

# STRINGdb Package Vignette

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## 1 INTRODUCTION

STRING (<https://www.string-db.org>) is a database of known and predicted protein-protein interactions. The interactions include direct (physical) and indirect (functional) associations. The database 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 v12.5 covers 59.3 million proteins from 12,535 organisms and more than 28 billion interactions. It also provides directed regulatory networks alongside the functional and physical networks.

As you will learn in this guide, the STRING database can be useful to add meaning to lists of genes, for example the best hits coming out from a screen or the most differentially expressed genes coming out from a microarray or RNA-seq experiment.

We provide the STRINGdb R package in order to facilitate our users in accessing the STRING database from R. In this guide we explain, with examples, most of the package's features and functionalities.

In the STRINGdb R package we use the new ReferenceClasses of R (search for "ReferenceClasses" in the R documentation.). Besides we make use of the iGraph package (<http://igraph.sourceforge.net>) as a data structure to represent our protein-protein interaction network.

To begin, you should first know the NCBI taxonomy identifiers of the organism on which you have performed the experiment (e.g. 9606 for Human, 10090 for mouse). If you don't know that, you can search the NCBI Taxonomy (<http://www.ncbi.nlm.nih.gov/taxonomy>) or start looking at our species table (that you can also use to verify that your organism is represented in the STRING database).

Hence, if your species is not Human (i.e. our default species), you can find it and their taxonomy identifiers on STRING webpage under the 'organisms' section ([https://string-db.org/cgi/input.pl?input\\_page\\_active\\_form=org](https://string-db.org/cgi/input.pl?input_page_active_form=org)) or download the full list in the download section of STRING website.

```
> library(STRINGdb)
> string_db <- STRINGdb$new( version="12.5", species=9606,
+                             score_threshold=400, network_type="full", link_data="detailed", input_data="full")
```

As it has been shown in the above commands, you start instantiating the STRINGdb reference class. In the constructor of the class you can also define the STRING version to be used and a threshold for the combined scores of the interactions, such that any interaction below that threshold is not loaded in the object (by default the score threshold is set to 400).

You can also specify the network type "full" (or its alias "functional") for the full functional STRING network, "physical" for the physical subnetwork, or "regulatory" for the directed regulatory subnetwork. In a regulatory network, an edge points from the regulator to its target. Use `network_flavor="typed"` with a full/functional network to show the typed network view in the STRING web interface; this view is not available for a regulatory network. The optional `typed_physical_edges`, `typed_regulatory_edges`, and `show_regulatory_signs` arguments select which typed-edge details are shown.

Besides, if you specify a local directory to the parameter `input-directory`, the database files will be downloaded into this directory and most of the methods can be used off-line. Otherwise, the database files will be saved and cached in a temporary directory that will be cleaned automatically when the R session is closed. By setting `link_data="detailed"` we also load the evidence score columns, such as the experimental score, in addition to the combined score.

For a better understanding of the package two other commands can be useful:

```
> STRINGdb$methods()           # To list all the methods available.

[1] ".objectPackage"           ".objectParent"
[3] "add_diff_exp_color"       "add_proteins_description"
[5] "benchmark_ppi"           "benchmark_ppi_pathway_view"
[7] "callSuper"               "copy"
[9] "enrichment_heatmap"      "export"
[11] "field"                   "get_aliases"
[13] "get_annotations"         "get_bioc_graph"
[15] "get_clusters"            "get_enrichment"
[17] "get_enrichment_figure"   "get_geneset_description"
[19] "get_graph"               "get_homologs"
[21] "get_homologs_besthits"    "get_homology_graph"
[23] "get_interaction_partners" "get_interactions"
[25] "get_link"                "get_neighbors"
[27] "get_paralogs"            "get_pathways_benchmarking_blackList"
[29] "get_png"                 "get_ppi_enrichment"
[31] "get_ppi_enrichment_full" "get_proteins"
[33] "get_pubmed"              "get_pubmed_interaction"
[35] "get_subnetwork"          "get_summary"
[37] "get_term_proteins"        "getClass"
[39] "getRefClass"             "import"
[41] "initFields"              "initialize"
[43] "load"                    "load_all"
[45] "map"                     "mp"
[47] "plot_network"            "plot_ppi_enrichment"
[49] "post_payload"            "ppi_enrichment"
[51] "remove_homologous_interactions" "set_background"
[53] "show"                    "show#envRefClass"
[55] "trace"                   "untrace"
[57] "usingMethods"
```

```
> STRINGdb$help("get_graph")   # To visualize their documentation.
```

```
Call:
$get_graph()
```

#### Description:

Return an igraph object with the entire STRING network.  
We invite the user to use the functions of the iGraph package to conveniently search/analyze the network.

