

Package: CDEnrich (via r-universe)

October 13, 2026

Title Enrichment Analysis for Cell Death Pathways

Version 0.99.1

Description Provides a curated collection of gene sets for major cell death modalities, together with tools for over-representation analysis, gene set enrichment analysis, single-sample gene set enrichment analysis, differential pathway analysis, and visualization.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

VignetteBuilder knitr

Imports clusterProfiler, enrichplot, ggplot2, stats, utils, ggrepel, stringr, tidyr, GSVA, pheatmap, rlang

Suggests BiocStyle, knitr, rmarkdown, testthat (>= 3.0.0), withr

Config/testthat/edition 3

LazyData true

Depends R (>= 4.5.0)

URL <https://github.com/Yushan-Chen-829/CDEnrich>

BugReports <https://github.com/Yushan-Chen-829/CDEnrich/issues>

biocViews GeneSetEnrichment, Pathways, GeneExpression, DifferentialExpression, CellBiology

Config/roxygen2/version 8.1.0

Config/pak/sysreqs

libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libglpk-dev make libmagick++-dev gsfonts libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev zlib1g-dev

Repository <https://biocstaging.r-universe.dev>

Date/Publication 2026-09-13 06:13:33 UTC

RemoteUrl <https://github.com/BiocStaging/CDEnrich>

RemoteRef HEAD

RemoteSha 7976584a298068e9eedbbe75fe9fa7373aea5712

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cd_Genesets

Curated Cell Death Pathway Gene Sets

Description

Curated cell death pathway gene sets collected from published literature, GeneCards and pathway databases. This is the underlying table loaded by [load_cell_death_genes](#).

Usage

```
data(cd_Genesets)
```

Format

A data frame with two columns:

term Pathway (gene set) name, e.g. Ferroptosis_FerrDb V2(36305834).

gene Gene symbol belonging to the pathway.

Source

Curated from public cell death literature and databases; see `data-raw/` for the construction scripts.

CDEnrich-data

Curated Data Included in CDEnrich

Description

Data objects used by CDEnrich to provide curated cell death pathway gene sets and representative pathway recommendations.

Details

- [cd_Genesets](#): curated cell death gene sets.
- [representative_genes](#): representative gene sets for the 13 cell death types with curated recommendations.
- [representative_pathways](#): metadata for the representative pathway recommendations.

Value

This help page is an overview of the curated datasets shipped with CDEnrich; see the linked pages for each dataset.

CDEnrich_demo_data	<i>CDEnrich Demonstration Data</i>
--------------------	------------------------------------

Description

Small simulated datasets used in CDEnrich examples and vignettes.

Details

The ORA and ssGSEA datasets are built from the recommended Ferroptosis gene set (FerrDb V2, PMID: 36305834), and the GSEA datasets from the representative Apoptosis gene set (PMID: 37968457). Background genes are synthetic placeholders (BackgroundGene_1 ... BackgroundGene_3000). All datasets are generated by data-raw/demo_data.R with a fixed random seed and are fully reproducible.

Value

This help page is an overview of the demonstration datasets shipped with CDEnrich; see the individual dataset pages for details.

celldeath_compare_enrich	<i>ORA Enrichment Analysis for Cell Death Pathways (Multi-Group Comparison)</i>
--------------------------	---

Description

Perform multi-group over-representation analysis (ORA) to compare cell death pathway enrichment across multiple gene lists. Support two modes:

1. Global mode: all groups vs all cell death pathways
2. Targeted mode: all groups vs one specific pathway

Usage

```
celldeath_compare_enrich(
  deg_list_list,
  term_select = NULL,
  use_recommended = TRUE,
  universe = NULL,
  pvalueCutoff = 1,
  qvalueCutoff = 1,
  minGSSize = 3,
  savefile = FALSE,
  filename = "celldeath_compareORA_result.csv"
)
```

Arguments

<code>deg_list_list</code>	A named list of gene vectors, where each element corresponds to a group of differentially expressed genes (gene symbols).
<code>term_select</code>	Character. Either an exact gene set name (e.g. "Disulfidptosis_Up_36747082") used directly, or a cell death type name (e.g. "Disulfidptosis"): for the 13 types with curated recommendations, the recommended representative gene set is used automatically (see get_representative_pathway); for other types with a single gene set, that gene set is used with a notice. Default NULL uses all cell death pathways (global mode).
<code>use_recommended</code>	Logical. Only takes effect when <code>term_select</code> is a cell death type with a curated recommendation: TRUE (default) uses only the recommended representative gene set; FALSE runs against ALL gene sets under that death type.
<code>universe</code>	Character vector of background genes. Default NULL uses all genes in the curated cell death collection. For formal analysis, pass all genes detected in your experiment (e.g. all expressed genes).
<code>pvalueCutoff</code>	P-value cutoff for significance (default: 0.05).
<code>qvalueCutoff</code>	Q-value cutoff for false positive control (default: 0.2).
<code>minGSSize</code>	Minimum gene set size to retain (default: 3).
<code>savefile</code>	Whether to save the results as a CSV file (default: FALSE)
<code>filename</code>	File name (default: "cell_death_ORA_result.csv")

Value

A `compareClusterResult` object for visualization. Returns NULL if no significant pathways are identified.

