Package 'wikiprofiler'

August 26, 2024

Type Package

Title 'WikiPathway' Based Data Integration and Visualization

Version 0.1.5

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

License Artistic-2.0

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

Author Guangchuang Yu [aut, cre, cph]
(<https://orcid.org/0000-0002-6485-8781>),
Yihao Chen [aut]

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

Repository CRAN

Date/Publication 2024-08-26 19:30:01 UTC

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)

Guangchuang Yu

---

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

```
if (yulab.utils::has_internet())
   wpplot('WP179')
```

---

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

Index