#### 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).
get_subnetwork(string_ids)   # returns a subgraph from the given input proteins
```

#### Author(s):

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For all the methods that we are going to explain below, you can always use the help function in order to get additional information/parameters with respect to those explained in this guide.

As an example, we use the analyzed data of a microarray study taken from GEO (Gene Expression Omnibus, GSE9008). This study investigates the activity of Resveratrol, a natural phytoestrogen found in red wine and a variety of plants, in A549 lung cancer cells. Microarray gene expression profiling after 48 hours exposure to Resveratrol has been performed and compared to a control composed by A549 lung cancer cells treated only with ethanol. This data is already analyzed for differential expression using the limma package: the genes are sorted by *fdr* corrected *p*values and the log fold change of the differential expression is also reported in the table.

```
> data(diff_exp_example1)
> head(diff_exp_example1)
```

|   | pvalue    | logFC    | gene         |
|---|-----------|----------|--------------|
| 1 | 0.0001018 | 3.333461 | VSTM2L       |
| 2 | 0.0001392 | 3.822383 | TBC1D2       |
| 3 | 0.0001720 | 3.306056 | LENG9        |
| 4 | 0.0001739 | 3.024605 | TMEM27       |
| 5 | 0.0001990 | 3.854414 | LOC100506014 |
| 6 | 0.0002393 | 3.082052 | TSPAN1       |

As a first step, we map the gene names to the STRING database identifiers using the "map" method. In this particular example, we map from gene HUGO names, but our mapping function supports several other common identifiers (e.g. Entrez GeneID, ENSEMBL proteins, RefSeq transcripts ... etc.).

The map function adds an additional column with STRING identifiers to the dataframe that is passed as first parameter.

```
> example1_mapped <- string_db$map( diff_exp_example1, "gene", removeUnmappedRows = TRUE )
```

