Package ‘wikiprofiler’

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Type Package

Title 'WikiPathway' Based Data Integration and Visualization

Version 0.1.6

Description Queries online 'WikiPathway' graphics and allows mapping user data (e.g., expression values) on the graph. The package designs a grammar of graphic syntax that using pipe operator to add graphic layer.

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

ByteCompile true

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

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

Encoding UTF-8

RoxygenNote 7.3.2

NeedsCompilation no

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Repository CRAN

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Contents

`read.wp` *read.wp*

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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`wpplot` *Input specific wikipathways ID to get an output in class of wpplot.*

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` *Save the 'wpplot' object to a file.*

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'

Value

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

`wp_bgfill` *Fill the background of gene with color according to amount of gene expression.*

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_shadowtext` *Add halo above gene name to get a clear view.*

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

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