Examples

```
group1 <- c("GPX4", "ACSL4", "SLC7A11", "GSDMD")
group2 <- c("BAX", "CASP3", "RIPK1", "FDX1")
deg_list <- list(Control = group1, Treatment = group2)

# 1. Global mode: all groups vs all cell death pathways
compare_res_all <- celldeath_compare_enrich(deg_list)

# 2. Targeted mode by death type: use the recommended gene set (default)
compare_res_rec <- celldeath_compare_enrich(deg_list, term_select = "Ferroptosis")

# 3. Targeted mode by death type: run against ALL Ferroptosis gene sets
compare_res_type <- celldeath_compare_enrich(deg_list, term_select = "Ferroptosis",
                                             use_recommended = FALSE)

# 4. Targeted mode by exact gene set name
compare_res_exact <- celldeath_compare_enrich(deg_list,
                                             term_select = "Disulfidptosis_Up_36747082")
```

celldeath_enrich

ORA Enrichment Analysis for Cell Death Pathways (Single Group)

Description

Perform Over-Representation Analysis (ORA) for a list of DEGs based on curated cell death gene sets. Support two modes:

1. Global mode: one group vs all cell death pathways
2. Targeted mode: one group vs one specific pathway

Usage

```
celldeath_enrich(
  deg,
  term_select = NULL,
  use_recommended = TRUE,
  universe = NULL,
  pvalueCutoff = 0.05,
  qvalueCutoff = 0.2,
  minGSSize = 3,
  savefile = FALSE,
  filename = "celldeath_ORA_result.csv"
)
```

Arguments

deg	A character vector of input genes (gene symbols) for enrichment analysis.
term_select	Character. Either an exact gene set name (e.g. "Disulfidptosis_Up_36747082") used directly, or a cell death type name (e.g. "Disulfidptosis"): for the 13 types with curated recommendations, the recommended representative gene set is used automatically (see get_representative_pathway); for other types with a single gene set, that gene set is used with a notice. Default NULL uses all cell death pathways (global mode).
use_recommended	Logical. Only takes effect when term_select is a cell death type with a curated recommendation: TRUE (default) uses only the recommended representative gene set; FALSE runs against ALL gene sets under that death type.
universe	Character vector of background genes. Default NULL uses all genes in the curated cell death collection. For formal analysis, pass all genes detected in your experiment (e.g. all expressed genes).
pvalueCutoff	P-value cutoff for significance (default: 0.05).
qvalueCutoff	Q-value cutoff for filtering false positives (default: 0.2).
minGSSize	Minimum gene set size to retain (default: 3).
savefile	Whether to save the results as a CSV file (default: FALSE)
filename	File name (default: "celldeath_ORA_result.csv")

Value

An `enrichResult` object for visualization and result export.

See Also

[get_representative_pathway](#) for recommendation details.

Examples

```
deg <- c("GPX4", "ACSL4", "SLC7A11", "GSDMD", "CASP3", "BAX")

# 1. Global ORA: vs all cell death pathways
enrich_res <- celldeath_enrich(deg)

# 2. Targeted ORA by death type: use the recommended gene set (default)
enrich_res_rec <- celldeath_enrich(deg, term_select = "Ferroptosis")

# 3. Targeted ORA by death type: run against ALL Ferroptosis gene sets
enrich_res_all <- celldeath_enrich(deg, term_select = "Ferroptosis",
                                   use_recommended = FALSE)

# 4. Targeted ORA by exact gene set name
enrich_res_exact <- celldeath_enrich(deg, term_select = "Disulfidptosis_Up_36747082")
```

celldeath_gsea

Cell Death Pathway GSEA Analysis

Description

This function performs GSEA using user-defined cell death gene sets. Support two modes:

1. Global mode: ranked gene list vs all cell death pathways
2. Targeted mode: ranked gene list vs one specific pathway

Usage

```
celldeath_gsea(
  genelist,
  term_select = NULL,
  use_recommended = TRUE,
  pvalueCutoff = 1,
  verbose = FALSE,
  savefile = FALSE,
  filename = "celldeath_gsea_result.csv"
)
```

Arguments

geneList	A named numeric vector, sorted descendingly.
term_select	Character. Either an exact gene set name (e.g. "Disulfidptosis_Up_36747082") used directly, or a cell death type name (e.g. "Disulfidptosis"): for the 13 types with curated recommendations, the recommended representative gene set is used automatically (see get_representative_pathway); for other types with a single gene set, that gene set is used with a notice. Default NULL uses all cell death pathways (global mode).
use_recommended	Logical. Only takes effect when term_select is a cell death type with a curated recommendation: TRUE (default) uses only the recommended representative gene set; FALSE runs against ALL gene sets under that death type.
pvalueCutoff	P-value cutoff.
verbose	Print messages.
savefile	Whether to save the results as a CSV file (default: FALSE)
filename	File name (default: "celldeath_gsea_result.csv")

Value

A gseaResult object.

See Also

[get_representative_pathway](#) for recommendation details.

Examples

```
# Prepare ranked gene vector (descending)
gene_rank <- c(GPX4=2.5, ACSL4=2.2, SLC7A11=1.8, BAX=-1.2, CASP3=-1.9)

# 1. Global GSEA: vs all cell death pathways
gsea_all <- celldeath_gsea(gene_rank)

# 2. Targeted GSEA by death type: use the recommended gene set (default)
gsea_rec <- celldeath_gsea(gene_rank, term_select = "Ferroptosis")

# 3. Targeted GSEA by death type: run against ALL Ferroptosis gene sets
gsea_all_type <- celldeath_gsea(gene_rank, term_select = "Ferroptosis",
                               use_recommended = FALSE)

# 4. Targeted GSEA by exact gene set name
gsea_exact <- celldeath_gsea(gene_rank, term_select = "Disulfidptosis_Up_36747082")
```

`celldeath_gsea_multiple`*Multiple Group Cell Death Pathway GSEA Analysis*

Description

This function performs GSEA for multiple gene lists. Support two modes:

1. Global mode: all groups vs all cell death pathways
2. Targeted mode: all groups vs one specific pathway

Usage

```
celldeath_gsea_multiple(  
  geneList_list,  
  term_select = NULL,  
  use_recommended = TRUE,  
  pvalueCutoff = 1,  
  verbose = FALSE,  
  savefile = FALSE  
)
```

Arguments

<code>geneList_list</code>	A named list of numeric vectors, each vector is sorted descendingly.
<code>term_select</code>	Character. Either an exact gene set name (e.g. "Disulfidptosis_Up_36747082") used directly, or a cell death type name (e.g. "Disulfidptosis"): for the 13 types with curated recommendations, the recommended representative gene set is used automatically (see get_representative_pathway); for other types with a single gene set, that gene set is used with a notice. Default NULL uses all cell death pathways (global mode).
<code>use_recommended</code>	Logical. Only takes effect when <code>term_select</code> is a cell death type with a curated recommendation: TRUE (default) uses only the recommended representative gene set; FALSE runs against ALL gene sets under that death type.
<code>pvalueCutoff</code>	P-value cutoff.
<code>verbose</code>	Print messages.
<code>savefile</code>	Whether to save all results as CSV files (default: FALSE)

Value

A named list of `gseaResult` objects.