```
Warning: we couldn't map to STRING 15% of your identifiers
```

As you may have noticed, the previous command prints a warning showing the number of genes that we failed to map. In this particular example, we cannot map all the probes of the microarray that refer to position of the chromosome that are not assigned to a real gene (i.e. all the LOC genes). If we remove all these LOC genes before the mapping we obtain a much lower percentage of unmapped genes (i.e. < 6 %).

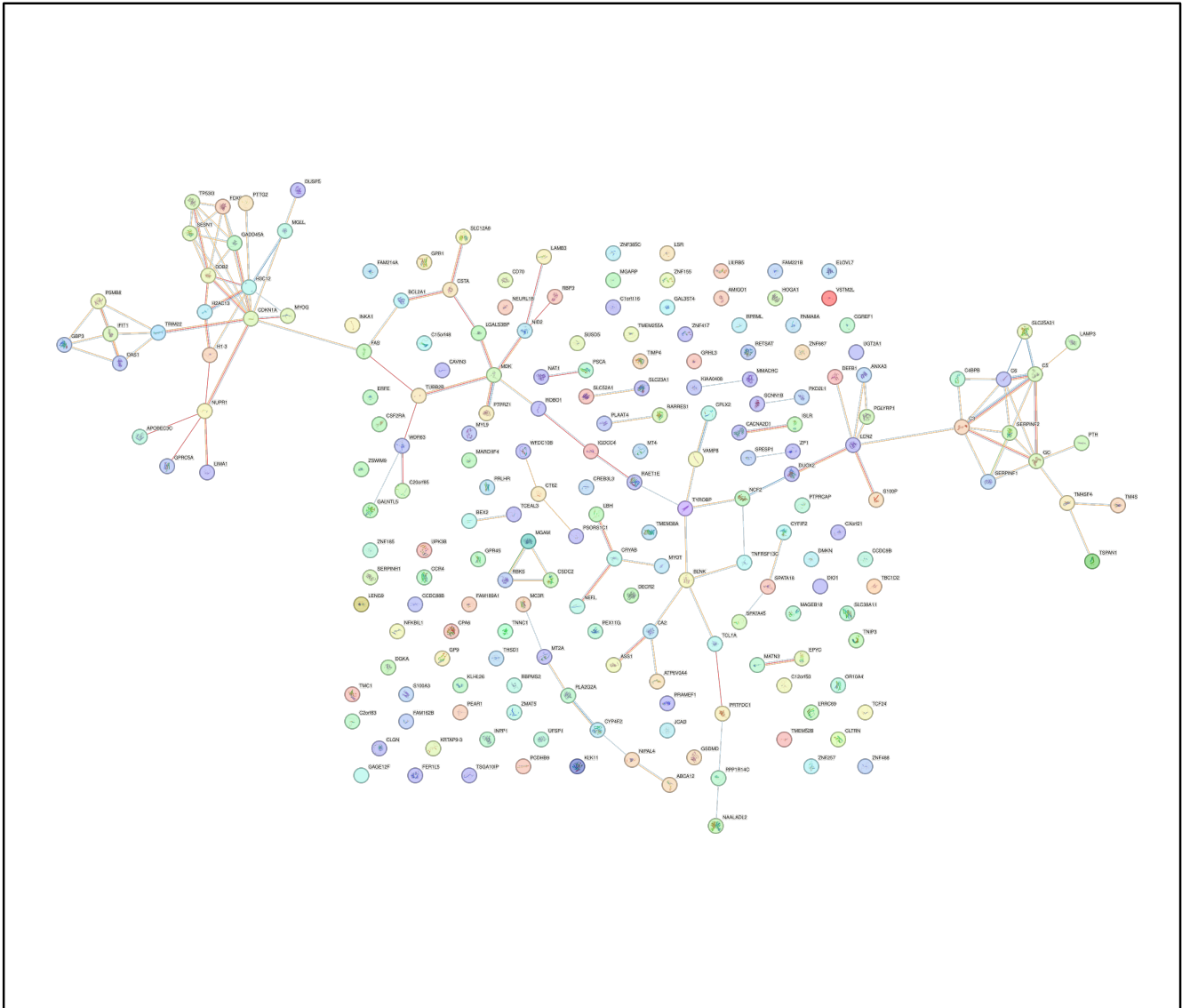
If you set to FALSE the "removeUnmappedRows" parameter, than the rows which corresponds to unmapped genes are left and you can manually inspect them.

Finally, we extract the genes with p-value < 0.05 and, for the examples below, we focus on the top 200 genes sorted by p-value. The image shows clearly the genes and how they are possibly functionally related. On the top of the plot, we insert a pvalue that represents the probability that you can expect such an equal or greater number of interactions by chance.

```
> example1_mapped_pval05 <- subset(example1_mapped, pvalue < 0.05)
> example1_mapped_pval05 <- example1_mapped_pval05[order(example1_mapped_pval05$pvalue), ]
> hits <- example1_mapped_pval05$STRING_id[1:200]

