

Package ‘GeSciLiVis’

March 14, 2023

Type Package

Title Gene-Based Publication Activity Visualiser

Version 1.1.0

Description

Visualising publication activity per gene based on a gene list and a user-defined set of keywords utilising R 'rentrez' <<https://cran.r-project.org/package=rentrez/>> that provides 'NCBI' <<https://www.ncbi.nlm.nih.gov>> database search like in 'PubMed' <<https://pubmed.ncbi.nlm.nih.gov>>. It summarises the retrieved number of publications for each gene in an overview bar plot (saved as 'png' file) and by choice a summary table (as 'csv') that including the most recent 100 'PubMed' IDs and publication titles.

License GPL (>= 3)

Depends R (>= 2.10)

Imports rentrez (>= 1.2.3), biomaRt (>= 2.54.0), biomart (>= 1.0.2), grDevices (>= 4.2.2), graphics (>= 4.2.2), utils (>= 4.2.2)

Encoding UTF-8

RoxygenNote 7.2.3

LazyData true

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

human_official_gene_names	2
mouse_official_gene_names	2
pub_activity_plot	3

Index	5
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human_official_gene_names
Human gene names data

Description

A set of human gene names in official symbol by HGNC retrieved from ensembl through biomaRt on Feb 5, 2023

Usage

human_official_gene_names

Format

human_official_gene_names:
A data frame with 40205 rows and 1 column:
symbol official symbol by HGNC

Source

https://www.ensembl.org/Homo_sapiens/Info/Index

mouse_official_gene_names
Mouse gene names data

Description

A set of mouse gene names in official symbol by MGNC retrieved from ensembl through biomaRt on Feb 5, 2023

Usage

mouse_official_gene_names

Format

mouse_official_gene_names:
A data frame with 55244 rows and 1 column:
symbol official symbol by MGNC

Source

http://www.ensembl.org/Mus_musculus/Info/Index

pub_activity_plot	<i>Visualize the publication activity for genes</i>
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Description

This function uses three input parameters, one gene list, one defined set of keywords and species, to run a PubMed database search, and returns an annotated overview of a publication activity plot.

Usage

```
pub_activity_plot(  
  g_list,  
  k_list,  
  species = "mouse",  
  output_dir = NULL,  
  use_preloaded_gene_names = TRUE,  
  show_progressbar = FALSE  
)
```

Arguments

g_list	list of official gene symbols <= 30 elements.
k_list	list of keywords <= 10 elements.
species	selecting the species of interest (species="mouse" or species="human").
output_dir	path to output directory to save resulting csv and png, NULL for not saving.
use_preloaded_gene_names	boolean: whether to use preloaded gene names (TRUE) or load from biomaRt (FALSE)
show_progressbar	boolean: whether to show progress bar

Value

None

Examples

```
gene_list_mouse = c("Mbl1")
keyword_list = c("stem cell")
pub_activity_plot(g_list = gene_list_mouse, k_list = keyword_list,
species = "mouse", output_dir=NULL, use_preloaded_gene_names=TRUE,
show_progressbar=FALSE)
```

Index

* datasets

human_official_gene_names, [2](#)

mouse_official_gene_names, [2](#)

human_official_gene_names, [2](#)

mouse_official_gene_names, [2](#)

pub_activity_plot, [3](#)