Package 'STRINGdb'

April 22, 2026

Type Package

Title STRINGdb - Protein-Protein Interaction Networks and Functional Enrichment Analysis

Version 2.23.0

Date 2024-06-05

Author Andrea Franceschini <andrea.franceschini@isb-sib.ch>

Maintainer Damian Szklarczyk <damian.szklarczyk@imls.uzh.ch>

Description The STRINGdb package provides an R interface to STRING, a protein-protein interaction database and functional enrichment analysis tool (https://string-db.org).

License GPL-2

Depends R (>= 2.14.0)

Imports png, sqldf, plyr, igraph, httr, methods, RColorBrewer, gplots, hash, plotrix

Suggests RUnit, BiocGenerics

biocViews Network

git_url https://git.bioconductor.org/packages/STRINGdb

git_branch devel

git_last_commit 071ea9e

git_last_commit_date 2026-04-13

Repository Bioconductor 3.24

Date/Publication 2026-04-21

Contents

`add_diff_exp_color` *add_diff_exp_color*

Description

Take in input a dataframe containing a logFC column that reports the logarithm of the difference in expression level. Add a "color" column to the data frame such that strongly downregulated genes are colored in green and strong upregulated genes are in red. When the down or up-regulation is instead weak the intensity of the color gets weaker as well, accordingly.

Usage

```
## S4 method for signature 'STRINGdb'
add_diff_exp_color(screen, logFcColStr="logFC" )
```

Arguments

`screen`	Dataframe containing the results of the experiment (e.g. the analyzed results of a microarray or RNAseq experiment)
`logFcColStr`	name of the colum that contains the logFC of the expression

Value

vector containing the colors

Author(s)

Andrea Franceschini

`add_proteins_description` *add_proteins_description*

Description

Add description coluns to the proteins that are present in the data frame given in input. The data frame must contain a column named "STRING_id".

Usage

```
## S4 method for signature 'STRINGdb'
add_proteins_description(screen)
```

Arguments

`screen`	Dataframe containing the results of the experiment (e.g. the analyzed results of a microarray or RNAseq experiment)

Value

returns the same dataframe given in input with an additional columns containing a description of the proteins.

Author(s)

Andrea Franceschini

`coeffOfvar` *coeffOfvar*

Description

coefficient of variation

Usage

```
coeffOfvar(x)
```

Arguments

`x`	input number

Details

coefficient of variation

Value

coefficient of variation

Author(s)

Andrea Franceschini

`delColDf` *delColDf*

Description

delete a column in the data frame

Usage

```
delColDf(df, colName)
```

Arguments

`df`	data frame
`colName`	name of the column to be deleted

Value

data frame

Author(s)

Andrea Franceschini

`diff_exp_example1` *example of microarray data (data processed from GEO GSE9008)*

Description

example of microarray data (data processed from GEO GSE9008)

Usage

```
data(diff_exp_example1)
```

Format

Data frames with 20861 observations on the following 3 variables.

`gene` a character vector

`pvalue` a numeric vector

`logFC` a numeric vector

Source

Whyte L, Huang YY, Torres K, Mehta RG. Molecular mechanisms of resveratrol action in lung cancer cells using dual protein and microarray analyses. Cancer Res 2007.

`downloadAbsentFile` *downloadAbsentFile*

Description

download a file only if it is not present.

Usage

```
downloadAbsentFile(urlStr, oD = tempdir())
```

Arguments

`urlStr`	url from which to download the file
`oD`	directory where to store the file

Author(s)

Andrea Franceschini

`downloadAbsentFileSTRING` *downloadAbsentFileSTRING*

Description

download a STRING file only if it is not present or if it is corrupted.

Usage

```
downloadAbsentFileSTRING(urlStr, oD = tempdir())
```

Arguments

`urlStr`	url from which to download the file
`oD`	directory where to store the file

Author(s)

Andrea Franceschini

get_aliases *get_aliases*

Description

Loads and returns STRING aliases. Depending on `takeFirst`, this returns either all alias mappings or a single preferred mapping for ambiguous aliases.