> string_db$plot_network( hits )
```

proteins: 200  
interactions: 127  
expected interactions: 77 (p-value: 1.19e-07)



If you want more control over the appearance of the network image, the `get_png` and `get_link` methods expose additional styling options. In particular, you can switch between **evidence** and **confidence** edge styles, hide node labels, hide disconnected proteins, disable the structure pictures inside bubbles, use the flat node design, center node labels, and change the label font size.

## 2 PAYLOAD MECHANISM

This R library provides the ability to interact with the STRING payload mechanism. The payload appears as an additional colored "halo" around the bubbles.

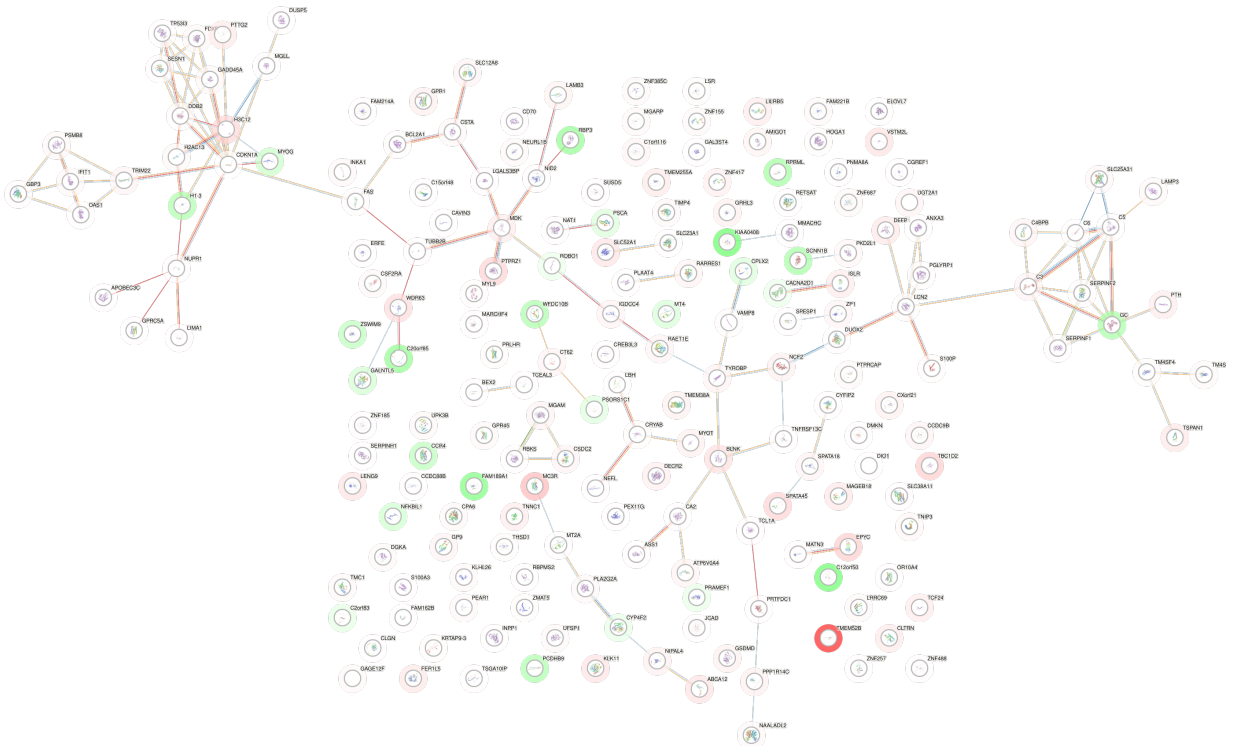
For example, this allows to color in green the genes that are down-regulated and in red the genes that are up-regulated. For this mechanism to work, we provide a function that posts the information on our web server.

```
> # filter by p-value and add a color column
> # (i.e. green down-regulated genes and red for up-regulated genes)
> example1_mapped_pval05 <- string_db$add_diff_exp_color( subset(example1_mapped, pvalue<0.05),
+                                                         logFcColStr="logFC" )

> # post payload information to the STRING server
> payload_id <- string_db$post_payload( example1_mapped_pval05$STRING_id,
+                                     colors=example1_mapped_pval05$color )

> # display a STRING network png with the "halo"
> string_db$plot_network( hits, payload_id=payload_id )
```

proteins: 200  
interactions: 127  
expected interactions: 77 (p-value: 1.19e-07)



### 3 ENRICHMENT

We provide a method to compute the enrichment in Gene Ontology (Process, Function and Component), KEGG and Reactome pathways, PubMed publications, UniProt Keywords, and PFAM/INTERPRO/SMART domains for your set of proteins all in one simple call. The enrichment itself is computed using an hypergeometric test and the FDR is calculated using Benjamini-Hochberg procedure.