See Also

[get_representative_pathway](#) for recommendation details.

Examples

```
# Multi-group ranked list
group1 <- c(GPX4=2.5, ACSL4=2.2, NUBPL=1.8, BAX=-1.2)
group2 <- c(GSDMD=2.8, SLC3A2=2.0, GPX4=-1.5)
gene_list <- list(Control = group1, Treatment = group2)

# 1. Global mode: all pathways
res_all <- celldeath_gsea_multiple(gene_list)

# 2. Targeted mode by death type: use the recommended gene set (default)
res_rec <- celldeath_gsea_multiple(gene_list, term_select = "Ferroptosis")

# 3. Targeted mode by death type: run against ALL Ferroptosis gene sets
res_all_type <- celldeath_gsea_multiple(gene_list, term_select = "Ferroptosis",
                                         use_recommended = FALSE)

# 4. Targeted mode by exact gene set name
res_exact <- celldeath_gsea_multiple(gene_list,
                                      term_select = "Disulfidptosis_Up_36747082")
```

celldeath_ssgsea

ssGSEA Analysis for Cell Death Pathways

Description

Perform single-sample Gene Set Enrichment Analysis (ssGSEA) on an expression matrix based on curated cell death gene sets. Unlike ORA/GSEA, ssGSEA computes an enrichment score for each sample on each pathway, enabling sample-level comparison of cell death activity. Support two modes:

1. Global mode: expression matrix vs all cell death pathways
2. Targeted mode: expression matrix vs one specific pathway

Usage

```
celldeath_ssgsea(
  expr,
  group = NULL,
  term_select = NULL,
  use_recommended = TRUE,
  min_size = 3,
  normalize = TRUE,
  savefile = FALSE,
  filename = "celldeath_ssgsea_score.csv"
)
```

Arguments

<code>expr</code>	A numeric matrix or data.frame of expression values, with genes (gene symbols) as rows and samples as columns.
<code>group</code>	An optional character or factor vector of group labels, with length equal to the number of samples (columns of <code>expr</code>). If provided, group information is attached to the result for downstream differential analysis and visualization. Default NULL.
<code>term_select</code>	Character. Either an exact gene set name (e.g. "Disulfidptosis_Up_36747082") used directly, or a cell death type name (e.g. "Disulfidptosis"): for the 13 types with curated recommendations, the recommended representative gene set is used automatically (see get_representative_pathway); for other types with a single gene set, that gene set is used with a notice. Default NULL uses all cell death pathways (global mode).
<code>use_recommended</code>	Logical. Only takes effect when <code>term_select</code> is a cell death type with a curated recommendation: TRUE (default) uses only the recommended representative gene set; FALSE scores ALL gene sets under that death type.
<code>min_size</code>	Minimum gene set size to retain (default: 3).
<code>normalize</code>	Logical. Whether to normalize ssGSEA scores by the difference between the maximum and minimum scores (default: TRUE).
<code>savefile</code>	Whether to save the results as a CSV file (default: FALSE)
<code>filename</code>	File name (default: "celldeath_ssgsea_score.csv")

Details

Multi-group comparison is supported via the `group` parameter. All samples are scored together on the same expression background to guarantee score comparability across groups.

Value

A named list of class `celldeath_ssgsea` with two elements:

- `score`: a numeric matrix of ssGSEA scores (pathways x samples);
- `group`: a factor of sample group labels (NULL if not provided).

See Also

[get_representative_pathway](#) for recommendation details.

Examples

```
# expr: gene x sample expression matrix (rows = genes, columns = samples)
gene_sets <- load_cell_death_genes()
all_genes <- unique(unlist(gene_sets))
set.seed(123)
expr <- matrix(rnorm(length(all_genes) * 10),
               nrow = length(all_genes), ncol = 10,
```

```

      dimnames = list(all_genes, paste0("Sample", 1:10)))
group <- rep(c("Control", "Treatment"), each = 5)

# 1. Global mode: all cell death pathways, no grouping
ssgsea_res <- celldeath_ssgsea(expr)

# 2. Multi-group mode: with group labels for downstream comparison
ssgsea_res_group <- celldeath_ssgsea(expr, group = group)

# 3. Targeted mode by death type: use the recommended gene set (default)
ssgsea_ferro <- celldeath_ssgsea(expr, group = group, term_select = "Ferroptosis")

# 4. Targeted mode by death type: score ALL Ferroptosis gene sets
ssgsea_ferro_all <- celldeath_ssgsea(expr, group = group, term_select = "Ferroptosis",
                                     use_recommended = FALSE)

# 5. Targeted mode by exact gene set name
ssgsea_exact <- celldeath_ssgsea(expr, group = group,
                                 term_select = "Disulfidptosis_Up_36747082")

```

celldeath_ssgsea_diff *Differential Analysis of ssGSEA Scores Between Groups*

Description

Perform group-wise differential analysis on cell death pathway ssGSEA scores. Wilcoxon rank-sum test is used for two groups, and Kruskal-Wallis test for three or more groups.

