
  label_size = 10,
  label_specific_rows = NULL,
  label_specific_rows_gp = grid::gpar(fontsize = 5),
  show_column_names = TRUE,
  cluster_rows = TRUE,
  show_row_dend = TRUE,
  cluster_columns = TRUE,
  kmeans_k = NULL,
  annotate_columns = FALSE,
  column_anno_palette = "Set2",
  color_default = TRUE,
  col = NULL,
  heatmap_name = NULL,
```

```

show_heatmap_legend = TRUE,
return_type = c("heatmap", "clusters", "both"),
...
)

```

### Arguments

<code>x</code>	A VISTA object with stored differential expression results.
<code>sample_comparisons</code>	Optional character vector of comparison names to include. Defaults to all available comparisons.
<code>genes</code>	Optional character vector of gene identifiers to display. When omitted, VISTA selects the top DE genes from each comparison by absolute log <sub>2</sub> fold-change.
<code>top_n</code>	Integer number of genes to select per comparison when <code>genes = NULL</code> . Defaults to 10.
<code>display_id</code>	Optional ID/column name to use for plot labels. If supplied
<code>display_from</code>	Optional source ID type for mapping (used when <code>display_id</code>
<code>display_orgdb</code>	Optional OrgDb object used for ID mapping when
<code>repair_genes</code>	Logical; attempt to simplify <code>gene_id</code> strings by removing prefixes.
<code>show_row_names</code>	Logical; draw row (gene) names. When <code>NULL</code> , VISTA turns labels on automatically for auto-selected genes.
<code>label_size</code>	Numeric font size for row names.
<code>label_specific_rows</code>	Optional character vector of genes to highlight with <code>anno_mark()</code> .
<code>label_specific_rows_gp</code>	<code>grid::gpar()</code> object controlling highlighted labels.
<code>show_column_names</code>	Logical; draw column labels.
<code>cluster_rows</code>	Logical; cluster rows.
<code>show_row_dend</code>	Logical; display the row dendrogram.
<code>cluster_columns</code>	Logical; cluster columns.
<code>kmeans_k</code>	Optional integer specifying the number of k-means clusters for rows.
<code>annotate_columns</code>	Logical; add annotation bars keyed to the sample grouping column.
<code>column_anno_palette</code>	Qualitative palette name used for column annotations.
<code>color_default</code>	Logical; use the default diverging palette when <code>TRUE</code> . Set to <code>FALSE</code> to supply <code>col</code> .
<code>col</code>	Optional <code>circlize::colorRamp2</code> color function used when <code>color_default = FALSE</code> .
<code>heatmap_name</code>	Optional legend title.
<code>show_heatmap_legend</code>	Logical; display the heatmap legend.
<code>return_type</code>	"heatmap", "clusters", or "both" selecting the returned value.
<code>...</code>	Additional arguments forwarded to <code>ComplexHeatmap::Heatmap()</code> .

**Value**

An object returned by this function.

A ComplexHeatmap object, a cluster data frame, or a list containing both depending on return\_type.

**Examples**

```
v <- example_vista()
comp <- names(comparisons(v))[1]
genes <- unique(stats::na.omit(as.character(comparisons(v)[[comp]]$gene_id)))[seq_len(20)]
if (requireNamespace('ComplexHeatmap', quietly = TRUE) &&
    requireNamespace('circlize', quietly = TRUE)) {
  hm <- get_foldchange_heatmap(
    v,
    sample_comparisons = comp,
    genes = genes,
    return_type = 'heatmap'
  )
  ComplexHeatmap::draw(hm)
}
v <- example_vista()
if (requireNamespace("ComplexHeatmap", quietly = TRUE) &&
    requireNamespace("circlize", quietly = TRUE)) {
  hm <- get_foldchange_heatmap(v, return_type = "heatmap")
  ComplexHeatmap::draw(hm)
}
```

---

get\_foldchange\_lineplot

*Fold-change line plot across comparisons*

---

**Description**

Plots log<sub>2</sub> fold-change trajectories for selected genes across multiple comparisons, optionally clustering genes.

**Usage**

```
get_foldchange_lineplot(
  x,
  sample_comparisons,
  genes = NULL,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  km = NULL,
  facet_by = c("none", "cluster"),
  facet_scales = "fixed",
  facet_nrow = NULL,
  facet_ncol = NULL,
  alpha = 0.5,
  palette = NULL,
  show_summary = TRUE,
```

```

summary_color = NULL,
summary_linewidth = 1,
summary_fun = c("median", "mean"),
base_size = 14
)

```

## Arguments

<code>x</code>	A VISTA object containing differential expression results.
<code>sample_comparisons</code>	Character vector of comparison names to include.
<code>genes</code>	Optional character vector of gene identifiers to plot. Defaults to all genes.
<code>display_id</code>	Optional ID/column name used to interpret genes and map the returned cluster table to display-friendly labels.
<code>display_from</code>	Optional source ID type for mapping when <code>display_id</code> is not present in <code>rowData(x)</code> .
<code>display_orgdb</code>	Optional <code>OrgDb</code> object used for identifier mapping when <code>display_id</code> is not present in <code>rowData(x)</code> .
<code>km</code>	Optional integer specifying the number of k-means clusters to compute; <code>NULL</code> disables clustering.
<code>facet_by</code>	Faceting mode: "none" (default) or "cluster" when k-means clustering is requested.
<code>facet_scales</code>	Facet scales argument passed to <code>facet_wrap()</code> when <code>facet_by = "cluster"</code> (default "fixed").
<code>facet_nrow, facet_ncol</code>	Optional layout passed to <code>facet_wrap()</code> when faceting.
<code>alpha</code>	Numeric alpha applied to individual gene lines.
<code>palette</code>	Optional named or unnamed color vector used for cluster lines.
<code>show_summary</code>	Logical; overlay a summary line per cluster when <code>TRUE</code> .
<code>summary_color</code>	Color used for the summary line. When <code>NULL</code> , uses the first comparison color (if stored) for consistency across plots.
<code>summary_linewidth</code>	Numeric line width for the summary line.
<code>summary_fun</code>	Character string selecting "median" or "mean" for the summary statistic.
<code>base_size</code>	Numeric base theme size.

## Value

An object returned by this function.

A list with `plot` (the `ggplot2` object) and `clustered_data` (gene-to-cluster assignments).

## Examples

```

v <- example_vista()
comp <- names(comparisons(v))[1]
genes <- head(as.character(comparisons(v)[[comp]]$gene_id), 5)
p <- get_foldchange_lineplot(v, sample_comparison = comp, genes = genes)
print(p)

```

---

 get\_foldchange\_lollipop

*Fold-change plotting helpers (overview)*


---

## Description

One-stop doc for fold-change plots:

- `get_foldchange_barplot()`: log2FC by comparison (bars).
- `get_foldchange_boxplot()`: log2FC distributions per comparison (boxes).
- `get_foldchange_lollipop()`: log2FC stems/dots; supports 1–2 comparisons.
- `get_foldchange_lineplot()`: log2FC trajectories across comparisons (optional clustering).

## Usage

```
get_foldchange_lollipop(
  x,
  sample_comparison,
  genes = NULL,
  sort_by = c("input", "log2fc", "abs_log2fc"),
  palette = NULL,
  point_size = 6,
  line_size = 1.2,
  label = TRUE,
  label_digits = 2,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  dodge_width = 0.5,
  facet_scales = "free_y",
  facet_nrow = NULL,
  facet_ncol = NULL,
  facet_by = c("auto", "gene", "comparison", "none")
)
```

## Arguments

<code>x</code>	A VISTA object.
<code>sample_comparison</code>	Character vector of length 1 or 2 naming the comparison(s) to plot (must exist in <code>metadata(x)\$de_results</code> ).
<code>genes</code>	Optional character vector of gene IDs to include. When NULL, all genes in the specified comparison(s) are shown.
<code>sort_by</code>	How to sort genes on the y-axis: "input" (use supplied order), "log2fc" (descending log2FC; for two comparisons uses the first comparison), or "abs_log2fc" (descending max abs log2FC across comparisons).
<code>palette</code>	For a single comparison, named vector of colors for "pos", "neg", and "zero" sign classes (set to NULL to disable color by sign). For two comparisons, a named or unnamed vector of colors with one entry per comparison (defaults to a qualitative palette).

<code>point_size</code>	Numeric size of dots.
<code>line_size</code>	Numeric size of stems (linewidth).
<code>label</code>	Logical; draw numeric labels next to the dots.
<code>label_digits</code>	Integer; digits to show in labels when <code>label = TRUE</code> .
<code>display_id</code>	Optional column in <code>rowData(x)</code> used to interpret genes and to label plotted genes.
<code>display_from</code>	Optional source ID type for mapping when <code>display_id</code> is not present in <code>rowData(x)</code> .
<code>display_orgdb</code>	Optional <code>OrgDb</code> object used for identifier mapping when <code>display_id</code> is not present in <code>rowData(x)</code> .
<code>dodge_width</code>	Horizontal separation between comparisons when plotting two comparisons on the same axis.
<code>facet_scales</code>	Facet scales argument passed to <code>facet_wrap()</code> when <code>facet_by != "none"</code> (default <code>"free_y"</code> ).
<code>facet_nrow, facet_ncol</code>	Optional layout passed to <code>facet_wrap()</code> when faceting.
<code>facet_by</code>	Faceting mode: <code>"auto"</code> (default), <code>"gene"</code> , <code>"comparison"</code> , or <code>"none"</code> .

## Details

Shared arguments: `x` (VISTA with DE results), `sample_comparisons/sample_comparison`, `genes`, `display_id` for label mapping, `sort_by` (where supported), faceting controls (`facet_*`), and comparison colours pulled from Plot log2 fold changes as a lollipop chart (one or two comparisons)

Extracts log2 fold changes from stored differential expression results and plots them as stems and dots, with labels and a zero reference line. You can optionally provide two comparisons; in that case both comparisons are drawn side-by-side, coloured by comparison.

## Value

An object returned by this function.

A `ggplot2` object.

## Examples