```
> enrichment <- string_db$get_enrichment( hits )
> head(enrichment, n=20)
```

|    | category     | term          | number_of_genes | number_of_genes_in_background |
|----|--------------|---------------|-----------------|-------------------------------|
| 1  | COMPARTMENTS | GOCC:0005576  | 44              | 1948                          |
| 2  | COMPARTMENTS | GOCC:1903561  | 19              | 552                           |
| 3  | Process      | GO:0006952    | 35              | 1486                          |
| 4  | Component    | GO:0070062    | 42              | 2045                          |
| 5  | Component    | GO:1903561    | 43              | 2075                          |
| 6  | Component    | GO:0005615    | 54              | 3120                          |
| 7  | Component    | GO:0005576    | 64              | 3988                          |
| 8  | TISSUES      | BT0:0000392   | 11              | 187                           |
| 9  | Keyword      | KW-0732       | 58              | 3506                          |
| 10 | Keyword      | KW-0964       | 28              | 1274                          |
| 11 | Keyword      | KW-1015       | 46              | 2493                          |
| 12 | PMID         | PMID:39331229 | 6               | 8                             |
| 13 | Hallmark     | M5939         | 11              | 198                           |

|    | ncbiTaxonId |
|----|-------------|
| 1  | 9606        |
| 2  | 9606        |
| 3  | 9606        |
| 4  | 9606        |
| 5  | 9606        |
| 6  | 9606        |
| 7  | 9606        |
| 8  | 9606        |
| 9  | 9606        |
| 10 | 9606        |
| 11 | 9606        |
| 12 | 9606        |
| 13 | 9606        |

```
1
2
3
4
5
6
7 9606. ENSP00000008938,9606. ENSP00000014914,9606. ENSP00000187762,9606. ENSP00000216286,9606. ENSP00000
8
9
10
11
12
13
```

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```

```

PGLYRP1,GPRC5A,TMEM38A,NID2,C5,RARRES1,C4BPB,C3,ISLR,SERPINF1,THSD1,LGALS3BP,C6,VAMP8,CSTA,ANXA3,Z
PGLYRP1,NID2,CYP4F2,C5,C4BPB,ISLR,SERPINF1,THSD1,EPYC,TYROBP,C6,L

```

|    | p_value  | fdr     |
|----|----------|---------|
| 1  | 4.08e-07 | 0.00070 |
| 2  | 5.33e-06 | 0.00460 |
| 3  | 3.22e-06 | 0.03970 |
| 4  | 8.59e-06 | 0.00920 |
| 5  | 5.23e-06 | 0.00920 |
| 6  | 4.46e-05 | 0.01580 |
| 7  | 6.79e-05 | 0.02000 |
| 8  | 5.42e-06 | 0.00490 |
| 9  | 7.58e-05 | 0.02220 |
| 10 | 1.10e-04 | 0.02220 |
| 11 | 4.35e-05 | 0.02220 |
| 12 | 2.69e-09 | 0.01380 |
| 13 | 9.06e-06 | 0.00045 |

```

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```

```

(2024) Identification of BBC3 as a novel indicator for predicting prostate cancer development and

```

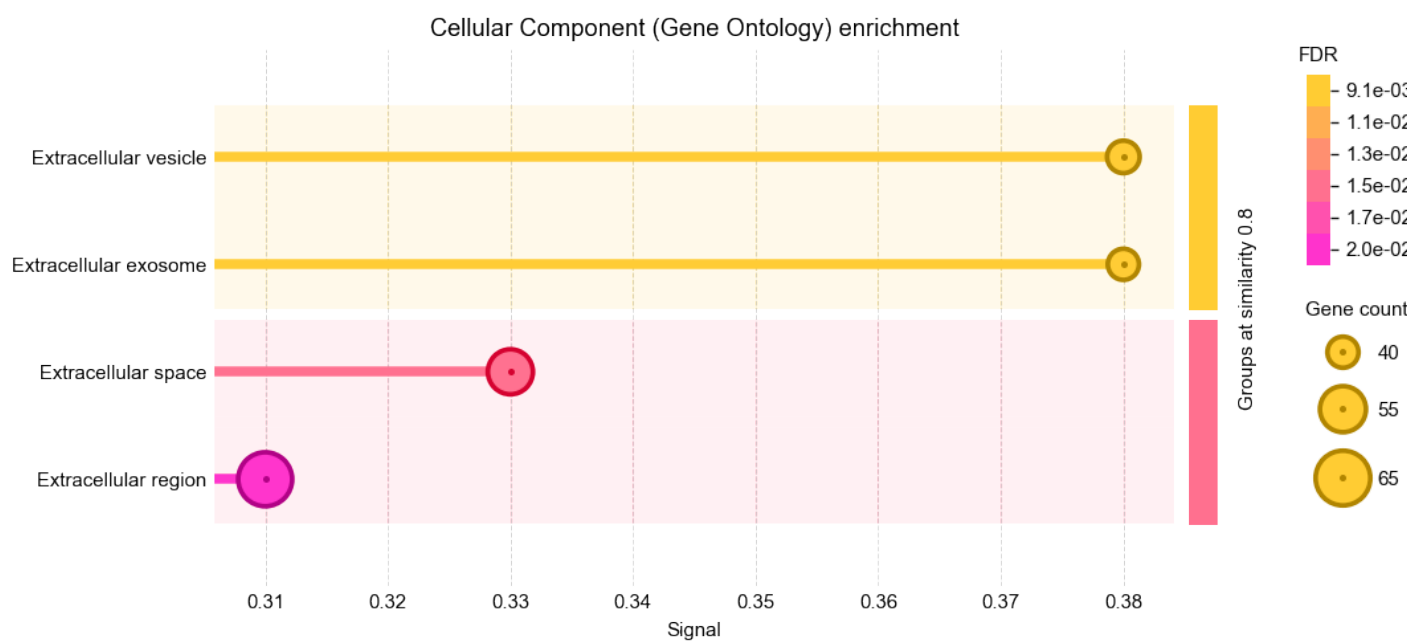
You can also retrieve an enrichment figure directly from STRING for a selected category. The image can be returned as a PNG array or as SVG markup, and you can customize the category, similarity-based grouping, color palette, the number of terms shown, and the variable displayed on the X-axis.

```

> enrichment_img <- string_db$get_enrichment_figure(
+   hits,

