

Package: wikiprofiler (via r-universe)

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Type Package

Title Data Integration and Visualization on 'WikiPathways' Graphics

Version 0.1.7

Description Retrieves pathway graphics from 'WikiPathways' and maps user-supplied quantitative data, such as gene expression values, onto pathway nodes. Provides a pipe-friendly grammar for building pathway visualizations with layered fills, text highlighting, condition-wise comparisons, data preparation helpers, and batch rendering utilities.

Imports ggplot2, ggplotify, grDevices, grid, gson, methods, rsvg, yulab.utils (>= 0.1.7)

Suggests clusterProfiler, DOSE, knitr, org.Hs.eg.db, quarto, rmarkdown

VignetteBuilder quarto

ByteCompile true

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URL <https://yulab-smu.top/contribution-knowledge-mining/>

BugReports <https://github.com/YuLab-SMU/wikiprofiler/issues>

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Repository <https://yulab-smu.r-universe.dev>

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read.wp	<i>read.wp</i>
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Description

parse wikipathway gmt file to a gson object

Usage

read.wp(file)

Arguments

file wikipathway gmt file downloaded from 'https://wikipathways-data.wmcloud.org/current/gmt/'

Value

a 'gson' object

Author(s)

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wp_bgfill	<i>Fill the background of gene with color according to amount of gene expression.</i>
-----------	---

Description

Generate a color array.Fill the gene then generate the legend.

Usage

```
wp_bgfill(
  p,
  value,
  high = "red",
  low = "blue",
  legend = TRUE,
  legend_x = 0.001,
  legend_y = 0.94
)
```

Arguments

p	p is
value	value is the amount of expression.
high	The color of highest gene.
low	The color of lowest gene.
legend	Whether you need legend.
legend_x	horizontal position of the legend
legend_y	vertical position of the legend

Value

A 'wpplot' object

wp_comparefill	<i>Visualize pathway differences between two conditions</i>
----------------	---

Description

Compute pathway-level comparison values from two symbol-keyed numeric vectors and render them through wp_bgfill().

Usage

```
wp_comparefill(
  p,
  value,
  control,
  mode = c("difference", "log2_ratio"),
  pseudocount = 1,
  high = "red",
  low = "blue",
  legend = TRUE,
  legend_x = 0.001,
  legend_y = 0.94
)
```

Arguments

p	A wplot object.
value	Case-condition values.
control	Control-condition values.
mode	Comparison mode: direct difference or log2 ratio.
pseudocount	Added before ratio calculation when mode = "log2_ratio".
high	High-end color passed to wp_bgfill().
low	Low-end color passed to wp_bgfill().
legend	Whether to draw the legend.
legend_x	Horizontal position of the legend.
legend_y	Vertical position of the legend.

Value

A wplot object.

wp_map

Map user values to pathway symbols

Description

Normalize a named numeric vector or a data.frame into a symbol-keyed numeric vector that can be used by wp_bgfill().

Usage

```
wp_map(  
  data,  
  value_col = NULL,  
  symbol_col = NULL,  
  id_col = NULL,  
  mapping = NULL,  
  mapping_from = NULL,  
  mapping_to = NULL,  
  aggregator = c("mean", "median", "max_abs", "first", "sum"),  
  na.rm = TRUE  
)
```

Arguments

data	A named numeric vector or a data.frame.
value_col	Value column name when data is a data.frame.
symbol_col	Symbol column name when data already contains gene symbols.
id_col	Identifier column name when data needs ID mapping.
mapping	Optional ID-to-symbol mapping. It can be a named character vector or a two-column data.frame.
mapping_from	Source ID column in mapping when mapping is a data.frame.
mapping_to	Target symbol column in mapping when mapping is a data.frame.
aggregator	Aggregation rule used when multiple rows map to the same symbol.
na.rm	Whether to remove NA values before aggregation.

Value

A named numeric vector keyed by gene symbol.

wp_render	<i>Render one or more WikiPathways entries</i>
-----------	--

Description

Render pathway IDs directly from a character vector, a result table, or an enrichment-like S4 object with a result slot.

Usage

```
wp_render(
  pathway,
  value = NULL,
  control = NULL,
  n = NULL,
  id_col = "ID",
  name_col = NULL,
  dir = NULL,
  file_ext = "png",
  filename_template = "{id}",
  width = NULL,
  height = NULL,
  shadowtext = FALSE,
  bg.r = 2,
  bg.col = "white",
  mode = c("difference", "log2_ratio"),
  pseudocount = 1,
  high = "red",
  low = "blue",
  legend = TRUE,
  legend_x = 0.001,
  legend_y = 0.94
)
```

Arguments

pathway	Pathway IDs, a data.frame, or an enrichment-like S4 object.
value	Optional symbol-keyed values for single-condition rendering.
control	Optional symbol-keyed control values for comparison rendering.
n	Maximum number of pathway IDs to render.
id_col	Column name that stores pathway IDs.
name_col	Optional column name used for output file naming when pathway is a data.frame or an enrichment-like result table.
dir	Optional output directory. When provided, PNG files are written there.
file_ext	Output file extension(s) passed to wpsave().
filename_template	Output filename template. Supported placeholders: {index}, {id}, and {name}.
width	Width passed to wpsave().
height	Height passed to wpsave().
shadowtext	Whether to add halo text after fill rendering.
bg.r	Halo width passed to wp_shadowtext().
bg.col	Halo color passed to wp_shadowtext().
mode	Comparison mode passed to wp_comparefill().

pseudocount	Pseudocount passed to wp_comparefill().
high	High-end color passed to fill functions.
low	Low-end color passed to fill functions.
legend	Whether to draw the legend.
legend_x	Horizontal position of the legend.
legend_y	Vertical position of the legend.

Value

A named list of wpplot objects.

wp_shadowtext	<i>Add halo above gene name to get a clear view.</i>
---------------	--

Description

Add use svghalo2 function to add halo.

Usage

```
wp_shadowtext(p, bg.r = 2, bg.col = "white")
```

Arguments

p	An wpplot class variance.
bg.r	The width of halo.
bg.col	The color of halo.

Value

A 'wpplot' object

wpplot	<i>Input specific wikipathways ID to get an output in class of wpplot.</i>
--------	--

Description

Use wikipathways ID to open a local svg file. Then extract related information from svg file and build a wpplot class variance.

Usage

```
wpplot(ID)
```

Arguments

ID	ID is wikipathways' ID.
----	-------------------------

Value

A 'wpplot' object

Examples

```
## Not run:  
wpplot('WP179')  
  
## End(Not run)
```

wpsave	<i>Save the 'wpplot' object to a file.</i>
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Description

Save the 'wpplot' object to a file.

Usage

```
wpsave(p, file, width = NULL, height = NULL, ...)
```

Arguments

p	A 'wpplot' object
file	the file to save the object
width	Width of the figure
height	Height of the figure
...	additional parameter passed to 'ggsave'

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Value

output the file and the input 'wpplot' object (invisible)

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