Usage

```

celldeath_ssgsea_diff(
  ssgsea_result,
  pAdjustMethod = "BH",
  savefile = FALSE,
  filename = "celldeath_ssgsea_diff.csv"
)

```

Arguments

ssgsea_result	A celldeath_ssgsea object returned by celldeath_ssgsea (must have non-NULL group).
pAdjustMethod	Multiple testing correction method passed to p.adjust (default: "BH").
savefile	Whether to save the results as a CSV file (default: FALSE)
filename	File name (default: "celldeath_ssgsea_diff.csv")

Value

A data.frame with per-pathway statistics, sorted by p-value: pathway name, mean score per group, test statistic, p-value and adjusted p-value.

Examples

```
# expr: gene x sample expression matrix (rows = genes, columns = samples)
gene_sets <- load_cell_death_genes()
all_genes <- unique(unlist(gene_sets))
set.seed(123)
expr <- matrix(rnorm(length(all_genes) * 10),
              nrow = length(all_genes), ncol = 10,
              dimnames = list(all_genes, paste0("Sample", 1:10)))
group <- rep(c("Control", "Treatment"), each = 5)

ssgsea_res <- celldeath_ssgsea(expr, group = group)
diff_res <- celldeath_ssgsea_diff(ssgsea_res)
head(diff_res)
```

demo_all_genes

*Demonstration Background Gene Universe***Description**

A character vector combining the recommended Ferroptosis gene set with 3000 synthetic background genes. Used as the ORA background universe.

Usage

```
data(demo_all_genes)
```

Format

A character vector of gene symbols.

demo_deg

*Demonstration DEG List for Single-Group ORA***Description**

Up to 100 real genes taken from the recommended Ferroptosis gene set, providing a strong and reproducible enrichment signal.

Usage

```
data(demo_deg)
```

Format

A character vector of gene symbols.

demo_deg_list	<i>Demonstration DEG Lists for Multi-Group ORA</i>
---------------	--

Description

A named list with two groups: Control (15 Ferroptosis genes) and Treatment (up to 100 Ferroptosis genes).

Usage

```
data(demo_deg_list)
```

Format

A named list of two character vectors.

demo_expr	<i>Demonstration Expression Matrix for ssGSEA</i>
-----------	---

Description

A numeric expression matrix with genes as rows and 12 samples as columns. Ferroptosis genes are shifted upwards in Treatment samples, creating higher Ferroptosis activity in that group.

Usage

```
data(demo_expr)
```

Format

A numeric matrix (genes x samples).

demo_group	<i>Demonstration Sample Groups for ssGSEA</i>
------------	---

Description

A factor assigning the 12 samples of demo_expr to Control and Treatment groups (6 samples each).

Usage

```
data(demo_group)
```

Format

A factor with two levels (Control, Treatment).

demo_rank_apop	<i>Demonstration Ranked Gene List for Single-Group GSEA</i>
----------------	---

Description

A decreasingly sorted named numeric vector. All genes from the representative Apoptosis gene set are assigned large positive ranking statistics, creating a clear enrichment signal.

Usage

```
data(demo_rank_apop)
```

Format

A decreasingly sorted named numeric vector.

demo_rank_apop_list	<i>Demonstration Ranked Gene Lists for Multi-Group GSEA</i>
---------------------	---

Description

A named list of two decreasingly sorted numeric vectors: Control has no intentionally introduced signal, Treatment carries the same strong Apoptosis signal as demo_rank_apop.

Usage

```
data(demo_rank_apop_list)
```

Format

A named list of two decreasingly sorted numeric vectors.

demo_targeted_deg	<i>Demonstration DEG List for Targeted ORA</i>
-------------------	--

Description

Identical to demo_deg; kept as a separate object so the targeted ORA example reads as an independent workflow.

Usage

```
data(demo_targeted_deg)
```

Format

A character vector of gene symbols.

```
get_representative_pathway
```

Get the Recommended Representative Gene Set for a Cell Death Type

Description

Look up the curated recommendation for a cell death type that has multiple PMID-based gene sets. 13 of the cell death types in this package have a recommended representative gene set.

Usage

```
get_representative_pathway(death_type)
```

Arguments

`death_type` `Character(1)`. A cell death type name, e.g. "Disulfidptosis". Matching is exact (case-sensitive).

Details

The lookup table can be overridden via `options(CDEnrich.representative_pathways = <data.frame>)` (mainly for testing); the override replaces the built-in table completely for the duration it is set.

Value

A one-row `data.frame` with the recommendation metadata (pathway name, PMID, source, etc.), or `NULL` if the death type has no recommendation.

Examples

```
get_representative_pathway("Disulfidptosis")
get_representative_pathway("Mitosis")    # returns NULL
```

```
load_cell_death_genes    Load Curated Cell Death Gene Sets
```

Description

Load and prepare cell death pathway gene sets for ORA and GSEA analysis. This function returns a gene list compatible with `clusterProfiler` functions. The 13 recommended representative gene sets are automatically merged in (see `representative_pathways` for their curation metadata).

Usage

```
load_cell_death_genes(.test_df = NULL, .test_rep = NULL)
```

Arguments

<code>.test_df</code>	Internal parameter for unit testing. A data.frame with term and gene columns; when provided, the built-in dataset and the representative gene sets are NOT used.
<code>.test_rep</code>	Internal parameter for unit testing. A named list of gene vectors used in place of the built-in representative gene sets; when provided together with <code>.test_df</code> , the merge step is still exercised

Value

A named list of gene vectors, each element representing a cell death pathway.

Examples

```
gene_sets <- load_cell_death_genes()
length(gene_sets)
names(gene_sets)
```

plot_death_compare_bubble

Visualization of Multi-Group Cell Death Enrichment Comparison

Description

Generate a dotplot for multi-group cell death pathway enrichment comparison. Support two analysis modes from `celldeath_compare_enrich()`:

1. Global mode: all groups compare against all cell death pathways
2. Targeted mode: all groups compare against one single specified pathway

Usage

```
plot_death_compare_bubble(
  compare_res,
  show_category = 10,
  palette = c("#2E8B57", "#F39C12", "#E74C3C"),
  title = "Cell Death Pathway Enrichment (Multi-Group)",
  filename = NULL,
  return_data = FALSE
)
```

Arguments

<code>compare_res</code>	A <code>compareClusterResult</code> object returned by <code>celldeath_compare_enrich()</code> .
<code>show_category</code>	Number of top pathways to display per group (sorted by p-value).
<code>palette</code>	Color palette for p.adjust (low to high). Default: <code>c("#2E8B57", "#F39C12", "#E74C3C")</code> .

title	Plot title. Default: "Cell Death Pathway Enrichment (Multi-Group)".
filename	If provided, save plot to file (e.g., "compare_bubble.png"). Default: NULL.
return_data	If TRUE, return the data frame used for plotting. Default: FALSE.