```
v <- example_vista()
comp <- names(comparisons(v))[1]
genes <- head(as.character(comparisons(v)[[comp]]$gene_id), 10)
p <- get_foldchange_lollipop(v, sample_comparison = comp, genes = genes)
print(p)
vista <- example_vista()
comp_name <- names(comparisons(vista))[1]
genes <- rownames(vista)[seq_len(3)]
get_foldchange_lollipop(vista, sample_comparison = comp_name, genes = genes)
```

---

get\_foldchange\_matrix *Extract a log2 fold-change matrix*

---

### Description

Returns a gene-by-comparison matrix of log2 fold changes stored in a VISTA object.

### Usage

```
get_foldchange_matrix(x, sample_comparisons = NULL, genes = NULL)
```

### Arguments

**x** A VISTA object containing differential expression results.

**sample\_comparisons** Optional character vector of comparison names. Defaults to all available comparisons.

**genes** Optional character vector of gene identifiers. When omitted, all genes present in `row_data(x)` are returned.

### Value

A numeric matrix with genes in rows and comparisons in columns.

### Examples

```
v <- example_vista()
mat <- get_foldchange_matrix(v)
dim(mat)
```

---

get\_foldchange\_raincloud

*Raincloud plot of fold-change distributions across comparisons*

---

### Description

Uses `gggrain::geom_rain()` to display log2 fold-change distributions for selected comparisons, with optional statistical testing across comparisons.

### Usage

```
get_foldchange_raincloud(
  x,
  genes = NULL,
  sample_comparisons = NULL,
  facet_scales = "free_x",
  facet_nrow = NULL,
  facet_ncol = NULL,
  facet_by = c("auto", "comparison", "none"),
```

```

rain_side = c("r", "l", "f", "f1x1", "f2x2"),
id.long.var = NULL,
alpha = 0.5,
point_size = 1.5,
p.label = "p.signif",
stats_group = FALSE,
stats_method = "t.test",
label = FALSE,
label_column = "gene_id",
label_size = 3,
label_max_overlaps = 50,
display_id = NULL,
display_from = NULL,
display_orgdb = NULL
)

```

### Arguments

<code>x</code>	A VISTA object containing differential expression results.
<code>genes</code>	Optional character vector of gene IDs to include.
<code>sample_comparisons</code>	Optional character vector of comparison names to plot.
<code>facet_scales</code>	Facet scales argument passed to <code>facet_wrap()</code> when <code>facet_by != "none"</code> (default <code>"free_x"</code> ).
<code>facet_nrow, facet_ncol</code>	Optional layout passed to <code>facet_wrap()</code> when faceting.
<code>facet_by</code>	Faceting mode: <code>"auto"</code> (default), <code>"comparison"</code> , or <code>"none"</code> .
<code>rain_side</code>	Side specification passed to <code>gggrain::geom_rain()</code> ; one of <code>"r"</code> , <code>"l"</code> , <code>"f"</code> , <code>"f1x1"</code> , or <code>"f2x2"</code> .
<code>id.long.var</code>	Optional column name passed to <code>gggrain::geom_rain()</code> as <code>id.long.var</code> to identify repeated measurements.
<code>alpha</code>	Alpha for jittered points.
<code>point_size</code>	Point size for jittered points.
<code>p.label</code>	Label type passed to <code>ggpubr::stat_compare_means()</code> .
<code>stats_group</code>	Logical; add pairwise statistical tests when TRUE.
<code>stats_method</code>	Statistical method passed to <code>ggpubr::stat_compare_means()</code> .
<code>label</code>	Logical; add text labels to points using <code>ggrepel</code> .
<code>label_column</code>	Column name in the plotting data used for labels. Defaults to <code>"gene_id"</code> for fold-change raincloud plots.
<code>label_size</code>	Text size for point labels.
<code>label_max_overlaps</code>	Maximum overlaps passed to <code>ggrepel::geom_text_repel()</code> .
<code>display_id</code>	Optional ID/column name to use for labels. If supplied and present in <code>rowData(x)</code> , those values are used; otherwise falls back to ID mapping.
<code>display_from</code>	Optional source ID type for mapping (used when <code>display_id</code> is not found in <code>rowData</code> ).
<code>display_orgdb</code>	Optional <code>OrgDb</code> object used for ID mapping when <code>display_id</code> is set but not found in <code>rowData</code> .

**Details**

id.long.var controls which repeated unit is connected by lines in `ggrain::geom_rain()`.

Recommended usage for fold-change raincloud plots:

- `id.long.var = NULL` (default): best for clean distribution summaries.
- `id.long.var = "gene_id"`: most useful option; connects each gene across comparisons.
- `id.long.var = "comparison"` is generally not useful because comparison is already on the x-axis.
- Continuous value columns (e.g. `log2FoldChange`) are not suitable identifiers for line connections.
- Point labels (`label = TRUE`) work best with `facet_by = "none"` unless only a small set of genes is shown.

For identifier display consistency with other VISTA plotting functions, set `display_id` (for example, "SYMBOL"). When provided, genes can be given in that ID space, and default point labels use the mapped display IDs.

**Value**

A `ggplot2` object.

**Examples**

```
v <- example_vista()
comp <- names(comparisons(v))[1]
genes <- head(as.character(comparisons(v)[[comp]]$gene_id), 20)
p <- get_foldchange_raincloud(v, sample_comparison = comp, genes = genes)
print(p)
```

---

get\_foldchange\_scatter

*Fold-change scatterplot between two comparisons*

---

**Description**

Plots  $\log_2$  fold changes from two stored comparisons against each other, with points coloured by concordant/discordant regulation based on the cutoffs saved in the VISTA object.

**Usage**

```
get_foldchange_scatter(
  x,
  sample_comparisons,
  genes = NULL,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  label_n = 0,
  alpha = 0.5,
  geometry = c("point", "hex"),
```

```

method = c("pearson", "spearman"),
colors = c(`Up/Up` = "#1b9e77", `Down/Down` = "#7570b3", `Up/Down` = "#d95f02",
  `Down/Up` = "#e7298a", Other = "grey70"),
point_size = 1.5,
label_size = 3,
base_size = 12
)

```

### Arguments

x	A VISTA object containing DE results.
sample_comparisons	Character vector of length 2 naming the comparisons.
genes	Optional character vector of gene identifiers used to subset the comparison overlap before plotting.
display_id	Optional ID/column name used to interpret genes and to label highlighted points.
display_from	Optional source ID type for mapping when display_id is not present in rowData(x).
display_orgdb	Optional OrgDb object used for identifier mapping when display_id is not present in rowData(x).
label_n	Integer; number of most extreme points to label (by $ \log_2FC1  +  \log_2FC2 $ ).
alpha	Point transparency.
geometry	Geometry used for the data layer: "point" or "hex".
method	Correlation method for the subtitle; "pearson" or "spearman".
colors	Named vector of concordance colours.
point_size	Point size used when geometry = "point".
label_size	Text size for labeled genes.
base_size	Base theme size.

### Details

Points are coloured by concordance status using fixed colours:

- Up/Up = #1b9e77
- Down/Down = #7570b3
- Up/Down = #d95f02
- Down/Up = #e7298a
- Other = grey70

Regulation is derived from the log2fc and pval cutoffs stored in cutoffs(x) (and p\_value\_type from the same list, defaulting to "padj").

### Value

A ggplot2 object.

**Examples**

```
## Not run:
data('count_data', package = 'VISTA')
data('sample_metadata', package = 'VISTA')
cell_levels <- unique(sample_metadata$cell)
if (length(cell_levels) >= 3) {
  v <- create_vista(count_data[seq_len(150), ], sample_metadata, column_geneid = 'gene_id', group_column = 'ce
                    group_numerator = cell_levels[2:3], group_denominator = rep(cell_levels[1], 2),
                    min_counts = 5, min_replicates = 1)
  comp_names <- names(comparisons(v))[seq_len(2)]
  p <- get_foldchange_scatter(v, sample_comparisons = comp_names)
  print(p)
}

## End(Not run)
```

---

```
get_genes_by_regulation
```

*Get Genes by Regulation*

---

**Description**

Extract gene IDs by regulation class from selected comparisons in a VISTA object.

**Usage**

```
get_genes_by_regulation(
  x,
  sample_comparisons,
  regulation = "Both",
  top_n = NULL,
  display_id = NULL,
  return_type = c("list", "table")
)
```

**Arguments**

x	A VISTA object.
sample_comparisons	Character vector of comparison names to include.
regulation	One of "Up", "Down", "Both", or "All" (default: "Both").
top_n	Optional integer limiting each comparison to the top DE genes ranked by absolute log <sub>2</sub> fold change after regulation filtering.
display_id	Optional column name in rowData(x) to append when return_type = "table", for example "SYMBOL".
return_type	Either "list" (default) to return gene ID vectors or "table" to return one data frame per comparison with gene metadata.

**Value**

A named list of character vectors (one per comparison) when return\_type = "list", or a named list of data frames when return\_type = "table".

**Examples**

```
v <- example_vista()
comp <- names(comparisons(v))[1]
genes <- get_genes_by_regulation(v, sample_comparisons = comp, regulation = 'Up', top_n = 20)
str(genes, max.level = 1)
```

---

get\_go\_enrichment      *Run GO enrichment directly from a VISTA comparison*

---

**Description**

Run GO enrichment directly from a VISTA comparison

**Usage**

```
get_go_enrichment(
  x,
  sample_comparison,
  regulation = c("Up", "Down", "Both", "All"),
  ont = c("BP", "MF", "CC"),
  from_type = "SYMBOL",
  orgdb = NULL,
  species = "Mus musculus",
  background = NULL,
  ...
)
```

**Arguments**

x	A VISTA object with DE results.
sample_comparison	Comparison name to use.
regulation	One of "Up", "Down", "Both", or "All"; selects genes.
ont	GO ontology: "BP", "MF", or "CC".
from_type	Identifier type in the DE tables (default "SYMBOL").
orgdb	OrgDb object; defaults to mouse/human based on species.
species	Species name to infer default OrgDb.
background	Optional background gene set; default uses all features.
...	Passed to clusterProfiler::enrichGO().

**Value**

A list with enrich containing an enrichResult.

**Examples**