Usage

```
## S4 method for signature 'STRINGdb'
get_aliases(takeFirst=TRUE, usePreferredSources=TRUE)
```

Arguments

`takeFirst`	boolean indicating whether ambiguous aliases should be collapsed to a single STRING identifier. If `FALSE`, all alias mappings are returned. If `TRUE`, one mapping is returned for each ambiguous alias.
`usePreferredSources`	boolean indicating whether preferred alias sources should be used to disambiguate aliases when `takeFirst=TRUE`. This parameter is ignored when `takeFirst=FALSE`.

Value

a data frame containing STRING aliases. With `takeFirst=FALSE`, all alias mappings are returned. With `takeFirst=TRUE`, ambiguous aliases are collapsed to one STRING identifier.

Author(s)

Andrea Franceschini

get_annotations *get_annotations*

Description

Loads and returns STRING annotations (i.e. GO annotations, KEGG pathways, domain databases). The annotations are stored in the "annotations" variable.

Usage

```
## S4 method for signature 'STRINGdb'
get_annotations( )
```

Value

a data frame containing the annotations to the STRING proteins (e.g. GeneOntology, KEGG pathways, InterPro domains)

Author(s)

Andrea Franceschini

get_annotations_desc *get_annotations_desc*

Description

Returns a data frame with the description of every STRING annotation term (it downloads and caches the information the first time that is called).

Usage

```
## S4 method for signature 'STRINGdb'
get_annotations_desc()
```

Value

data frame with the description of every STRING annotation term.

Author(s)

Andrea Franceschini

get_bioc_graph *get_bioc_graph*

Description

Returns the interaction graph as an object of the graph package in Bioconductor.

Usage

```
## S4 method for signature 'STRINGdb'
get_bioc_graph()
```

Value

interaction graph as an object of the graph package in Bioconductor.

Author(s)

Andrea Franceschini

get_clusters *get_clusters*

Description

Returns a list of clusters of interacting proteins. See the iGraph (http://igraph.sourceforge.net/) documentation for additional information on the algorithms.

Usage

```
## S4 method for signature 'STRINGdb'
get_clusters(string_ids, algorithm="fastgreedy")
```

Arguments

string_ids	a vector of STRING identifiers.
algorithm	algorithm to use for the clustering. You can choose between "fastgreedy", "walktrap", "spinglass" and "edge.betweenness").

Value

list of clusters of interacting proteins.

Author(s)

Andrea Franceschini

get_enrichment *get_enrichment*

Description

Returns the enrichment in pathways of the vector of STRING proteins that is given in input.

Usage

```
## S4 method for signature 'STRINGdb'
get_enrichment(string_ids, category = "Process", methodMT = "fdr", iea = TRUE, minScore=NULL)
```

Arguments

string_ids	a vector of STRING identifiers.
category	category for which to compute the enrichment (i.e. "Process", "Component", "Function", "KEGG", "Pfam", "InterPro"). The default category is "Process".
methodMT	method to be used for the multiple testing correction. (i.e. "fdr", "bonferroni"). The default is "fdr".
iea	specify whether you also want to use electronic inference annotations
minScore	with Tissue and Disease categories is possible to filter the annotations having an annotation score higher than this threshold (from 0 to 5)

Value

Data frame containing the enrichment in pathways of the vector of STRING proteins that is given in input.