Value

A ggplot2 object (or data frame if return_data = TRUE).

Examples

```
data("demo_deg_list", package = "CDEnrich")
data("demo_all_genes", package = "CDEnrich")
data("representative_genes", package = "CDEnrich")

compare_result <- celldeath_compare_enrich(
  deg_list_list = demo_deg_list,
  universe = demo_all_genes
)

plot_death_compare_bubble(
  compare_result,
  show_category = 10
)
```

plot_death_compare_heatmap

*Visualization of Multi-Group Cell Death Enrichment Comparison
(Heatmap)*

Description

Generate a heatmap for multi-group cell death pathway enrichment comparison, showing $-\log_{10}(p.adjust)$ for each pathway-group pair. Compatible with two analysis modes from celldeath_compare_enrich():

1. Global mode: all groups compare against all cell death pathways
2. Targeted mode: all groups compare against one single specified pathway

Usage

```
plot_death_compare_heatmap(
  compare_res,
  show_category = 10,
  palette = c("#2E8B57", "#F39C12", "#E74C3C"),
  title = "Cell Death Pathway Enrichment (Multi-Group Heatmap)",
  filename = NULL,
  return_data = FALSE
)
```

Arguments

compare_res	A compareClusterResult object returned by celldeath_compare_enrich().
show_category	Number of top pathways to display (selected by lowest p.adjust across groups).
palette	Color palette for fill (low to high). Default: c("#2E8B57", "#F39C12", "#E74C3C").
title	Plot title. Default: "Cell Death Pathway Enrichment (Multi-Group Heatmap)".
filename	If provided, save plot to file (e.g., "compare_heatmap.png"). Default: NULL.
return_data	If TRUE, return the data frame used for plotting. Default: FALSE.

Value

A ggplot2 object (or data frame if return_data = TRUE).

Examples

```
data("demo_deg_list", package = "CDEnrich")
data("demo_all_genes", package = "CDEnrich")
data("representative_genes", package = "CDEnrich")

compare_result <- celldeath_compare_enrich(
  deg_list_list = demo_deg_list,
  universe = demo_all_genes
)

plot_death_compare_heatmap(
  compare_result,
  show_category = 10
)
```

plot_death_enrich_bubble

Visualization of Cell Death Enrichment Results (Bubble Plot)

Description

Generate a dotplot for single-group cell death pathway enrichment analysis. Automatically adapt for two modes:

1. Global mode: multiple pathways bubble plot
2. Targeted mode: single-pathway ORA plot layout adjustment

Usage

```
plot_death_enrich_bubble(  
  enrich_res,  
  show_category = 10,  
  palette = c("#2E8B57", "#F39C12", "#E74C3C"),  
  size_range = c(2, 8),  
  title = "Cell Death Pathway Enrichment",  
  filename = NULL,  
  return_data = FALSE  
)
```

Arguments

enrich_res	An enrichResult object returned by celldeath_enrich().
show_category	Number of top pathways to display (sorted by p-value).
palette	Color palette for p.adjust (low to high). Default: c("#2E8B57", "#F39C12", "#E74C3C").
size_range	Range of point size (min, max). Default: c(2, 8).
title	Plot title. Default: "Cell Death Pathway Enrichment".
filename	If provided, save plot to file (e.g., "bubble.png"). Default: NULL.
return_data	If TRUE, return the data frame used for plotting. Default: FALSE.

Value

A ggplot2 object (or data frame if return_data = TRUE).

Examples

```
data("demo_deg", package = "CDEnrich")  
data("demo_all_genes", package = "CDEnrich")  
data("representative_genes", package = "CDEnrich")  
  
ora_result <- celldeath_enrich(  
  deg = demo_deg,  
  universe = demo_all_genes  
)  
  
plot_death_enrich_bubble(  
  ora_result,  
  show_category = 10  
)
```

plot_death_enrich_network

Visualization of Cell Death Enrichment Results (Enrichment Network)

Description

Generate an enrichment network plot for single-group cell death pathway enrichment analysis. Automatically adapt two analysis modes from `celldeath_enrich()`:

1. Global mode: multiple pathways, full gene overlap network with edges
2. Targeted mode: single specified pathway, simple single-node plot. Nodes represent pathways, edges represent gene overlaps (similarity)(only for multi-pathway).

Usage

```
plot_death_enrich_network(
  enrich_res,
  show_category = 30,
  color = "p.adjust",
  filename = NULL,
  ...
)
```

Arguments

<code>enrich_res</code>	An <code>enrichResult</code> object returned by <code>celldeath_enrich()</code> .
<code>show_category</code>	Number of top pathways to display (sorted by p-value). Default: 30.
<code>color</code>	Which variable to use for node color. Options: "p.adjust" (default), "pvalue", "qvalue", "Count", etc.
<code>filename</code>	If provided, save plot to file (e.g., "enrich_network.png"). Default: NULL.
<code>...</code>	Additional arguments passed to <code>enrichplot::emapplot</code> (e.g., <code>node_label</code> , <code>cex_label_group</code>).

Value

A `ggplot2` object.