```
## Not run:
v <- example_vista()
comp <- names(comparisons(v))[1]
if (requireNamespace('org.Mm.eg.db', quietly = TRUE)) {
  out <- try(get_go_enrichment(v, sample_comparison = comp, ont = 'BP', from_type = 'ENSEMBL',
                             orgdb = org.Mm.eg.db::org.Mm.eg.db), silent = TRUE)
  if (!inherits(out, 'try-error')) out
}

## End(Not run)
```

get\_gsea

*Gene set enrichment analysis (GSEA) from a VISTA comparison***Description**

Gene set enrichment analysis (GSEA) from a VISTA comparison

**Usage**

```
get_gsea(
  x,
  sample_comparison,
  set_type = c("msigdb", "go", "kegg"),
  from_type = "SYMBOL",
  orgdb = NULL,
  species = "Mus musculus",
  msigdb_category = "H",
  msigdb_subcategory = NULL,
  ...
)
```

**Arguments**

x	A VISTA object with DE results.
sample_comparison	Comparison name to use.
set_type	One of "msigdb", "go", or "kegg" selecting the gene set source.
from_type	Identifier type in the DE tables (default "SYMBOL").
orgdb	OrgDb object; defaults to mouse/human based on species.
species	Species name to infer default OrgDb.
msigdb_category, msigdb_subcategory	Passed to msigdb::msigdb() when set_type = "msigdb".
...	Additional arguments forwarded to the underlying GSEA function: clusterProfiler::GSEA() (msigdb TERM2GENE), gseGO(), or gseKEGG() depending on set_type.

**Value**

An object returned by this function.

**Examples**

```
## Not run:
v <- example_vista()
comp <- names(comparisons(v))[1]
if (requireNamespace('msigdb', quietly = TRUE)) {
  out <- try(get_gsea(v, sample_comparison = comp, set_type = 'msigdb', from_type = 'ENSEMBL', species = 'Homo s
  if (!inherits(out, 'try-error')) out
}

## End(Not run)
```

---

get\_kegg\_enrichment     *Run KEGG enrichment directly from a VISTA comparison*

---

**Description**

Run KEGG enrichment directly from a VISTA comparison

**Usage**

```
get_kegg_enrichment(
  x,
  sample_comparison,
  regulation = c("Up", "Down", "Both", "All"),
  from_type = "SYMBOL",
  orgdb = NULL,
  species = "Mus musculus",
  kegg_species = NULL,
  background = NULL,
  ...
)
```

**Arguments**

x	A VISTA object with DE results.
sample_comparison	Comparison name to use.
regulation	One of "Up", "Down", "Both", or "All"; selects genes.
from_type	Identifier type in the DE tables (default "SYMBOL").
orgdb	OrgDb object; defaults to mouse/human based on species.
species	Species name to infer default OrgDb.
kegg_species	KEGG organism code (e.g., "mmu" or "hsa"). If NULL, inferred from species.
background	Optional background gene set; default uses all features.
...	Passed to clusterProfiler::enrichGO().

**Value**

An object returned by this function.

**Examples**

```
v <- example_vista()
comp <- names(comparisons(v))[1]
if (requireNamespace('org.Mm.eg.db', quietly = TRUE)) {
  out <- try(get_kegg_enrichment(v, sample_comparison = comp, from_type = 'ENSEMBL', orgdb = org.Mm.eg.db::org.
  if (!inherits(out, 'try-error')) out
}
```

get\_ma\_plot

*Generate MA plot from a VISTA object***Description**

Create an MA plot (log2 fold change vs mean expression) for a selected comparison contained in a VISTA object. Genes are coloured by their regulation class and the top results can be optionally labeled with gene IDs.

**Usage**

```
get_ma_plot(
  x,
  sample_comparison,
  point_size = 1.2,
  alpha = 0.6,
  colors = c(Up = "#a40000", Down = "#16317d", Other = "gray70"),
  label_n = 0,
  label_size = 3,
  repair_genes = FALSE,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL
)
```

**Arguments**

x	A <a href="#">VISTA</a> object.
sample_comparison	Character scalar naming the comparison to plot. Must match one of <code>names(comparisons(x))</code> .
point_size	Numeric point size. Default: 1.2.
alpha	Numeric transparency (0-1). Default: 0.6.
colors	Named character vector of colors for "Up", "Down", and "Other" genes.
label_n	Integer number of genes to label. Default: 0.
label_size	Text size for labels. Default: 3.
repair_genes	Logical; if TRUE, attempt to shorten gene identifiers to symbols by stripping prefixes. Default: FALSE.
display_id	Optional ID/column name to use for labels. If supplied and present in <code>rowData(x)</code> , those values are used; otherwise falls back to ID mapping.
display_from	Optional source ID type for mapping (used when <code>display_id</code> is not found in <code>rowData</code> ).
display_orgdb	Optional OrgDb used for ID mapping when <code>display_id</code> is set but not found in <code>rowData</code> .

**Value**

A `ggplot` MA plot.

**Examples**

```
v <- example_vista()
p <- get_ma_plot(v, sample_comparison = names(comparisons(v))[1])
print(p)
```

---

get\_mds\_plot

*Generate an MDS plot for samples in a VISTA object*

---

**Description**

Runs classical multidimensional scaling on normalized counts, optionally restricting to groups or genes.

**Usage**

```
get_mds_plot(
  x,
  sample_group = NULL,
  group_column = NULL,
  genes = NULL,
  top_n_genes = NULL,
  label = FALSE,
  label_size = 3,
  point_size = 10,
  shape_by = NULL,
  shape_values = NULL,
  color_by = NULL,
  use_vista_colors = NULL,
  palette = NULL,
  colors = NULL,
  use_group_colors = TRUE
)
```

**Arguments**

<code>x</code>	A VISTA object.
<code>sample_group</code>	Optional character vector of groups to include (based on the column specified by <code>group_column</code> ).
<code>group_column</code>	Optional column name in <code>sample_info</code> to use for grouping/filtering.
<code>genes</code>	Optional character vector of gene identifiers to restrict the matrix.
<code>top_n_genes</code>	Optional integer selecting the top variable genes to include.
<code>label</code>	Logical; draw sample labels when TRUE.
<code>label_size</code>	Numeric size of sample labels when <code>label = TRUE</code> .
<code>point_size</code>	Numeric size for points.

shape_by	Optional column name in sample_info used to map point shape. When NULL, shapes are not mapped.
shape_values	Optional vector of shapes passed to scale_shape_manual() when shape_by is set. Use a named vector to map shapes to specific levels.
color_by	Optional column name in sample_info used for point colour. Defaults to the active grouping column.
use_vista_colors	Deprecated alias for use_group_colors. When supplied, it overrides use_group_colors.
palette	Optional qualitative palette name used when generating colours for non-group metadata levels.
colors	Optional named character vector of manual colours overriding both palette and stored VISTA colours.
use_group_colors	Logical; when TRUE, prefer the stored VISTA group colours when colouring by the grouping column.

**Value**

An object returned by this function.

**Examples**

```
v <- example_vista()
p <- get_mds_plot(v)
print(p)
```

---

get\_msigdb\_enrichment *Run MSigDB enrichment directly from a VISTA comparison*

---

**Description**

Convenience wrapper that pulls regulated genes from a stored differential expression comparison in a VISTA object and runs `enrichMsigDB()` on them.

**Usage**

```
get_msigdb_enrichment(
  x,
  sample_comparison,
  regulation = c("Up", "Down", "Both", "All"),
  from_type = "SYMBOL",
  orgdb,
  msigdb_category = "H",
  msigdb_subcategory = NULL,
  species = "Mus musculus",
  background = NULL,
  col_genetype = "GENETYPE",
  feature_type = "protein-coding",
  ...
)
```

**Arguments**

x	A VISTA object with DE results in <code>metadata(x)\$de_results</code> .
sample_comparison	Character scalar naming the comparison to use.
regulation	One of "Up", "Down", "Both", or "All"; selects which genes to send to enrichment.
from_type	Identifier type of the genes in the DE table (passed to <code>enrichMsigDB()</code> , default "SYMBOL"). Ensembl versions are stripped automatically.
orgdb	An OrgDb object used for ID conversion (passed through). If omitted, the default is chosen from species (mouse/human).
msigdb_category	MSigDB category (e.g., "H", "C2", "C5"). Default "H".
msigdb_subcategory	Optional MSigDB sub-collection. Default NULL.
species	Species name for MSigDB (default "Mus musculus").
background	Optional background gene set (passed to <code>enrichMsigDB()</code> ). Default NULL uses all features in x (optionally filtered by <code>feature_type</code> ).
col_geneid	Column in <code>rowData(x)</code> used to filter background by gene type. Default "GENETYPE".
feature_type	Gene type to retain in the background when filtering. Default "protein-coding".
...	Additional arguments forwarded to <code>enrichMsigDB()</code> .

**Value**

A list with `enrich` containing an `enrichResult`.

**Examples**

```
if (requireNamespace("msigdb", quietly = TRUE)) {
  vista <- example_vista()
  comp <- names(comparisons(vista))[1]
  msig <- get_msigdb_enrichment(
    vista,
    sample_comparison = comp,
    regulation = "Both",
    msigdb_category = "H",
    from_type = "ENSEMBL"
  )
  class(msig$enrich)
}
```

```
# Create VISTA object
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")
```

```
vista <- create_vista(
  counts = count_data[seq_len(200), ],
  sample_info = sample_metadata[seq_len(6), ],
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
```

```

    group_denominator = "control"
  )
  comp <- names(comparisons(vista))[1]