```

```
+   category = "Component",
+   group_by_similarity = 0.8,
+   color_palette = "yellow_pink",
+   x_axis = "signal"
+ )
> grid::grid.newpage()
> grid::grid.raster(enrichment_img, interpolate = FALSE)
```



If you have performed your experiment on a predefined set of proteins, it is important to run the enrichment statistics using that set as a background (otherwise you would get a wrong p-value!). Hence, before to launch the method above, you may want to set the background:

```
> backgroundV <- example1_mapped$STRING_id
> string_db$set_background(backgroundV)

IGRAPH 0e27587 UN-- 17440 1990788 --
+ attr: name (v/c), neighborhood (e/n), fusion (e/n), cooccurrence
| (e/n), coexpression (e/n), experimental (e/n), database (e/n),
| textmining (e/n), combined_score (e/n)
+ edges from 0e27587 (vertex names):
[1] 9606.ENSP00000000233--9606.ENSP00000054666
[2] 9606.ENSP00000000233--9606.ENSP00000158762
[3] 9606.ENSP00000000233--9606.ENSP00000160827
[4] 9606.ENSP00000000233--9606.ENSP00000216446
[5] 9606.ENSP00000000233--9606.ENSP00000217402
[6] 9606.ENSP00000000233--9606.ENSP00000219479
+ ... omitted several edges
```

If you already have a `STRINGdb` object, calling `set_background` is sufficient and you do not need to instantiate a new object again. Passing `backgroundV` to the constructor is simply an alternative when you already know the background at initialization time:

```
> string_db <- STRINGdb$new( score_threshold=400, backgroundV = backgroundV )
```

Once the background has been set, the enrichment results can change substantially because the statistical test is now performed against the selected background rather than the whole proteome. In many cases the enrichment signals become smaller, which is expected: the test is now calibrated against the proteins that were actually measurable or considered in the experiment, rather than against all proteins in the organism.

```
> enrichment_background_corrected <- string_db$get_enrichment( hits )
> head(enrichment_background_corrected, n=20)
```

|   | category     | term          | number_of_genes | number_of_genes_in_background |
|---|--------------|---------------|-----------------|-------------------------------|
| 1 | COMPARTMENTS | GOCC:0005576  | 44              | 1867                          |
| 2 | COMPARTMENTS | GOCC:1903561  | 19              | 541                           |
| 3 | TISSUES      | BT0:0000392   | 11              | 183                           |
| 4 | PMID         | PMID:39331229 | 6               | 8                             |
| 5 | Hallmark     | M5939         | 11              | 196                           |

```
ncbiTaxonId
```

```
1 9606
2 9606
3 9606
4 9606
5 9606
```

```
1 9606.ENSP00000008938,9606.ENSP00000014914,9606.ENSP00000216286,9606.ENSP00000223642,9606.ENSP00000000000
2
3
4
5
```

```

1 PGLYRP1,GPRC5A,NID2,C5,RARRES1,C4BPB,C3,ISLR,SERPINF1,THSD1,LGALS3BP,C6,VAMP8,CSTA,ANXA3,ZP1,CA2,TI
2
3
4
5
    p_value    fdr
1 3.26e-06 0.0056
2 2.12e-05 0.0181
3 1.35e-05 0.0117
4 5.45e-09 0.0197
5 2.47e-05 0.0012

1
2
3
4 (2024) Identification of BBC3 as a novel indicator for predicting prostate cancer development and c
5