Examples

```
data("demo_deg", package = "CDEnrich")
data("demo_all_genes", package = "CDEnrich")
data("representative_genes", package = "CDEnrich")

ora_result <- celldeath_enrich(
  deg = demo_deg,
  universe = demo_all_genes
)
```

```
plot_death_enrich_network(
  ora_result,
  show_category = 10
)
```

```
plot_death_enrich_targeted
```

Targeted Single-Pathway ORA Summary Plot

Description

Generate a compact summary plot for a targeted ORA result containing exactly one pathway. The bar shows the number of overlapping genes and the annotation reports GeneRatio, BgRatio, and adjusted P-value.

Usage

```
plot_death_enrich_targeted(
  enrich_res,
  color = "#F39C12",
  title = "Targeted Cell Death Pathway Enrichment",
  filename = NULL,
  return_data = FALSE
)
```

Arguments

<code>enrich_res</code>	An <code>enrichResult</code> object or data frame returned by <code>celldeath_enrich()</code> .
<code>color</code>	Bar color. Default: "#F39C12".
<code>title</code>	Plot title. Default: "Targeted Cell Death Pathway Enrichment".
<code>filename</code>	If provided, save plot to file. Default: NULL.
<code>return_data</code>	If TRUE, return the data frame used for plotting. Default: FALSE.

Value

A `ggplot2` object (or data frame if `return_data = TRUE`).

Examples

```
data("demo_targeted_deg", package = "CDEnrich")
data("demo_all_genes", package = "CDEnrich")
data("representative_pathways", package = "CDEnrich")

ora_ferroptosis <- celldeath_enrich(
  deg = demo_targeted_deg,
  universe = demo_all_genes,
  term_select = "Ferroptosis"
```

```
)

plot_death_enrich_targeted(ora_ferroptosis)
```

plot_death_gsea_curve *Plot GSEA Curve for Cell Death Pathways*

Description

Generate standard three-panel GSEA enrichment plot for cell death pathway. Support both global multi-pathway mode and targeted single-pathway mode.

Usage

```
plot_death_gsea_curve(gsea_res, pathway, use_recommended = TRUE)
```

Arguments

gsea_res	Result from celldeath_gsea().
pathway	Character. Either an exact pathway ID present in the result, or a cell death type name (e.g. "Ferroptosis"), which is resolved to the recommended representative gene set when available (see get_representative_pathway).
use_recommended	Logical. Only takes effect when pathway is a cell death type with a curated recommendation: TRUE (default) plots the recommended representative gene set; FALSE plots ALL gene sets of this type present in the result.

Value

A ggplot2 object.

Examples

```
data("demo_rank_apop", package = "CDEnrich")
data("representative_pathways", package = "CDEnrich")

apoptosis_id <- get_representative_pathway("Apoptosis")$Pathway

gsea_result <- celldeath_gsea(
  geneList = demo_rank_apop
)

plot_death_gsea_curve(
  gsea_result,
  pathway = apoptosis_id
)
```

plot_death_gsea_curve_multiple

Plot GSEA Curves for Multiple Group Cell Death Pathways

Description

Plot GSEA Curves for Multiple Group Cell Death Pathways

Usage

```
plot_death_gsea_curve_multiple(
  gsea_res_list,
  pathway,
  use_recommended = TRUE,
  filename_prefix = NULL,
  ...
)
```

Arguments

gsea_res_list	Named list of GSEA results from <code>celldeath_gsea_multiple()</code> .
pathway	Character. Either an exact pathway ID present in the results, or a cell death type name (e.g. "Ferroptosis"), which is resolved to the recommended representative gene set when available (see get_representative_pathway).
use_recommended	Logical. Only takes effect when pathway is a cell death type with a curated recommendation: TRUE (default) plots the recommended representative gene set; FALSE plots ALL gene sets of this type present in each group's result.
filename_prefix	If provided, save each plot as "prefix_groupname.png". Default: NULL.
...	Additional arguments passed to <code>plot_death_gsea_curve</code> .

Value

A named list of ggplot2 objects, each containing one GSEA curve.

Examples

```
data("demo_rank_apop_list", package = "CDEnrich")
data("representative_pathways", package = "CDEnrich")

apoptosis_id <- get_representative_pathway("Apoptosis")$Pathway

gsea_groups <- celldeath_gsea_multiple(
  geneList_list = demo_rank_apop_list,
  pvalueCutoff = 1
)
```

```

curves <- plot_death_gsea_curve_multiple(
  gsea_groups,
  pathway = apoptosis_id
)

curves$Control
curves$Treatment

```

plot_death_gsea_heatmap_multiple

Heatmap for Multi-Group GSEA Results

Description

Generate a heatmap to compare pathway statistics (e.g., NES, $-\log_{10}$ p.adjust) across multiple GSEA groups. Compatible with two modes from `celldeath_gsea()`:

1. Global mode: ranked list vs all cell death pathways
2. Targeted mode: ranked list vs one specific single pathway Missing pathway in certain group will be shown as grey tile.

Usage

```

plot_death_gsea_heatmap_multiple(
  gsea_res_list,
  show_category = 10,
  statistic = c("NES", "p.adjust"),
  palette = c("#2E8B57", "#F39C12", "#E74C3C"),
  title = "GSEA Multi-Group Enrichment Heatmap",
  filename = NULL,
  return_data = FALSE
)

```

Arguments

<code>gsea_res_list</code>	A named list of GSEA result objects (from <code>celldeath_gsea_multiple</code>).
<code>show_category</code>	Number of top pathways to display. Default: 10.
<code>statistic</code>	Which statistic to plot. Options: "NES" (default) or "p.adjust".
<code>palette</code>	Color palette for fill (low to high). Default: <code>c("#2E8B57", "#F39C12", "#E74C3C")</code> .
<code>title</code>	Plot title. Default: "GSEA Multi-Group Enrichment Heatmap".
<code>filename</code>	If provided, save plot to file. Default: NULL.
<code>return_data</code>	If TRUE, return the data frame used for plotting. Default: FALSE.

Value

A `ggplot2` object (or data frame if `return_data = TRUE`).