  # Run MSigDB enrichment on upregulated genes
  msig_up <- get_msigdb_enrichment(
    vista,
    sample_comparison = comp,
    regulation = "Up",
    msigdb_category = "H", # Hallmark gene sets
    from_type = "ENSEMBL"
  )

  if (!is.null(msig_up$enrich)) {
    # View results
    head(msig_up$enrich)
    # Visualize enrichment
    get_enrichment_plot(msig_up$enrich)
  }

  # Enrichment for downregulated genes
  msig_down <- get_msigdb_enrichment(
    vista,
    sample_comparison = comp,
    regulation = "Down",
    msigdb_category = "C2" # Curated gene sets
  )

```

---

```
get_pairwise_corr_plot
```

*Plot pairwise correlations between samples*

---

## Description

Uses GGally::ggpairs on normalized expression to display correlations among samples from selected groups/genes.

## Usage

```

get_pairwise_corr_plot(
  x,
  sample_group = NULL,
  group_column = NULL,
  genes = NULL,
  sample_order = c("input", "group"),
  value_transform = c("log2", "none"),
  title = "Pairwise Sample Correlations"
)

```

**Arguments**

x	A VISTA object.
sample_group	Optional character vector of groups (from the column specified by group_column) used to subset samples.
group_column	Optional column name in sample_info defining the grouping used for filtering.
genes	Optional character vector of gene IDs to include; defaults to all genes.
sample_order	Ordering for selected samples: "input" keeps the current order, while "group" sorts by group_column.
value_transform	Value transformation: "log2" (default) or "none".
title	Plot title.

**Value**

An object returned by this function.

**Examples**

```
v <- example_vista()
p <- get_pairwise_corr_plot(v)
print(p)
```

---

get_pathway_genes	<i>Extract genes from enriched pathways</i>
-------------------	---

---

**Description**

Parses pathway-level gene members from an enrichment result and returns either a long table, pathway-indexed list, or a unique vector of genes.

**Usage**

```
get_pathway_genes(
  x,
  pathways = NULL,
  top_n = 10,
  pathway_column = c("Description", "ID"),
  gene_column = c("auto", "geneID", "core_enrichment"),
  gene_sep = "/",
  return_type = c("long", "list", "vector")
)
```

**Arguments**

x	An enrichResult/gseaResult, or a list containing element enrich (e.g. output from get_msigdb_enrichment()).
pathways	Optional character vector of pathway names to keep. Matches against pathway_column.
top_n	Number of top pathways to use when pathways is NULL. Ranking uses p.adjust (then pvalue) when available. Default: 10.

pathway_column	Which enrichment column to match pathway names against: "Description" (default) or "ID".
gene_column	Which column stores pathway members. "auto" (default) uses "geneID" when present, otherwise "core_enrichment".
gene_sep	Delimiter used in pathway gene strings (default "/").
return_type	One of "long", "list", or "vector".

### Value

Depending on return\_type:

- "long": data frame with pathway\_id, pathway, and gene.
- "list": named list of character vectors (genes per pathway).
- "vector": unique character vector of genes.

### Examples

```
if (requireNamespace("msigdb", quietly = TRUE)) {
  vista <- example_vista()
  msig <- get_msigdb_enrichment(
    vista,
    sample_comparison = names(comparisons(vista))[1],
    regulation = "Both",
    msigdb_category = "H",
    from_type = "ENSEMBL"
  )
  pathway_tbl <- get_pathway_genes(msig, top_n = 5, return_type = "long")
  head(pathway_tbl)
}
```

```
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")
```

```
vista <- create_vista(
  counts = count_data,
  sample_info = sample_metadata,
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control"
)
```

```
msig <- get_msigdb_enrichment(
  vista,
  sample_comparison = names(comparisons(vista))[1],
  regulation = "Up",
  species = "Homo sapiens",
  from_type = "ENSEMBL"
)
```

```
pathway_tbl <- get_pathway_genes(msig, top_n = 5, return_type = "long")
head(pathway_tbl)
```

---

get\_pathway\_heatmap *Plot pathway-specific expression heatmaps from enrichment output*

---

### Description

This wrapper bridges enrichment results and expression heatmaps. It extracts genes from selected pathways (via [get\\_pathway\\_genes\(\)](#)), maps them to the VISTA feature IDs, and forwards to [get\\_expression\\_heatmap\(\)](#).

### Usage

```
get_pathway_heatmap(
  x,
  enrichment,
  sample_group = NULL,
  pathways = NULL,
  top_n = 5,
  pathway_column = c("Description", "ID"),
  gene_column = c("auto", "geneID", "core_enrichment"),
  gene_sep = "/",
  gene_mode = c("union", "intersection"),
  gene_id_column = NULL,
  max_genes = NULL,
  return_type = c("heatmap", "both", "genes"),
  ...
)
```

### Arguments

x	A VISTA object.
enrichment	An enrichResult/gseaResult, or a list with element enrich as returned by <a href="#">get*_enrichment()</a> helpers.
sample_group	Character vector of group labels to include (same semantics as <a href="#">get_expression_heatmap()</a> ).
pathways	Optional pathway names to include. When NULL, top pathways are selected using top_n.
top_n	Number of top pathways used when pathways = NULL. Default: 5.
pathway_column	Pathway matching column, "Description" (default) or "ID".
gene_column	Pathway gene-member column. "auto" uses "geneID" or "core_enrichment" based on availability.
gene_sep	Delimiter used to parse pathway gene strings (default "/").
gene_mode	How to combine pathway genes for plotting: "union" (default) or "intersection".
gene_id_column	Optional column in rowData(x) used to map enrichment genes back to VISTA rownames (e.g., "SYMBOL" or "ENTREZID"). Leave NULL when enrichment genes already match VISTA rownames.
max_genes	Optional cap on the number of genes passed to the heatmap.
return_type	One of "heatmap" (default), "both", or "genes".
...	Additional arguments passed to <a href="#">get_expression_heatmap()</a> .

**Value**

Depending on return\_type:

- "heatmap": a ComplexHeatmap object from `get_expression_heatmap()`.
- "both": list with heatmap, genes, and pathway\_genes.
- "genes": character vector of mapped genes selected for plotting.

**Examples**

```
if (requireNamespace("msigdb", quietly = TRUE)) {
  vista <- example_vista()
  msig <- get_msigdb_enrichment(
    vista,
    sample_comparison = names(comparisons(vista))[1],
    regulation = "Both",
    msigdb_category = "H",
    from_type = "ENSEMBL"
  )
  genes <- get_pathway_heatmap(
    vista,
    enrichment = msig,
    sample_group = c("control", "treatment1"),
    top_n = 3,
    return_type = "genes"
  )
  head(genes)
}
```

```
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")
```

```
vista <- create_vista(
  counts = count_data,
  sample_info = sample_metadata,
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control"
)
```

```
msig <- get_msigdb_enrichment(
  vista,
  sample_comparison = names(comparisons(vista))[1],
  regulation = "Up",
  species = "Homo sapiens",
  from_type = "ENSEMBL"
)
```

```
get_pathway_heatmap(
  vista,
  enrichment = msig,
  sample_group = c("control", "treatment1"),
  top_n = 3,
  value_transform = "zscore",
  annotate_columns = TRUE,
```

```

    summarise_replicates = FALSE
  )

```

---

get\_pca\_plot

*PCA plot*


---

### Description

Uses normalized counts to compute principal components and plot samples, optionally restricting to selected groups or genes.

### Usage

```

get_pca_plot(
  x,
  sample_group = NULL,
  group_column = NULL,
  genes = NULL,
  top_n_genes = NULL,
  label = FALSE,
  label_size = 3,
  point_size = 10,
  shape_by = NULL,
  shape_values = NULL,
  sample.seed = 123,
  show_clusters = FALSE,
  color_by = NULL,
  use_vista_colors = NULL,
  palette = NULL,
  colors = NULL,
  use_group_colors = TRUE
)

```

### Arguments

x	A VISTA object containing normalized counts.
sample_group	Optional character vector of group labels (taken from the column specified by group_column, defaulting to the stored grouping column) used to subset samples prior to PCA. Use NULL to include all samples.
group_column	Optional column name in sample_info to use for grouping. Defaults to the stored grouping column.
genes	Optional character vector of gene identifiers to restrict the PCA input matrix. When NULL, all genes are used.
top_n_genes	Optional integer selecting the top most variable genes to include. Ignored when genes is supplied.
label	Logical; if TRUE, sample names are drawn next to the points.
label_size	Numeric size of sample labels when label = TRUE.

point_size	Numeric size of the plotted points.
shape_by	Optional column name in <code>sample_info</code> used to map point shape. When NULL, shapes are not mapped.
shape_values	Optional vector of shapes passed to <code>scale_shape_manual()</code> when <code>shape_by</code> is set. Use a named vector to map shapes to specific levels.
sample.seed	Deprecated/unused; retained for backward compatibility.
show_clusters	Logical; add normal ellipses per group when TRUE.
color_by	Optional column name in <code>sample_info</code> used to map point colour. Defaults to the active grouping column.
use_vista_colors	Deprecated alias for <code>use_group_colors</code> . When supplied, it overrides <code>use_group_colors</code> .
palette	Optional qualitative palette name used when generating colours for non-group metadata levels.
colors	Optional named character vector of manual colours overriding both <code>palette</code> and stored VISTA colours.
use_group_colors	Logical; when TRUE, prefer the stored VISTA group colours when colouring by the grouping column.

## Value

A ggplot object showing the first two PCs.

## Examples

```
# Create VISTA object
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

vista <- create_vista(
  counts = count_data[seq_len(200), ],
  sample_info = sample_metadata[seq_len(6), ],
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control"
)

# Basic PCA plot
get_pca_plot(vista)

# With sample labels
get_pca_plot(vista, label = TRUE)

# Using top variable genes
get_pca_plot(vista, top_n_genes = 100)

# With confidence ellipses
get_pca_plot(vista, show_clusters = TRUE)
```

---

<code>get_umap_plot</code>	<i>Generate a UMAP plot for samples in a VISTA object</i>
----------------------------	---

---

### Description

Runs UMAP on normalized counts, optionally restricting to selected groups or genes. UMAP is intended for exploratory sample-level structure.

### Usage

