

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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`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	<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'

Value

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

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

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

Add use svghalo2 function to add halo.

Usage

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

Arguments

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

Value

A 'wplot' object

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