Examples

```
data("demo_rank_apop_list", package = "CDEnrich")
data("representative_genes", package = "CDEnrich")

gsea_groups <- celldeath_gsea_multiple(
  geneList_list = demo_rank_apop_list,
  pvalueCutoff = 1
)

plot_death_gsea_heatmap_multiple(
  gsea_groups,
  statistic = "NES",
  show_category = 10
)
```

```
plot_death_gsea_ranked
```

Plot GSEA Ranking Score Curve for Cell Death Pathways

Description

Generate a running score plot (ranked list metric) for a single GSEA result. Compatible with two modes from `celldeath_gsea()`:

1. Global mode: ranked list vs all cell death pathways
2. Targeted mode: ranked list vs one specific single pathway This plot shows the enrichment score as a function of the ranked gene list.

Usage

```
plot_death_gsea_ranked(
  gsea_res,
  pathway,
  use_recommended = TRUE,
  color = "#2E8B57",
  base_size = 10,
  title = NULL,
  filename = NULL,
  ...
)
```

Arguments

<code>gsea_res</code>	Result from <code>celldeath_gsea()</code> .
<code>pathway</code>	Character. Either an exact pathway ID present in the result, or a cell death type name (e.g. "Ferroptosis"), which is resolved to the recommended representative gene set when available (see get_representative_pathway).

use_recommended	Logical. Only takes effect when pathway is a cell death type with a curated recommendation: TRUE (default) plots the recommended representative gene set; FALSE plots ALL gene sets of this type present in the result.
color	Color of the running score line. Default: "#2E8B57".
base_size	Base font size. Default: 10.
title	Plot title. If NULL, uses the pathway name. Default: NULL.
filename	If provided, save plot to file (e.g., "gsea_ranked.png"). Default: NULL.
...	Additional arguments passed to <code>enrichplot::gseaplot</code> .

Value

A `ggplot2` object.

Examples

```
data("demo_rank_apop", package = "CDEnrich")
data("representative_pathways", package = "CDEnrich")

apoptosis_id <- get_representative_pathway("Apoptosis")$Pathway

gsea_result <- celldeath_gsea(
  geneList = demo_rank_apop
)

plot_death_gsea_ranked(
  gsea_result,
  pathway = apoptosis_id
)
```

`plot_death_ssgsea_bar` *Visualization of Cell Death ssGSEA Scores (Mean Barplot)*

Description

Generate a horizontal barplot of mean ssGSEA scores per group, with SEM (standard error of mean) error bars. Suitable for comparing overall pathway activity across groups when many pathways are involved.

Usage

```
plot_death_ssgsea_bar(
  ssgsea_res,
  show_category = 20,
  palette = c("#2E8B57", "#F39C12", "#E74C3C", "#8E44AD"),
  title = "Mean Cell Death Pathway ssGSEA Score",
```

```

    filename = NULL,
    return_data = FALSE
  )

```

Arguments

ssgsea_res	A celldeath_ssgsea object returned by celldeath_ssgsea() (must have non-NULL group).
show_category	Number of top pathways to display, ordered by mean absolute score. The default is 20.
palette	Group colors. Default: c("#2E8B57", "#F39C12", "#E74C3C", "#8E44AD").
title	Plot title. Default: "Mean Cell Death Pathway ssGSEA Score".
filename	If provided, save plot to file (e.g., "barplot.png"). Default: NULL.
return_data	If TRUE, return the data frame used for plotting. Default: FALSE.

Value

A ggplot2 object (or data frame if return_data = TRUE).

Examples

```

data("demo_expr", package = "CDEnrich")
data("demo_group", package = "CDEnrich")
data("representative_genes", package = "CDEnrich")

ssgsea_result <- celldeath_ssgsea(
  expr = demo_expr,
  group = demo_group
)

plot_death_ssgsea_bar(
  ssgsea_result,
  show_category = 10
)

```

plot_death_ssgsea_boxplot

Visualization of Cell Death ssGSEA Scores (Grouped Boxplot)

Description

Generate boxplots comparing ssGSEA score distributions across groups. Best companion for celldeath_ssgsea_diff() results. Automatically adapt for two modes:

1. Global mode: pathways on x-axis (faceted or dodged by group)
2. Targeted mode: single-pathway group comparison layout

Usage

```
plot_death_ssgsea_boxplot(
  ssgsea_result,
  show_category = 10,
  palette = c("#2E8B57", "#F39C12", "#E74C3C", "#8E44AD"),
  add_points = TRUE,
  title = "Cell Death Pathway ssGSEA Score Comparison",
  filename = NULL,
  return_data = FALSE
)
```

Arguments

ssgsea_result	A celldeath_ssgsea object returned by celldeath_ssgsea() (must have non-NULL group).
show_category	Number of top pathways to display (ordered by mean absolute score). Default: 10.
palette	Colors for groups. Default: c("#2E8B57", "#F39C12", "#E74C3C", "#8E44AD").
add_points	Logical. Whether to overlay jittered sample points. Default: TRUE.
title	Plot title. Default: "Cell Death Pathway ssGSEA Score Comparison".
filename	If provided, save plot to file (e.g., "boxplot.png"). Default: NULL.
return_data	If TRUE, return the data frame used for plotting. Default: FALSE.

Value

A ggplot2 object (or data frame if return_data = TRUE).