```
get_umap_plot(
  x,
  sample_group = NULL,
  group_column = NULL,
  color_by = NULL,
  genes = NULL,
  top_n_genes = NULL,
  label = FALSE,
  label_size = 3,
  point_size = 10,
  shape_by = NULL,
  shape_values = NULL,
  n_neighbors = 15,
  min_dist = 0.1,
  metric = "euclidean",
  seed = 123,
  use_vista_colors = NULL,
  palette = NULL,
  colors = NULL,
  use_group_colors = TRUE
)
```

### Arguments

<code>x</code>	A VISTA object.
<code>sample_group</code>	Optional character vector of groups to include (based on <code>group_column</code> ).
<code>group_column</code>	Optional column name in <code>sample_info</code> used for filtering/grouping. Defaults to the stored grouping column.
<code>color_by</code>	Optional column name in <code>sample_info</code> used for point color. Defaults to <code>group_column</code> .
<code>genes</code>	Optional character vector of gene identifiers to restrict the matrix.
<code>top_n_genes</code>	Optional integer selecting top variable genes to include.
<code>label</code>	Logical; draw sample labels when TRUE.
<code>label_size</code>	Numeric label size when <code>label = TRUE</code> .
<code>point_size</code>	Numeric point size.
<code>shape_by</code>	Optional column name in <code>sample_info</code> used to map point shape.
<code>shape_values</code>	Optional vector passed to <code>scale_shape_manual()</code> when <code>shape_by</code> is set.
<code>n_neighbors</code>	UMAP <code>n_neighbors</code> parameter.

min_dist	UMAP min_dist parameter.
metric	UMAP distance metric.
seed	Integer random seed passed to UMAP.
use_vista_colors	Deprecated alias for use_group_colors. When supplied, it overrides use_group_colors.
palette	Optional qualitative palette name used when generating colours for non-group metadata levels.
colors	Optional named character vector of manual colours overriding both palette and stored VISTA colours.
use_group_colors	Logical; when TRUE, prefer the stored VISTA group colours when colouring by the grouping column.

**Value**

A ggplot object with UMAP1/UMAP2 coordinates.

**Examples**

```
if (requireNamespace("uwot", quietly = TRUE)) {
  vista <- example_vista()
  get_umap_plot(vista, top_n_genes = 50)
}
```

---

get_volcano_plot	<i>Generate a volcano plot for a comparison in a VISTA object</i>
------------------	---

---

**Description**

Wraps EnhancedVolcano to visualize log<sub>2</sub>FC vs p-values for a selected comparison.

**Usage**

```
get_volcano_plot(
  x,
  sample_comparison,
  log2fc_cutoff = 1,
  pval_cutoff = 0.05,
  label_genes = NULL,
  label_size = 3,
  point_size = 1,
  colors = c(Up = "#a40000", Down = "#007e2f", Other = "grey"),
  repair_genes = TRUE,
  display_id = NULL,
  display_from = NULL,
  display_orgdb = NULL,
  ...
)
```

**Arguments**

x	A VISTA object containing differential expression results.
sample_comparison	Character scalar naming the comparison to display.
log2fc_cutoff	Numeric absolute log2 fold-change threshold used to color significant points.
pval_cutoff	Numeric p-value threshold used to color significant points.
label_genes	Optional character vector of gene identifiers to force-label.
label_size	Numeric label text size.
point_size	Numeric point size.
colors	Named colour vector with entries for "Up", "Down", and "Other".
repair_genes	Logical; when TRUE, split gene_id values like ID:SYMBOL to display the symbol.
display_id	Optional ID/column name to use for plot labels. If supplied and present in rowData(x), those values are used; otherwise falls back to ID mapping.
display_from	Optional source ID type for mapping (used when display_id is not found in rowData).
display_orgdb	Optional OrgDb object used for ID mapping when display_id is set but not found in rowData.
...	Additional parameters forwarded to EnhancedVolcano::EnhancedVolcano().

**Value**

A ggplot2 object.

**Examples**

```
vista <- example_vista()
comps <- names(comparisons(vista))
get_volcano_plot(vista, sample_comparison = comps[1])

# Create VISTA object
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

vista <- create_vista(
  counts = count_data,
  sample_info = sample_metadata,
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control"
)

# Basic volcano plot
comps <- names(comparisons(vista))
get_volcano_plot(vista, sample_comparison = comps[1])

# With custom thresholds
get_volcano_plot(
  vista,
  sample_comparison = comps[1],
```

```

    log2fc_cutoff = 1.5,
    pval_cutoff = 0.01
  )

  # Highlight specific genes
  genes_of_interest <- rownames(vista)[seq_len(5)]
  get_volcano_plot(
    vista,
    sample_comparison = comps[1],
    label_genes = genes_of_interest
  )

```

---

match_vista_inputs	<i>Match count and metadata inputs for VISTA</i>
--------------------	--

---

### Description

match\_vista\_inputs() aligns standardized counts and sample metadata so they can be passed directly to create\_vista(). It accepts the raw output from read\_vista\_counts() or a count data frame/matrix plus sample metadata.

### Usage

```

match_vista_inputs(
  counts,
  sample_info,
  column_geneid = NULL,
  sample_column = NULL,
  reorder = TRUE,
  drop_unmatched = FALSE,
  verbose = TRUE
)

```

### Arguments

counts	Standardized counts from read_vista_counts(), or a compatible count matrix/data frame.
sample_info	Sample metadata from read_vista_metadata() or a data frame coercible to that format.
column_geneid	Optional gene identifier column for raw tabular counts. Ignored when counts is the list output of read_vista_counts().
sample_column	Optional sample identifier column in sample_info.
reorder	Logical; if TRUE (default), reorder sample_info to match count columns.
drop_unmatched	Logical; if TRUE, keep only the intersection of count samples and metadata samples. Otherwise mismatches raise an error.
verbose	Logical; print an informational alignment summary.

**Value**

A list with standardized counts, aligned sample\_info, column\_geneid, sample\_names, sample\_name\_map, row\_data, and a small report.

**Examples**

```
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

cnt <- read_vista_counts(
  count_data[seq_len(25), ],
  format = "matrix",
  gene_id_column = "gene_id",
  verbose = FALSE
)
si <- read_vista_metadata(
  sample_metadata[sample_metadata$sample_names %in% cnt$sample_names, ],
  verbose = FALSE
)
matched <- match_vista_inputs(cnt, si, verbose = FALSE)

matched$column_geneid
identical(matched$sample_info$sample_names, colnames(matched$counts)[-1])
```

---

print.VISTA

---

*Print a VISTA object like a SummarizedExperiment*


---

**Description**

Forwards to SummarizedExperiment's show() so the output is identical to a plain SE. Invisibly returns x.

**Usage**

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

**Arguments**

```
x          A VISTA object.
...        Ignored.
```

**Value**

The input object x, returned invisibly.

**Examples**

```
v <- example_vista()
print(v)
```

---

read\_vista\_counts      *Read and standardize count inputs for VISTA*

---

## Description

read\_vista\_counts() helps standardize common RNA-seq count inputs into a count table that can be passed directly to create\_vista(). It supports plain matrices/data frames, featureCounts outputs, STAR gene counts, HTSeq-count outputs, tximport-like lists, and RSEM gene result files.

## Usage

```
read_vista_counts(
  x,
  format = c("auto", "matrix", "featurecounts", "star", "htseq", "tximport", "rsem"),
  gene_id_column = NULL,
  sample_columns = NULL,
  sample_names = NULL,
  annotation_columns = NULL,
  count_column = NULL,
  tx2gene = NULL,
  counts_from = c("counts", "abundance", "length"),
  drop_technical = TRUE,
  remove_special_rows = TRUE,
  make_unique_ids = FALSE,
  repair_sample_names = c("auto", "none"),
  return_type = c("list", "data.frame", "matrix"),
  verbose = TRUE
)
```

## Arguments

x	Count input. Supported values depend on format and include a matrix, data frame, single file path, vector of file paths, or a tximport-like list with counts, abundance, and/or length.
format	Input format. One of "auto", "matrix", "featurecounts", "star", "htseq", "tximport", or "rsem".
gene_id_column	Optional gene identifier column in tabular inputs. When omitted, VISTA uses common names such as gene_id/Geneid, or falls back to rownames for matrices/data frames with unique rownames.
sample_columns	Optional character vector of sample count columns to retain from tabular inputs.
sample_names	Optional sample names to use when x is a vector of per-sample files.
annotation_columns	Optional feature annotation columns to retain in the returned row_data.
count_column	Optional count column selector for formats that expose multiple count choices. For STAR, use one of "unstranded", "stranded_first", or "stranded_second". For RSEM, this defaults to "expected_count".
tx2gene	Optional two-column mapping used to summarize transcript-level tximport-like inputs to genes. The first column should contain transcript IDs and the second column gene IDs.

counts_from	Which matrix to extract from a tximport-like input: "counts", "abundance", or "length".
drop_technical	Logical; when TRUE, drop known technical summary rows from STAR/HTSeq inputs.
remove_special_rows	Logical; alias for drop_technical, retained for clarity in file-based imports.
make_unique_ids	Logical; if TRUE, duplicate gene IDs are repaired with <code>make.unique()</code> . Otherwise duplicated gene IDs raise an error.
repair_sample_names	<p>Strategy for repairing sample column names. "auto" (default) strips common file-path and alignment/count suffixes when the repaired names are unique, while "none" leaves sample columns unchanged. In automatic mode VISTA currently:</p> <ul style="list-style-type: none"> <li>• strips directory paths to the basename</li> <li>• uses the parent directory for generic quantification files such as <code>quant.sf</code> or <code>abundance.tsv</code></li> <li>• removes common RNA-seq output suffixes such as <code>Aligned.sortedByCoord.out.bam</code>, <code>ReadsPerGene.out.tab</code>, <code>.genes.results</code>, <code>.isoforms.results</code>, <code>.bam</code>, and <code>.fastq.gz</code></li> <li>• removes common lane/read suffixes such as <code>_S1_L001_R1_001</code>, <code>_L001_R2_001</code>, <code>_R1</code>, and <code>_R2</code></li> </ul> <p>Repaired names are only applied when they remain non-empty and unique. Otherwise VISTA keeps the original count column names and records the unchanged mapping in <code>sample_name_map</code>.</p>
return_type	Return "list" (default), standardized "data.frame", or numeric "matrix".
verbose	Logical; print an informational import summary.

## Details

Internally, VISTA uses a format-specific importer for each supported input type, then normalizes the result into a common structure with:

- a count table with a `gene_id` column plus sample columns
- optional feature metadata in `row_data`
- sample names inferred from columns or file names
- an auditable `sample_name_map` showing original and repaired names

## Value

If `return_type = "list"`, a list with:

**counts** A standardized count table with `gene_id` plus sample columns.

**row\_data** Feature metadata aligned to the count table.

**column\_geneid** Always "gene\_id" for the standardized output.

**sample\_names** Sample columns in the standardized count table.

**sample\_name\_map** A two-column mapping of original and repaired sample names.

**input\_format** Resolved import format.

**report** Basic import summary.

If `return_type = "data.frame"`, returns the standardized count table. If `return_type = "matrix"`, returns a numeric matrix with gene IDs as rownames.

**Examples**