Author(s)

Andrea Franceschini

`get_graph` *get_graph*

Description

Return an igraph object with the STRING network (for information about iGraph visit http://igraph.sourceforge.net)

Usage

```
## S4 method for signature 'STRINGdb'
get_graph()
```

Value

igraph object with the STRING network

Author(s)

Andrea Franceschini

References

Csardi G, Nepusz T: The igraph software package for complex network research, InterJournal, Complex Systems 1695. 2006. http://igraph.sf.net

See Also

In order to simplify the most common tasks, we do also provide convenient functions that wrap some iGraph functions. get_interactions(string_ids) # returns the interactions in between the input proteins get_neighbors(string_ids) # Get the neighborhoods of a protein (or of a vector of proteins) that is given in input. get_subnetwork(string_ids) # returns a subgraph from the given input proteins

get_homologs_besthits *get_homologs_besthits*

Description

Returns the list of closest homologs (as measured by bitscore) of the given input identifiers in all STRING species or single target species.

Usage

```
## S4 method for signature 'STRINGdb'
get_homologs_besthits(string_ids, target_species_id=NULL)
```

Arguments

string_ids	a vector of STRING identifiers.
target_species_id	NCBI taxonomy identifier of the species to query for homologs (the species must be present in the STRING database)

Value

Data frame containing the best blast hits x species of the given input identifiers.

Author(s)

Andrea Franceschini

get_interactions *get_interactions*

Description

Shows the interactions in between the proteins that are given in input.

Usage

```
## S4 method for signature 'STRINGdb'
get_interactions(string_ids)
```

Arguments

string_ids	a vector of STRING identifiers

Value

Data frame containing the interactions in between the input proteins. The leading columns are `from`, `to`, `combined_score`, `from_name` and `to_name`, followed by any additional loaded edge attributes.

Author(s)

Damian Szklarczyk

get_interaction_partners *get_interaction_partners*

Description

Returns the interaction partners of the input proteins using the locally loaded STRING graph. The returned data frame preserves the edge attributes available for the current `link_data` setting.

Usage

```
## S4 method for signature 'STRINGdb'
get_interaction_partners(string_ids, required_score=NULL, limit=NULL)
```

Arguments

`string_ids`	a vector of STRING identifiers
`required_score`	optional minimum combined score for returned partners. This value cannot be below the `score_threshold` used to load the local graph.
`limit`	optional maximum number of partner rows returned per query protein

Value

Data frame containing one row per query-partner interaction. The leading columns are `from`, `to`, `combined_score`, `from_name` and `to_name`, followed by any additional edge attributes loaded for the current `link_data` mode. Here `from` is the queried protein and `to` is its interaction partner. If `limit` is used, rows are ordered by `combined_score`.

Author(s)

Damian Szklarczyk

get_link *get_link*

Description

Returns a short link to the network page of the STRING website that shows the protein interactions between the given identifiers.

Usage

```
## S4 method for signature 'STRINGdb'
get_link(string_ids=NULL, required_score=NULL, network_flavor="evidence", payload_id=NULL, networ
```

Arguments

string_ids	a vector of STRING identifiers. Can be omitted when network_term_id is provided.
required_score	minimum STRING combined score of the interactions (if left NULL we get the combined score of the object, which is 400 by default).
network_flavor	specify the flavor of the network ("evidence" or "confidence". Default "evidence").
payload_id	an identifier of payload data on the STRING server (see method post_payload for additional informations).
network_term_id	functional term identifier used by STRING instead of explicit protein identifiers.
hide_node_labels	hides all protein names from the picture. Accepts TRUE/FALSE or 0/1.
hide_disconnected_nodes	hides proteins that are not connected to any other protein in the network. Accepts TRUE/FALSE or 0/1.
block_structure_pics_in_bubbles	disables structure pictures inside the bubbles. Accepts TRUE/FALSE or 0/1.
flat_node_design	disables 3D bubble design. Accepts TRUE/FALSE or 0/1. Default is TRUE.
center_node_labels	centers protein names on nodes. Accepts TRUE/FALSE or 0/1.
custom_label_font_size	changes the font size of the protein names (from 5 to 50).
caller_identity	caller identifier sent to STRING.

Value

short link to the network page of the STRING website that shows the protein interactions between the input identifiers.