```

If you just want to know which terms are assigned to your set of proteins, and not necessarily which ones are enriched, you can use "get\_annotations" method. This method outputs the terms from most categories (the exceptions are KEGG terms due to licensing issues and PubMed due to the size of the output) that are associated with your set of proteins.

```

> annotations <- string_db$get_annotations( hits )
> head(annotations, n=20)

```

|    | category     | term_id      | number_of_genes | ratio_in_set | species |
|----|--------------|--------------|-----------------|--------------|---------|
| 1  | COMPARTMENTS | GOCC:0000139 | 2               | 0.010        | 9606    |
| 2  | COMPARTMENTS | GOCC:0000151 | 2               | 0.010        | 9606    |
| 3  | COMPARTMENTS | GOCC:0000323 | 6               | 0.030        | 9606    |
| 4  | COMPARTMENTS | GOCC:0000502 | 1               | 0.005        | 9606    |
| 5  | COMPARTMENTS | GOCC:0000785 | 1               | 0.005        | 9606    |
| 6  | COMPARTMENTS | GOCC:0000791 | 1               | 0.005        | 9606    |
| 7  | COMPARTMENTS | GOCC:0001533 | 1               | 0.005        | 9606    |
| 8  | COMPARTMENTS | GOCC:0001650 | 1               | 0.005        | 9606    |
| 9  | COMPARTMENTS | GOCC:0001669 | 1               | 0.005        | 9606    |
| 10 | COMPARTMENTS | GOCC:0001725 | 2               | 0.010        | 9606    |
| 11 | COMPARTMENTS | GOCC:0001726 | 2               | 0.010        | 9606    |
| 12 | COMPARTMENTS | GOCC:0005576 | 44              | 0.220        | 9606    |
| 13 | COMPARTMENTS | GOCC:0005577 | 1               | 0.005        | 9606    |
| 14 | COMPARTMENTS | GOCC:0005579 | 3               | 0.015        | 9606    |
| 15 | COMPARTMENTS | GOCC:0005581 | 1               | 0.005        | 9606    |
| 16 | COMPARTMENTS | GOCC:0005604 | 2               | 0.010        | 9606    |
| 17 | COMPARTMENTS | GOCC:0005610 | 1               | 0.005        | 9606    |
| 18 | COMPARTMENTS | GOCC:0005615 | 23              | 0.115        | 9606    |
| 19 | COMPARTMENTS | GOCC:0005622 | 102             | 0.510        | 9606    |
| 20 | COMPARTMENTS | GOCC:0005634 | 34              | 0.170        | 9606    |

```

1

```

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9  
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12  
13  
14  
15  
16  
17  
18  
19 9606. ENSP00000008938, 9606. ENSP00000078445, 9606. ENSP00000187762, 9606. ENSP00000219481, 9606. ENSP00000

20  
  
1  
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3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19 PGLYRP1, CREB3L3, TMEM38A, DECR2, PEX11G, CYP4F2, BLNK, TNNC1, MYOT, MYOG, H1-3, C3, ISLR, PLAAT4, DDB2, THSD1, TU

20  
  
1  
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3  
4  
5  
6  
7  
8  
9  
10

description  
Golgi membrane  
Ubiquitin ligase complex  
Lytic vacuole  
Proteasome complex  
Chromatin  
Euchromatin  
Cornified envelope  
Fibrillar center  
Acrosomal vesicle  
Stress fiber

```

11                               Ruffle
12           Extracellular region
13           Fibrinogen complex
14           Membrane attack complex
15           Collagen trimer
16           Basement membrane
17           laminin-5 complex
18           Extracellular space
19 Intracellular anatomical structure
20                               Nucleus