```
data("count_data", package = "VISTA")

cnt <- read_vista_counts(
  count_data[seq_len(25), ],
  format = "matrix",
  gene_id_column = "gene_id"
)

head(cnt$counts[, seq_len(4)])
cnt$sample_names
```

---

read\_vista\_metadata     *Read and standardize sample metadata for VISTA*

---

**Description**

read\_vista\_metadata() standardizes a sample sheet for use as sample\_info in create\_vista(). It infers or creates the required sample\_names column using the same conventions VISTA already accepts in the constructor.

**Usage**

```
read_vista_metadata(
  x,
  sample_column = NULL,
  required_columns = NULL,
  drop_empty = TRUE,
  standardize_names = TRUE,
  verbose = TRUE
)
```

**Arguments**

x	Sample metadata as a data frame or file path.
sample_column	Optional column to use as sample_names. If omitted, VISTA uses an existing sample_names column, non-default rownames, or common aliases such as sample, sample_id, or Run.
required_columns	Optional character vector of columns that must be present after import.
drop_empty	Logical; if TRUE, remove columns that are entirely NA or empty strings.
standardize_names	Logical; if TRUE, coerce the final sample_names column to character and set rownames to match it.
verbose	Logical; print an informational import summary.

**Value**

A data frame suitable for use as sample\_info in create\_vista().

**Examples**

```
data("sample_metadata", package = "VISTA")

si <- read_vista_metadata(sample_metadata[seq_len(6), ])
head(si$sample_names)
```

---

```
run_cell_deconvolution
```

*Run Cell Deconvolution on Bulk RNA-seq from VISTA Object*

---

**Description**

Estimates cell-type proportions in bulk RNA-seq using single-cell reference or xCell2.

**Usage**

```
run_cell_deconvolution(
  x,
  method = c("xCell2"),
  single_cell_reference = NULL,
  reference_labels = NULL,
  gene_id_type = c("auto", "symbol", "ensembl", "ensembl_symbol"),
  xcell2_reference = NULL,
  xcell2_min_shared_genes = NULL,
  transform = c("log2", "raw"),
  ...
)
```

**Arguments**

<code>x</code>	A VISTA object.
<code>method</code>	Deconvolution method. Currently only "xCell2" is supported.
<code>single_cell_reference</code>	Reserved for future reference-based methods (ignored).
<code>reference_labels</code>	Reserved for future reference-based methods (ignored).
<code>gene_id_type</code>	Type of gene identifiers: "auto", "symbol", "ensembl", or "ensembl_symbol".
<code>xcell2_reference</code>	Optional xCell2 reference object or dataset name (e.g., "DICE_demo.xCell2Ref"). Used when xCell2 exposes xCell2Analysis().
<code>xcell2_min_shared_genes</code>	Optional numeric shortcut for xCell2's minSharedGenes argument (when supported by the installed xCell2 API).
<code>transform</code>	Expression transformation: "log2" or "raw".
<code>...</code>	Additional arguments passed to the specific method.

**Value**

VISTA object with cell\_fractions added to metadata.

## Examples

```
v <- example_vista()
if (requireNamespace('xCell2', quietly = TRUE)) {
  out <- try(run_cell_deconvolution(v, method = 'xCell2'), silent = TRUE)
  if (!inherits(out, 'try-error')) out
}
```

---

run_deseq_analysis	<i>Run Differential Expression Analysis with DESeq2, edgeR, or limma-voom</i>
--------------------	---

---

## Description

These functions encapsulate the standard RNA-seq analysis workflow using DESeq2 ([run\\_deseq\\_analysis](#)), edgeR ([run\\_edger\\_analysis](#)), or limma-voom ([run\\_limma\\_analysis](#)), including: gene filtering, design matrix setup, normalization, model fitting, differential testing, DEG classification ("Up", "Down", "Other"), and result formatting.

Both methods return output in a harmonized structure ready for downstream use in [create\\_vista](#) or standalone DEG summaries.

## Usage

```
run_deseq_analysis(
  counts,
  sample_info,
  column_geneid,
  group_column,
  group_numerator,
  group_denominator,
  covariates = NULL,
  design_formula = NULL,
  min_counts = 10,
  min_replicates = 1,
  log2fc_cutoff = 1,
  pval_cutoff = 0.05,
  p_value_type = "padj"
)
```

```
run_edger_analysis(
  counts,
  sample_info,
  column_geneid,
  group_column,
  group_numerator,
  group_denominator,
  covariates = NULL,
  design_formula = NULL,
  min_counts = 10,
  min_replicates = 1,
  log2fc_cutoff = 1,
  pval_cutoff = 0.05,
```

```

    p_value_type = "FDR"
  )

run_limma_analysis(
  counts,
  sample_info,
  column_geneid,
  group_column,
  group_numerator,
  group_denominator,
  covariates = NULL,
  design_formula = NULL,
  min_counts = 10,
  min_replicates = 1,
  log2fc_cutoff = 1,
  pval_cutoff = 0.05,
  p_value_type = "FDR"
)

```

### Arguments

counts	A data frame or matrix of raw counts with one gene per row. Must include a column defined by <code>column_geneid</code> , and column names must match entries in <code>sample_info\$sample_names</code> .
sample_info	A data frame with sample metadata. Must contain <code>sample_names</code> and the specified grouping column.
column_geneid	A string identifying the column name containing gene identifiers.
group_column	The name of the column in <code>sample_info</code> that defines experimental groups.
group_numerator	A character vector of numerator group(s) for fold-change comparisons.
group_denominator	A character vector of denominator group(s) for fold-change comparisons.
covariates	Optional character vector of additional <code>sample_info</code> columns to adjust for.
design_formula	Optional model formula (or formula string). When provided, it overrides automatic design construction from <code>group_column + covariates</code> . Must include <code>group_column</code> .
min_counts	Minimum total read count across all samples to retain a gene. Default: 10.
min_replicates	Minimum number of replicates within each group that must exceed <code>min_counts</code> . Default: 1.
log2fc_cutoff	Absolute log <sub>2</sub> fold-change threshold to define DEGs. Default: 1.
pval_cutoff	P-value or adjusted p-value cutoff for significance. Default: 0.05.
p_value_type	For DESeq2: one of "padj" or "pvalue". For edgeR/limma: one of "FDR" or "PValue".

### Details

Perform differential expression (DE) analysis across multiple group comparisons using DESeq2, edgeR, or limma-voom. These functions process raw count data, normalize it, execute pairwise group-level tests, and return standardized DEG outputs compatible with VISTA-based visualization and analysis.

- For DESeq2, normalization is performed via [DESeq](#), and DE testing uses [results](#).
- For edgeR, normalization uses [calcNormFactors](#), and testing uses [glmLRT](#).
- For limma, normalization uses [calcNormFactors](#) + [voom](#), and testing uses [eBayes](#).

Low-abundance filtering is applied before model fitting. Gene regulation status is determined via `.categorize_deg_results()` based on user thresholds.

All output comparison results are internally standardized via `.tidy_de_results()` to ensure a uniform column schema compatible with VISTA plotting tools.

## Value

A named list with components:

- `norm_counts`: Matrix of normalized expression values (CPM for edgeR/limma, DESeq2-normalized counts).
- `sample_info`: Updated sample metadata.
- `row_data`: Gene-level metadata, including mean expression.
- `comparisons`: Named list of DEG result tibbles (one per comparison), each containing standardized columns: `gene_id`, `log2fc`, `pvalue`, `p.adj`, and `regulation`.
- `deg_summary`: List of summary tables showing DEG regulation counts.

## See Also

[create\\_vista](#), [DESeq](#), [glmLRT](#), [voom](#)

## Examples

```
v <- example_vista()
si <- as.data.frame(sample_info(v))
data("count_data", package = "VISTA")
counts_small <- count_data[seq_len(200), c("gene_id", si$sample_names), drop = FALSE]
limma_results <- run_limma_analysis(
  counts = counts_small,
  sample_info = si,
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control",
  min_counts = 5,
  min_replicates = 1
)
names(limma_results$comparisons)
```

---

run_vista_report	<i>Generate a publication-ready VISTA workflow report</i>
------------------	---

---

### Description

Builds a VISTA object (or uses a precomputed one), computes a comprehensive single-comparison analysis panel, exports publication assets, and renders an automated Quarto HTML/PDF report from YAML-driven parameters.

### Usage