Author(s)

Damian Szklarczyk

---

get_neighbors *get_neighbors*

Description

Get the neighborhoods of a protein (or of a vector of proteins) that is given in input.

Usage

```
## S4 method for signature 'STRINGdb'
get_neighbors(string_ids)
```

Arguments

string_ids	a vector of STRING identifiers

Value

vector containing the neighborhoods of a protein (or of a vector of proteins) that is given in input.

Author(s)

Andrea Franceschini

---

get_paralogs *get_paralogs*

Description

Returns the list of paralogs of the given input in their species.

Usage

```
## S4 method for signature 'STRINGdb'
get_paralogs(string_ids)
```

Arguments

string_ids	a vector of STRING identifiers.

Value

Data frame containing the within-species homology hits of the input identifiers, with columns ncbiTaxonId_A, stringId_A, ncbiTaxonId_B, stringId_B, and bitscore.

Author(s)

Andrea Franceschini

---

get_png *get_png*

Description

Returns a STRING network image for the given identifiers or for a STRING functional term.

Usage

```
## S4 method for signature 'STRINGdb'
get_png(string_ids=NULL, required_score=NULL, network_flavor="evidence", file=NULL, payload_id=NU
```

Arguments

string_ids	a vector of STRING identifiers. Can be omitted when network_term_id is provided.
required_score	minimum STRING combined score of the interactions (if left NULL we get the combined score of the object, which is 400 by default).
network_flavor	specify the flavor of the network ("evidence" or "confidence". Default "evidence").
file	file where to save the image output.
payload_id	identifier of the payload.
output_format	STRING image output format: "image", "highres_image" or "svg".
network_term_id	functional term identifier used by STRING instead of explicit protein identifiers.
hide_node_labels	hides all protein names from the picture. Accepts TRUE/FALSE or 0/1.
hide_disconnected_nodes	hides proteins that are not connected to any other protein in the network. Accepts TRUE/FALSE or 0/1.
block_structure_pics_in_bubbles	disables structure pictures inside the bubbles. Accepts TRUE/FALSE or 0/1.
flat_node_design	disables 3D bubble design. Accepts TRUE/FALSE or 0/1. Default is TRUE.
center_node_labels	centers protein names on nodes. Accepts TRUE/FALSE or 0/1.
custom_label_font_size	changes the font size of the protein names (from 5 to 50).
caller_identity	caller identifier sent to STRING.

Value

For output_format="image" and output_format="highres_image", returns a PNG image array. For output_format="svg", returns the SVG markup as text.

Author(s)

Damian Szklarczyk

---

get_ppi_enrichment *get_ppi_enrichment*

Description

Returns a pvalue representing the enrichment in interactions of the list of proteins (i.e. the probability to obtain such a number of interactions by chance).

Usage

```
## S4 method for signature 'STRINGdb'
get_ppi_enrichment(string_ids)
```

Arguments

string_ids	a vector of STRING identifiers

Value

Returns a pvalue representing the enrichment in interactions of the list of proteins (i.e. the probability to obtain such a number of interactions by chance).

Author(s)

Andrea Franceschini

---

get_proteins *get_proteins*

Description

Returns the STRING proteins data frame. (it downloads and caches the information the first time that is called).

Usage

```
## S4 method for signature 'STRINGdb'
get_proteins()
```

Value

STRING proteins data frame.

Author(s)

Andrea Franceschini

---

get_subnetwork *get_subnetwork*

Description

Returns the subgraph generated by the given input proteins.

Usage

```
## S4 method for signature 'STRINGdb'
get_subnetwork(string_ids )
```

Arguments

string_ids	a vector of STRING identifiers

Value

Returns the subgraph (i.e. an iGraph object) generated by the given input proteins.

Author(s)

Andrea Franceschini

`get_summary` *get_summary*

Description

Returns a summary of the STRING sub-network containing the identifiers provided in input.

