Package ‘STRINGdb’

October 2, 2023

Type Package
Title STRINGdb - Protein-Protein Interaction Networks and Functional Enrichment Analysis
Version 2.12.1
Date 2020-01-10
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Description The STRINGdb package provides a R interface to the STRING protein-protein interactions database (https://string-db.org).
License GPL-2
Depends R (&gt;= 2.14.0)
Imports png, sqldf, plyr, igraph, RCurl, methods, RColorBrewer,
gplots, hash, plotrix
Suggests RUnit, BiocGenerics
biocViews Network
git_url https://git.bioconductor.org/packages/STRINGdb
git_branch RELEASE_3_17
git_last_commit 843ae6a
git_last_commit_date 2023-08-08
Date/Publication 2023-10-01

R topics documented:

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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

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

**Arguments**

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

- **logFcColStr**
  - name of the column that contains the logFC of the expression

**Value**

- vector containing the colors

**Author(s)**

Andrea Franceschini

---

**Description**

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

**Usage**

```r
## 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**

**Description**
coefficient of variation

**Usage**
coeffOfvar(x)

**Arguments**
x input number

**Details**
coefficient of variation

**Value**
coefficient of variation

**Author(s)**
Andrea Franceschini

---

**delColDf**

**Description**
delete a column in the data frame

**Usage**
delColDf(df, colName)

**Arguments**

<table>
<thead>
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</thead>
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<tr>
<td>df</td>
<td>data frame</td>
</tr>
<tr>
<td>colName</td>
<td>name of the column to be deleted</td>
</tr>
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**Value**
data frame
**diff_exp_example1**

**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**
```r
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**

---

**downloadAbsentFile**  *downloadAbsentFile*

**Description**
download a file only if it is not present.

**Usage**
```r
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 the STRING alias table.

Usage

## S4 method for signature 'STRINGdb'
get_aliases()

Value

a data frame containing the STRING alias table

Author(s)

Andrea Franceschini
**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**

```r
## 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**

**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**

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

**Value**

data frame with the description of every STRING annotation term.

**Author(s)**

Andrea Franceschini
Description

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

Usage

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

Value

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

Author(s)

Andrea Franceschini

Description

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

Usage

```r
## 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

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

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**


**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**

**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**

```r
## 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

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

Usage
```r
## 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.

Author(s)
Andrea Franceschini

get_link

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

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

Arguments
- `string_ids`: a vector of STRING identifiers.
- `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", "confidence" or "actions". default "evidence").
- `payload_id`: an identifier of payload data on the STRING server (see method post_payload for additional informations)
Value
short link to the network page of our STRING website that shows the protein interactions between
the input identifiers.

Author(s)
Andrea Franceschini

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

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.
**get_png**

**Value**

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

**Author(s)**

Andrea Franceschini

---

**Description**

Returns a png image of a STRING protein network with the given identifiers.

**Usage**

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

**Arguments**

- `string_ids`: a vector of STRING identifiers.
- `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", "confidence" or "actions". default "evidence").
- `file`: file where to save the image
- `payload_id`: identifier of the payload

**Value**

Returns a png image of a STRING protein network with the given identifiers.

**Author(s)**

Andrea Franceschini
**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**

```r
## 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**

**Description**

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

**Usage**

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

**Value**

STRING proteins data frame.

**Author(s)**

Andrea Franceschini
get_subnetwork

**Description**

Returns the subgraph generated by the given input proteins.

**Usage**

```r
## 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

**Description**

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

**Usage**

```r
## 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

```r
## 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

```r
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
Description

Downloads and returns the STRING network (the network is set also in the graph variable of the STRING_db object).

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

```r
## 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

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

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

Author(s)

Andrea Franceschini
Description

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

Usage

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

Arguments

- `my_data_frame` data frame provided as input.
- `my_data_frame_id_col_names` vector containing 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.

Value

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

Author(s)

Andrea Franceschini

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

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**

### Description

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

#### Usage

```r
## 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**

### 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

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

Description

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

Usage

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

Arguments

interactions_dataframe
   a data frame containing 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
**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**

**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.

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

- background_vector: vector of STRING protein identifiers

Author(s)

Andrea Franceschini

Description

The R package STRINGdb provides a convenient interface to the STRING protein-protein interactions database for the R/biocductor users. Please look at the manual/vignette to get 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 various evidences. STRING is regularly updated, the latest version 9.05 contains information on 5 millions proteins from more than 1100 species. The STRING web interface is freely accessible at: http://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, minVal): ~~
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): ~~
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get_ppi_enrichment_full(string_ids, sliceWindow, edgeWindow, windowExtendedReferenceThreshold, growingWindowLimit): ~~
get_ppi_enrichment(string_ids): ~~
get_proteins(): ~~
get_png(string_ids, required_score, network_flavor, file, payload_id): ~~
get_neighbors(string_ids): ~~
get_link(string_ids, required_score, network_flavor, payload_id): ~~
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
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See Also

http://stitch-db.org

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