```
run_vista_report(config, output_file = "vista-report.html")
```

### Arguments

config	Path to a YAML config file (see template at <code>inst/reports/vista-report-template.yml</code> ) or a named list of parameters.
output_file	Optional output filename overriding <code>config\$output_file</code> .

### Details

The report focuses on one differential comparison (`primary_comparison`) and includes:

- QC plots (PCA, MDS, correlation heatmap),
- DE plots (volcano, MA, DEG bar/pie/donut summaries),
- expression-focused views (boxplot, fold-change barplot, expression heatmap),
- enrichment outputs (MSigDB/GO/KEGG when available),
- downloadable artifacts (tables + plots + optional zip bundle),
- interactive HTML tables via **DT** when installed.

### Value

Invisibly, the normalized output report path.

### Examples

```
## Not run:
data('count_data', package = 'VISTA')
data('sample_metadata', package = 'VISTA')
cfg <- list(
  counts = count_data[seq_len(100), ],
  sample_info = sample_metadata[seq_len(6), ],
  column_geneid = 'gene_id',
  group_column = 'cond_long',
  group_numerator = 'treatment1',
  group_denominator = 'control',
  include_msigdb = FALSE, include_go = FALSE, include_kegg = FALSE
)
if (requireNamespace('quarto', quietly = TRUE)) {
  out <- tempfile(fileext = '.html')
  try(run_vista_report(cfg, output_file = out), silent = TRUE)
```

```
}  
## End(Not run)
```

---

sample_metadata	<i>Sample metadata accompanying the VISTA airway example counts</i>
-----------------	---

---

## Description

Metadata describing each column in `count_data`, including friendly sample names and the experimental group assignment used throughout the vignettes and tests.

## Usage

```
data(sample_metadata)
```

## Format

A tibble with 8 rows and 13 columns:

**sample\_names** Character identifiers matching the column names in `count_data`.

**groups** Group labels used in examples ("control", "treatment1").

**cond\_long** Long-form condition labels ("control", "treatment1").

**cond\_short** Short-form condition labels ("CTRL", "TREAT1").

**SampleName** Original sample label from the airway `colData`.

**dex** Original airway treatment labels ("untrt"/"trt").

**cell** Donor/cell-line identifiers from airway.

**albut** Original airway albuterol indicator.

**Run** SRA run identifier (also copied into `sample_names`).

**avgLength** Average transcript length metadata from airway.

**Experiment** SRA experiment accession from airway.

**Sample** SRA sample accession from airway.

**BioSample** NCBI BioSample accession from airway.

## Source

Derived from the airway Bioconductor dataset.

## See Also

[count\\_data](#)

---

save_vista_data	<i>Save VISTA tabular outputs to disk</i>
-----------------	---

---

### Description

Exports selected data components from a VISTA object to CSV/TSV/RDS/XLSX.

### Usage

```
save_vista_data(  
  x,  
  what = c("comparison", "comparisons", "norm_counts", "sample_info", "row_data",  
           "deg_summary", "cutoffs"),  
  file,  
  sample_comparison = NULL,  
  format = NULL,  
  include_rownames = TRUE  
)
```

### Arguments

x	A VISTA object.
what	Character vector specifying which object(s) to export. Supported values are "comparison", "comparisons", "norm_counts", "sample_info", "row_data", "deg_summary", and "cutoffs".
file	Output file path.
sample_comparison	Optional comparison name used when what includes "comparison". Defaults to the first comparison in comparisons(x).
format	Output format. One of "csv", "tsv", "rds", "xlsx". If NULL, inferred from file extension.
include_rownames	Logical; include meaningful row identifiers (e.g., gene IDs or sample names) as explicit columns where applicable.

### Value

Invisibly, the normalized output file path.

### Examples

```
v <- example_vista()  
save_vista_data(v, what = "comparison", file = tempfile(fileext = ".csv"), format = "csv")
```

---

save_vista_plot	<i>Save a VISTA plot object to disk</i>
-----------------	---

---

### Description

Saves plot objects returned by VISTA plotting functions to file. Supports both ggplot-like objects (saved via `ggplot2::ggsave()`) and `ComplexHeatmap` objects (`Heatmap` / `HeatmapList`) saved via graphics devices.

### Usage

```
save_vista_plot(  
  plot,  
  file,  
  width = 8,  
  height = 6,  
  units = "in",  
  dpi = 300,  
  device = NULL,  
  ...  
)
```

### Arguments

plot	A plot object. Typically <code>ggplot</code> , <code>patchwork</code> , <code>Heatmap</code> , or <code>HeatmapList</code> .
file	Output file path.
width	Plot width.
height	Plot height.
units	Units for width and height. One of "in", "cm", "mm", or "px".
dpi	Resolution for raster outputs.
device	Optional graphics device (e.g. "png", "pdf"). If NULL, inferred from file extension (defaults to "png" when missing).
...	Additional arguments passed to <code>ggplot2::ggsave()</code> for ggplot-like objects.

### Value

Invisibly, the normalized output file path.

### Examples

```
v <- example_vista()  
p <- get_pca_plot(v)  
out_file <- tempfile(fileext = ".pdf")  
save_vista_plot(p, file = out_file, width = 7, height = 5, units = "in")
```

---

set_de_source	<i>Set active DE source in a VISTA object</i>
---------------	---

---

### Description

Switches the DE result source used by all downstream VISTA plotting and accessor functions that read the active metadata slots.

### Usage

```
set_de_source(
  object,
  source = c("deseq2", "edger", "limma", "consensus", "active")
)
```

### Arguments

object	A VISTA object.
source	One of "active", "deseq2", "edger", "limma", or "consensus". When "active", the currently active DE source is kept.

### Value

A modified VISTA object with updated active DE source.

### Examples

```
v <- example_vista(method = "both")
v <- set_de_source(v, "edger")
names(comparisons(v, source = "active"))
```

---

set_rowdata	<i>Set or append rowData annotations on a VISTA object</i>
-------------	--

---

### Description

Accepts a data.frame/tibble/DataFrame of gene-level annotations, aligns it to the VISTA row order, and stores it in `rowData(x)`. Rows are matched by a key column (default: tries `gene_id` or `rownames`); Ensembl version suffixes can be stripped for matching.

### Usage

```
set_rowdata(
  x,
  annotations = NULL,
  orgdb = NULL,
  key_col = NULL,
  keytype = NULL,
  columns = c("SYMBOL", "GENENAME", "ENSEMBL", "ENTREZID", "TXCHROM", "TXSTART", "TXEND"),
  drop_version = TRUE,
  overwrite = FALSE
)
```

**Arguments**

x	A VISTA object.
annotations	Optional data.frame/tibble/DataFrame with one row per gene and a column containing the gene IDs to match against rownames(x). If omitted, annotations are pulled from orgdb.
orgdb	Optional OrgDb object; when supplied (and annotations is NULL), annotations are retrieved via AnnotationDbi::select().
key_col	Name of the column in annotations that holds the gene IDs. If NULL, the function will try gene_id, gene, ENSEMBL, SYMBOL, or use rownames(annotations). Ignored when annotations is NULL and orgdb is used.
keytype	Key type for orgdb lookups (e.g., "ENSEMBL", "SYMBOL"). If NULL, inferred from rownames(x) (ENSEMBL if they start with "ENS", otherwise SYMBOL).
columns	Character vector of OrgDb columns to retrieve when using orgdb. Default: c("SYMBOL", "GENENAME", "ENSEMBL", "ENTREZID", "TXCHROM", "TXSTART", "TXEND"). The TXCHROM/TXSTART/TXEND fields carry basic genomic coordinates when available in the OrgDb.
drop_version	Logical; if TRUE, strips Ensembl version suffixes (e.g., .1) from both the VISTA rownames and the key column/keys before matching.
overwrite	Logical; if TRUE, replaces existing rowData. If FALSE, new columns are appended (overwriting by name when names collide).

**Details**

OrgDb packages rarely include full genomic coordinates; the default TXCHROM/TXSTART/TXEND columns may therefore be NA unless your OrgDb provides them. For reliable coordinates, fetch them from an EnsDb/TxDb (via genes() or biomaRt/AnnotationHub), build an annotation table keyed on your gene IDs, and supply that via the annotations argument. When fetching from an OrgDb, only columns available in that database will be filled.

**Value**

The updated VISTA object with rowData populated/appended.

**Examples**

```
vista <- example_vista()
custom_annot <- data.frame(
  gene_id = rownames(vista)[seq_len(10)],
  custom_info = paste0("Info_", seq_len(10))
)
vista2 <- set_rowdata(vista, annotations = custom_annot, key_col = "gene_id")
head(SummarizedExperiment::rowData(vista2)$custom_info)

# Load example VISTA object
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

vista <- create_vista(
  counts = count_data[seq_len(100), ],
  sample_info = sample_metadata[seq_len(6), ],
  column_geneid = "gene_id",
```

```

    group_column = "cond_long",
    group_numerator = "treatment1",
    group_denominator = "control"
  )

  # Add annotations from OrgDb (human)
  if (requireNamespace("org.Hs.eg.db", quietly = TRUE)) {
    vista <- set_rowdata(
      vista,
      orgdb = org.Hs.eg.db::org.Hs.eg.db,
      columns = c("SYMBOL", "GENENAME", "ENTREZID")
    )

    # View updated rowData
    head(SummarizedExperiment::rowData(vista))
  }

  # Or provide custom annotations
  custom_annot <- data.frame(
    gene_id = rownames(vista)[seq_len(10)],
    custom_info = paste0("Info_", seq_len(10))
  )
  vista <- set_rowdata(vista, annotations = custom_annot, key_col = "gene_id")

```

---

```
set_vista_comparison_colors
```

*Set manual comparison colors in a VISTA object*

---

## Description

Updates `metadata(x)$comparison$colors` using a user-supplied named color vector. Comparison colors are used in fold-change and comparison-level plots. The color map must include all currently active comparisons.

## Usage

```
set_vista_comparison_colors(object, color_map)
```

## Arguments

<code>object</code>	A VISTA object.
<code>color_map</code>	Named character vector of colors, with names equal to comparison names (for example "A_VS_B").

## Value

A modified VISTA object with updated comparison colors.

**Examples**