Examples

```
data("demo_expr", package = "CDEnrich")
data("demo_group", package = "CDEnrich")
data("representative_genes", package = "CDEnrich")

ssgsea_result <- celldeath_ssgsea(
  expr = demo_expr,
  group = demo_group
)

plot_death_ssgsea_boxplot(
  ssgsea_result,
  show_category = 10
)
```

plot_death_ssgsea_heatmap

Visualization of Cell Death ssGSEA Scores (Heatmap)

Description

Generate a heatmap of ssGSEA scores (pathways x samples) with optional group annotation. This is the most common visualization for ssGSEA results in publications. Automatically adapt for two modes:

1. Global mode: multiple pathways heatmap with row scaling
2. Targeted mode: single-pathway heatmap without row scaling

Usage

```
plot_death_ssgsea_heatmap(
  ssgsea_result,
  show_category = 30,
  scale_rows = TRUE,
  cluster_cols = TRUE,
  palette = c("#2E8B57", "white", "#E74C3C"),
  group_palette = c("#2E8B57", "#F39C12", "#E74C3C", "#8E44AD"),
  title = "Cell Death Pathway ssGSEA Scores",
  filename = NULL,
  width = 10,
  height = 8
)
```

Arguments

ssgsea_result	A celldeath_ssgsea object returned by celldeath_ssgsea().
show_category	Number of top pathways to display, ordered by mean absolute score. The default is 30.
scale_rows	Logical. Whether to z-score scale each pathway across samples (recommended for multi-pathway mode). Default: TRUE.
cluster_cols	Logical. Whether to cluster samples. Default: TRUE. Ignored automatically if only one pathway is present.
palette	Color palette for score values (low to high). Default: c("#2E8B57", "white", "#E74C3C").
group_palette	Named or unnamed colors for group annotation. Default: c("#2E8B57", "#F39C12", "#E74C3C", "#8E44AD").
title	Plot title. Default: "Cell Death Pathway ssGSEA Scores".
filename	If provided, save plot to file (e.g., "heatmap.png"). Default: NULL.
width	Plot width in inches when saving. Default: 10.
height	Plot height in inches when saving. Default: 8.

Value

Invisibly returns the pheatmap object.

Examples

```
data("demo_expr", package = "CDEnrich")
data("demo_group", package = "CDEnrich")
data("representative_genes", package = "CDEnrich")

ssgsea_result <- celldeath_ssgsea(
  expr = demo_expr,
  group = demo_group
)

plot_death_ssgsea_heatmap(
  ssgsea_result,
  show_category = 10
)
```

plot_death_volcano	<i>Volcano Plot for Cell Death Enrichment Results</i>
--------------------	---

Description

Generate a volcano-style plot for single-group enrichment analysis (ORA or GSEA), showing effect size (GeneRatio for ORA, NES for GSEA) versus significance ($-\log_{10}$ p.adjust). Support both global multi-pathway mode and targeted single-pathway mode.

Usage

```
plot_death_volcano(
  enrich_res,
  label_top = 5,
  color_point = "lightblue",
  color_signif = "darkred",
  point_size = 2,
  alpha = 0.8,
  label_size = 3.5,
  x_lab = NULL,
  y_lab = expression(-log[10]("Adjusted P-value")),
  title = NULL,
  filename = NULL,
  ...
)
```

Arguments

<code>enrich_res</code>	An <code>enrichResult</code> (ORA) or <code>gseaResult</code> (GSEA) object.
<code>label_top</code>	Number of top significant pathways to label (sorted by <code>p.adjust</code>). Default: 5.
<code>color_point</code>	Color of non-significant points. Default: "#D3D3D3".
<code>color_signif</code>	Color of significant points (<code>p.adjust</code> < 0.05). Default: "#D62728".
<code>point_size</code>	Size of points. Default: 2.
<code>alpha</code>	Transparency of points. Default: 0.8.
<code>label_size</code>	Size of pathway labels. Default: 3.5.
<code>x_lab</code>	X-axis label. If <code>NULL</code> , auto-detected ("Gene Ratio" for ORA, "NES" for GSEA). Default: <code>NULL</code> .
<code>y_lab</code>	Y-axis label. Default: <code>"-log10(Adjusted P-value)"</code> .
<code>title</code>	Plot title. If <code>NULL</code> , auto-generated. Default: <code>NULL</code> .
<code>filename</code>	If provided, save plot to file (e.g., "volcano.png"). Default: <code>NULL</code> .
<code>...</code>	Additional arguments passed to <code>ggrepel::geom_text_repel</code> (e.g., <code>max.overlaps</code> , <code>force</code>).

Value

A `ggplot2` object.

Examples

```
data("demo_deg", package = "CDEnrich")
data("demo_all_genes", package = "CDEnrich")
data("representative_genes", package = "CDEnrich")

ora_result <- celldeath_enrich(
  deg = demo_deg,
  universe = demo_all_genes
)

plot_death_volcano(
  ora_result,
  label_top = 5
)
```

```
print.celldeath_ssgsea
```

Print Method for celldeath_ssgsea Objects

Description

Print Method for `celldeath_ssgsea` Objects

Usage

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

Arguments

x	A celldeath_ssgsea object.
...	Additional arguments (ignored).

Value

Invisibly returns x.

representative_genes	<i>Representative Gene Sets for Cell Death Types</i>
----------------------	--

Description

The recommended representative gene set for each of the 13 cell death types with curated recommendations. These are merged into the result of [load_cell_death_genes](#) and are used as the default gene set in targeted analysis modes.

Usage

```
data(representative_genes)
```

Format

A named list of character vectors; names are pathway names (e.g. Ferroptosis_FerrDb V2(36305834)) and each element is a vector of gene symbols.

Source

Curated from the seminal publication of each cell death type; see [representative_pathways](#) for the curation metadata.

`representative_pathways`*Representative Pathway Recommendation Metadata*

Description

Curated recommendation table recording, for each cell death type with multiple PMID-based gene sets, which gene set is the recommended representative. Used by [get_representative_pathway](#).

Usage

```
data(representative_pathways)
```

Format

A data frame with one row per recommended cell death type and the following columns:

Type Cell death type name, e.g. Ferroptosis.

PMID PubMed ID of the source publication.

IF Journal impact factor of the source publication.

Cite Citation count of the source publication.

Pathway Name of the recommended representative gene set, e.g. Ferroptosis_FerrDb V2(36305834).

Source Where the gene set was obtained from in the publication, e.g. Supplementary-table1.

Description Free-text description of how the gene set was curated.

Notes Additional curation notes (may be empty).

Source

Curated manually from the primary literature; see `data-raw/representative_pathways.csv`.

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