Usage

```
## S4 method for signature 'STRINGdb'
get_summary(string_ids)
```

Arguments

`string_ids`	a vector of STRING identifiers

Value

Returns a summary (i.e. a text description) of the STRING sub-network containing the identifiers provided in input.

Author(s)

Andrea Franceschini

`get_term_proteins` *get_term_proteins*

Description

Returns the proteins annotated to belong to a given term.

Usage

```
## S4 method for signature 'STRINGdb'
get_term_proteins(term_ids, string_ids=NULL, enableIEA=TRUE)
```

Arguments

`term_ids`	vector of terms
`string_ids`	a vector of STRING identifiers. If the variable is set, the method returns only the proteins that are present in this vector.
`enableIEA`	whether to consider also Electronic Inferred Annotations

Value

Returns the proteins annotated to belong to a given term.

Author(s)

Andrea Franceschini

---

interactions_example *example of a protein-protein interactions sorted data frame*

Description

example of a sorted list of protein-protein interactions, resulta our cooccurrence algorithm (SVD_Phy)

Usage

```
data(interactions_example)
```

Format

Data frames with 20861 observations on the following 3 variables.

`proteinA` a character vector

`proteinB` a character vector

`score` a numeric vector

---

load *load*

Description

Downloads and returns the STRING network (the network is set also in the graph variable of the STRING_db object). When possible, the download uses the threshold-specific streamed network file matching the current `score_threshold`.

It makes use of the variables: "backgroundV" vector containing STRING identifiers to be used as background (i.e. the STRING network loaded will contain only the proteins that are present also in this vector) "score_threshold" STRING combined score threshold (the network loaded contains only interactions having a combined score greater than this threshold)

Usage

```
## S4 method for signature 'STRINGdb'
load()
```

Value

STRING network (i.e. an iGraph object. For info look to http://igraph.sourceforge.net)

Author(s)

Andrea Franceschini and Damian Szklarczyk

load_all *load_all*

Description

Force download and loading of all the files (so that you can later store the object on the hard disk if you like). It makes use of the variables: "backgroundV" vector containing STRING identifiers to be used as background (i.e. the STRING network loaded will contain only the proteins that are present also in this vector) "score_threshold" STRING combined score threshold (the network loaded contains only interactions having a combined score greater than this threshold)

Usage

```
## S4 method for signature 'STRINGdb'
load_all()
```

Author(s)

Andrea Franceschini

map *map*

Description

Maps the gene identifiers of the input dataframe to STRING identifiers. It returns the input dataframe with the "STRING_id" additional column.

Usage

```
## S4 method for signature 'STRINGdb'
map(my_data_frame, my_data_frame_id_col_names, takeFirst=TRUE, removeUnmappedRows=FALSE, quiet=FA
```

Arguments

my_data_frame	data frame provided as input.
my_data_frame_id_col_names	vector contatining the names of the columns of "my_data_frame" that have to be used for the mapping.
takeFirst	boolean indicating what to do in case of multiple STRING proteins that map to the same name. If TRUE, only the first of those is taken. Otherwise all of them are used. (default TRUE)
removeUnmappedRows	remove the rows that cannot be mapped to STRING (by default those lines are left and their STRING_id is set to NA).
quiet	Setting this variable to TRUE we can avoid printing the warning relative to the unmapped values.
usePreferredSources	when takeFirst=TRUE, prioritize aliases using the preferred source order.

Value

Returns the dataframe that is given in input with the "STRING_id" additional column.

Author(s)

Andrea Franceschini

`mp` *mp*

Description

Maps the gene identifiers of the input vector to STRING identifiers (using a take first approach). It returns a vector with the STRING identifiers of the mapped proteins.

Usage

```
## S4 method for signature 'STRINGdb'
mp(protein_aliases)
```

Arguments

`protein_aliases`
vector of protein aliases that we want to convert to STRING identifiers

Value

It returns a vector with the STRING identifiers of the mapped proteins.