```
v <- example_vista()
comps <- names(comparisons(v))
if (length(comps)) {
  cmap <- stats::setNames(rep('#1b9e77', length(comps)), comps)
  set_vista_comparison_colors(v, cmap)
}
```

---

set\_vista\_group\_colors

*Set manual group colors in a VISTA object*

---

**Description**

Updates `metadata(x)$group$colors` using a user-supplied named color vector. This controls group-level coloring across VISTA plots that use group mapping (for example PCA, MDS, and expression plots). The color map must include all groups currently present in the object.

**Usage**

```
set_vista_group_colors(object, color_map)
```

**Arguments**

<code>object</code>	A VISTA object.
<code>color_map</code>	Named character vector of colors, with names equal to group labels.

**Value**

A modified VISTA object with updated group colors.

**Examples**

```
v <- example_vista()
groups <- unique(as.character(sample_info(v)$cond_long))
gmap <- stats::setNames(c('#1b9e77', '#d95f02')[seq_along(groups)], groups)
set_vista_group_colors(v, gmap)
```

---

validate\_vista

*Validate a VISTA object*

---

**Description**

Performs structural and metadata contract checks on a VISTA object. Use `level = "core"` for invariants that all VISTA objects must satisfy, or `level = "full"` to additionally validate method-specific metadata used by advanced workflows.

**Usage**

```
validate_vista(x, level = c("core", "full"), error = TRUE)
```

**Arguments**

x	A VISTA object.
level	Validation depth. One of "core" or "full".
error	Logical; if TRUE, aborts on validation failures. If FALSE, returns the validation report and emits a warning when issues are found.

**Value**

Invisibly returns a list with fields `valid`, `level`, and `issues`.

**Examples**

```
mat <- matrix(rnorm(60), nrow = 10)
rownames(mat) <- paste0("gene", seq_len(nrow(mat)))
colnames(mat) <- paste0("sample", seq_len(ncol(mat)))
se <- SummarizedExperiment::SummarizedExperiment(
  assays = list(norm_counts = mat),
  colData = S4Vectors::DataFrame(
    cond = rep(c("A", "B"), each = 3),
    row.names = colnames(mat)
  ),
  rowData = S4Vectors::DataFrame(
    gene_id = rownames(mat),
    row.names = rownames(mat)
  )
)
v <- as_vista(se, group_column = "cond")
validate_vista(v)
```

---

validate\_vista\_deep    *Deep validation of VISTA differential-expression fidelity*

---

**Description**

This validator combines `validate_vista()` with backend-to-backend numerical equivalence checks against standalone DESeq2, edgeR, and limma runs.

**Usage**

```
validate_vista_deep(
  counts,
  sample_info,
  column_geneid,
  group_column,
  group_numerator,
  group_denominator,
  methods = c("deseq2", "edger", "limma"),
  min_counts = 10,
  min_replicates = 1,
  log2fc_cutoff = 1,
  pval_cutoff = 0.05,
```

```

    p_value_type = "padj",
    covariates = NULL,
    design_formula = NULL,
    tolerance = 1e-08,
    return_plots = FALSE,
    error = TRUE
  )

```

### Arguments

counts	Raw counts (matrix/data.frame) with a gene-id column and sample columns.
sample_info	Data frame with sample metadata.
column_geneid	Column name in counts that contains gene identifiers.
group_column	Column in sample_info used to group samples.
group_numerator	Character vector of numerator groups for pairwise comparisons.
group_denominator	Character vector of denominator groups.
methods	Character vector of backends to benchmark. Any subset of c("deseq2", "edger", "limma").
min_counts	Minimum total counts per gene to retain.
min_replicates	Minimum samples per group meeting filtering criteria.
log2fc_cutoff	Absolute log <sub>2</sub> fold-change threshold for DEG calling.
pval_cutoff	P-value (or adjusted p-value) threshold.
p_value_type	Either "padj" or "pvalue".
covariates	Optional character vector of additional sample_info columns.
design_formula	Optional model formula (or formula string) including group_column.
tolerance	Numeric tolerance used for floating-point comparisons.
return_plots	Logical; if TRUE, return paired VISTA/reference plots for MA, volcano, DEG count, and PCA views.
error	Logical; if TRUE, abort when any discrepancy is detected.

### Value

Invisibly returns the full benchmark report.

### Examples

```

v <- example_vista()
si <- as.data.frame(sample_info(v))
data("count_data", package = "VISTA")
count_subset <- count_data[seq_len(500), c("gene_id", si$sample_names), drop = FALSE]

report <- validate_vista_deep(
  counts = count_subset,
  sample_info = si,
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",

```

```

    group_denominator = "control",
    methods = "limma",
    min_counts = 5,
    min_replicates = 1,
    error = FALSE
  )

report$valid

data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

target_groups <- c("control", "treatment1")
sample_subset <- sample_metadata[sample_metadata$cond_long %in% target_groups, ]
count_subset <- count_data[seq_len(150), c("gene_id", sample_subset$sample_names)]

validate_vista_deep(
  counts = count_subset,
  sample_info = sample_subset,
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control",
  methods = c("deseq2", "edger"),
  min_counts = 5,
  min_replicates = 1
)

```

---

VISTA-accessors

*Accessor Methods for VISTA Object*


---

## Description

These accessor functions expose the analysis components stored in a VISTA object. Core expression matrices and annotations live in the underlying SummarizedExperiment, while differential expression results, summaries, and configuration details are kept inside `metadata(x)`.

## Usage

```

## S4 method for signature 'VISTA'
comparisons(object, source = "active")

## S4 method for signature 'VISTA'
deg_summary(object, source = "active")

## S4 method for signature 'VISTA'
cutoffs(object)

## S4 method for signature 'VISTA'
norm_counts(object, summarise = FALSE)

```

```
## S4 method for signature 'VISTA'
sample_info(object)

## S4 method for signature 'VISTA'
row_data(object)

## S4 method for signature 'VISTA'
group_colors(object)

## S4 method for signature 'VISTA'
group_palette(object)
```

### Arguments

<code>object</code>	An object of class VISTA.
<code>source</code>	Which DE result source to use for <code>comparisons()</code> / <code>deg_summary()</code> . One of "active", "deseq2", "edger", "limma", or "consensus". "active" uses the currently selected source stored in metadata.
<code>summarise</code>	Logical. If TRUE, returns mean-normalized counts grouped by the grouping column stored in the VISTA object (e.g., condition or treatment). Default is FALSE.

### Value

The content of the respective slot or processed data:

**comparisons** A named list of differential expression tables stored in `metadata(x)$de_results`.

**deg\_summary** A named list of DEG summary tables stored in `metadata(x)$de_summary`.

**cutoffs** A list of analysis thresholds held in `metadata(x)$de_cutoffs` (empty list if absent).

**norm\_counts** A matrix of normalized counts, optionally averaged by group.

**sample\_info** A DataFrame of sample metadata.

**row\_data** A DataFrame of gene-level annotation (e.g., baseMean, gene ID).

**group\_colors** A named character vector of colours from `metadata(x)$group$colors`.

**group\_palette** The qualitative palette name stored in `metadata(x)$group$palette`.

### See Also

[create\\_vista\(\)](#), [as\\_vista\(\)](#), [run\\_deseq\\_analysis\(\)](#)

### Examples

```
# Create example VISTA object
data("count_data", package = "VISTA")
data("sample_metadata", package = "VISTA")

vista <- create_vista(
  counts = count_data[seq_len(100), ],
  sample_info = sample_metadata[seq_len(6), ],
  column_geneid = "gene_id",
  group_column = "cond_long",
  group_numerator = "treatment1",
  group_denominator = "control"
```

```
)  
  
# Access differential expression comparisons  
comps <- comparisons(vista)  
names(comps)  
comparisons(vista, source = "active")  
  
# View DEG summary statistics  
deg_summary(vista)  
  
# Get analysis cutoffs  
cutoffs(vista)  
  
# Access normalized counts  
nc <- norm_counts(vista)  
head(nc)  
  
# Get group-summarized counts  
nc_summary <- norm_counts(vista, summarise = TRUE)  
head(nc_summary)  
  
# Access sample metadata  
sample_info(vista)  
  
# Access gene-level annotations  
head(row_data(vista))  
  
# Get group colors  
group_colors(vista)  
  
# Get palette name  
group_palette(vista)  
  
# For method = "both", inspect method-specific outputs  
  
vista_both <- create_vista(  
  counts = count_data,  
  sample_info = sample_metadata,  
  column_geneid = "gene_id",  
  group_column = "cond_long",  
  group_numerator = "treatment1",  
  group_denominator = "control",  
  method = "both",  
  result_source = "consensus"  
)  
comparisons(vista_both, source = "deseq2")  
comparisons(vista_both, source = "edger")  
vista_both <- set_de_source(vista_both, "edger")
```

## Description

The VISTA class extends SummarizedExperiment. All analysis metadata (DE results, summaries, cutoffs, grouping info, etc.) is stored in the `metadata()` slot of the object.

## Details

Core elements stored in `metadata(v)`:

- `$de_results`: named SimpleList of DE result tables.
- `$de_summary`: named SimpleList of DEG summary tables.
- `$de_cutoffs`: named list of thresholds (log2FC, p-value type/cutoff, method settings).
- `$group`: list with column, palette, colors describing the grouping/fill scheme.
- `$provenance`: list with constructor version, timestamp, session info.
- `$vista_schema_version`: metadata schema tag used for compatibility checks.

Feature-level annotations live in `rowData(v)`, sample metadata in `colData(v)`, and normalized counts (and any additional assays) in `assay(v, "norm_counts")` by default. Use `create_vista()` as the primary end-user constructor. Advanced users can convert an existing SummarizedExperiment with `as_vista()`.

## Value

A VISTA S4 object.

## See Also

[create\\_vista](#), [as\\_vista](#), [validate\\_vista](#)

## Examples

```
methods::showClass('VISTA')
```

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