Author(s)

Andrea Franceschini

`multi_map_df` *multi_map_df*

Description

mapping function (it add the possibility to map using more than one column of the data frame)

Usage

```
multi_map_df(dfToMap, dfMap, strColsFrom, strColFromDfMap, strColToDfMap, caseSensitive=FALSE)
```

Arguments

dfToMap	input data frame (that contains the columns that need to be mapped)
dfMap	data frame containing the mapping data
strColsFrom	sorted vector containing the names of the columns to be used in the input data frame for the mapping (the order of the elements in the vector defines the priority for the mapping)
strColFromDfMap	name of the column in the mapping data frame to be used as source for the mapping
strColToDfMap	name of the column in the mapping data frame to be used as target for the mapping
caseSensitive	specify whether the mapping should be case sensitive

Value

data frame with an additional column containing the result of the mapping

Author(s)

Andrea Franceschini

---

plot_network *plot_network*

Description

Plots an image of the STRING network with the given proteins.

Usage

```
## S4 method for signature 'STRINGdb'
plot_network(string_ids, payload_id=NULL, required_score=NULL, add_link=TRUE, add_summary=TRUE)
```

Arguments

string_ids	a vector of STRING identifiers
payload_id	an identifier of payload data on the STRING server (see method post_payload for additional informations)
required_score	a threshold on the score that overrides the default score_threshold, that we use only for the picture
add_link	parameter to specify whether you want to generate and add a short link to the relative page in STRING. As default this option is active but we suggest to deactivate it in case one is generating many images (e.g. in a loop). Deactivating this option avoids to generate and store a lot of short-urls on our server.
add_summary	parameter to specify whether you want to add a summary text to the picture. This summary includes a p-value and the number of proteins/interactions.

Author(s)

Andrea Franceschini

post_payload *post_payload*

Description

Posts the input to STRING and returns an identifier that you can use to access the payload when you enter in our website.

Usage

```
## S4 method for signature 'STRINGdb'
post_payload(stringIds, colors=NULL, comments=NULL, links=NULL, iframe_urls=NULL, logo_imgF=NULL,
```

Arguments

stringIds	vector of STRING identifiers.
colors	vector containing the colors to use for a every STRING identifier (the order of the elements must match those in the string_ids vector)
comments	vector containing the comments to use for every STRING identifier (the order of the elements must match those in the string_ids vector)
links	vector containing the links to use for every STRING identifier (the order of the elements must match those in the string_ids vector)
iframe_urls	vector containing the urls of the iframes to use for every STRING identifier (the order of the elements must match those in the string_ids vector).
logo_imgF	path to a file containing the logo image to be display in the STRING website
legend_imgF	path to a file containing a legend image to be display in the STRING website

Value

identifier of the payload.

Author(s)

Andrea Franceschini

remove_homologous_interactions *remove_homologous_interactions*

Description

With this method it is possible to remove the interactions that are composed by a pair of homologous/similar proteins, having a similarity bitscore between each other higher than a threshold.

Usage

```
## S4 method for signature 'STRINGdb'
remove_homologous_interactions(interactions_dataframe, bitscore_threshold = 60)
```

Arguments

`interactions_dataframe`
: a data frame contaning the sorted interactions to be benchmarked. The data frame should have the following column names: proteinA, proteinB, score

`bitscore_threshold`
: filter out pairs of homologous proteins, having a similarity bitscore higher than this parameter

Value

interactions data frame where the homologous pairs have been removed, from the input interactions' data frame

Author(s)

Andrea Franceschini

`renameColDf` *renameColDf*

Description

Rename a column of a data frame

Usage

```
renameColDf(df, colOldName, colNewName)
```

Arguments

`df`	input data frame
`colOldName`	column name to be changed
`colNewName`	new column name

Value

data frame with the column name changed

Author(s)

Andrea Franceschini

set_background *set_background*

Description

With this method you can specify a vector of proteins to be used as background. The network is reloaded and only the proteins that are present in the background vector are inserted in the graph. Besides, the background is taken in consideration for all the enrichment statistics. If you already created a STRINGdb object, calling set_background is sufficient and you do not need to instantiate a new object again.

Usage

```
## S4 method for signature 'STRINGdb'
set_background(background_vector )
```

Arguments

background_vector
: vector of STRING protein identifiers

Author(s)

Andrea Franceschini

STRINGdb-class *Class "STRINGdb"*

Description

The R package STRINGdb provides a convenient interface to STRING, a protein-protein interaction database and functional enrichment analysis tool, for R/Bioconductor users. Please look at the manual/vignette for additional information and examples on how to use the package. STRING is a database of known and predicted protein-protein interactions. It contains information from numerous sources, including experimental repositories, computational prediction methods, and public text collections. Each interaction is associated with a combined confidence score that integrates the different evidence channels. STRING v12.0 contains information on 59.3 million proteins from 12,535 organisms and more than 20 billion interactions. The STRING web interface is freely accessible at: https://string-db.org/

Extends

All reference classes extend and inherit methods from "envRefClass".

Fields

annotations: Object of class data.frame ~~

annotations_description: Object of class data.frame ~~

graph: Object of class igraph ~~

proteins: Object of class data.frame ~~

speciesList: Object of class data.frame ~~

species: Object of class numeric ~~

version: Object of class character ~~

input_directory: Object of class character ~~

backgroundV: Object of class vector ~~

score_threshold: Object of class numeric ~~

Methods

set_background(background_vector): ~~

post_payload(stringIds, colors, comments, links, iframe_urls, logo_imgF, legend_imgF): ~~

plot_network(string_ids, payload_id, required_score): ~~

plot_ppi_enrichment(string_ids, file, sliceWindow, edgeWindow, windowExtendedReferenceThreshold, m ~~

map(my_data_frame, my_data_frame_id_col_names, takeFirst, removeUnmappedRows, quiet): ~~

load(): ~~

get_term_proteins(term_ids, string_ids, enableIEA): ~~

get_summary(string_ids): ~~

get_subnetwork(string_ids): ~~

get_ppi_enrichment_full(string_ids, sliceWindow, edgeWindow, windowExtendedReferenceThreshold, gro ~~

get_ppi_enrichment(string_ids): ~~

get_proteins(): ~~

get_enrichment_figure(string_ids, category="Process", file, output_format="image", group_by_simila ~~

get_png(string_ids, required_score, network_flavor, file, payload_id, output_format, network_term_i ~~

get_neighbors(string_ids): ~~

get_interaction_partners(string_ids, required_score, limit): ~~

get_link(string_ids, required_score, network_flavor, payload_id, network_term_id, hide_node_labels ~~

get_interactions(string_ids): ~~

get_homologs_besthits(string_ids, symbets, target_species_id, bitscore_threshold): ~~

get_homologs(string_ids, target_species_id, bitscore_threshold): ~~

get_graph(): ~~

`get_enrichment(string_ids, category, methodMT, iea)`: ~~

`get_clusters(string_ids, algorithm)`: ~~

`get_annotations_desc()`: ~~

`get_annotations()`: ~~

`load_all()`: ~~

`initialize(...)`: ~~

`add_proteins_description(screen)`: ~~

`add_diff_exp_color(screen, logFcColStr)`: ~~

`show()`: ~~

Author(s)

Andrea Franceschini and Damian Szklarczyk

References

Szklarczyk D, Kirsch R, Koutrouli M, Nastou K, Mehryary F, Hachilif R, Gable AL, Fang T, Doncheva NT, Pyysalo S, Bork P, Jensen LJ, von Mering C. The STRING database in 2023: protein-protein association networks and functional enrichment analyses for any sequenced genome of interest. Nucleic Acids Res. 2023 Jan 6;51(D1):D638-D646. doi: 10.1093/nar/gkac1000.

Examples

```
showClass("STRINGdb")
```

Index