```

## 4 CLUSTERING

The iGraph package provides several clustering/community algorithms: "fastgreedy", "walktrap", "springlass", "edge.betweenness". We encapsulate this in an easy-to-use function that returns the clusters in a list.

```

> # get clusters
> clustersList <- string_db$get_clusters(example1_mapped_pval05$STRING_id[1:600])

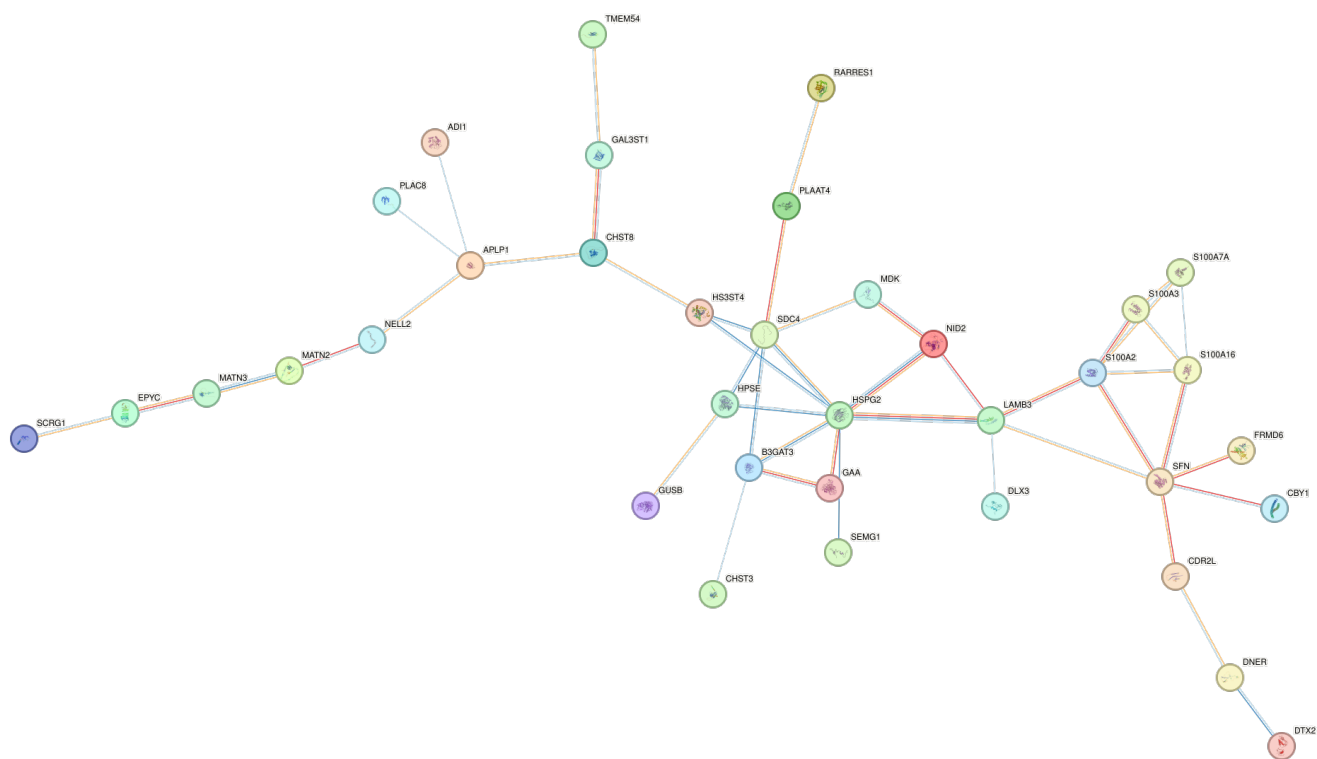
```

Now we visualize the first four clusters one by one.

```

> par(mar = c(0, 0, 0.5, 0))
> string_db$plot_network(clustersList[[1]], add_summary = FALSE)
> par(mar = c(0, 0, 0.5, 0))
> string_db$plot_network(clustersList[[2]], add_summary = FALSE)
> par(mar = c(0, 0, 0.5, 0))
> string_db$plot_network(clustersList[[3]], add_summary = FALSE)
> par(mar = c(0, 0, 0.5, 0))
> string_db$plot_network(clustersList[[4]], add_summary = FALSE)

```



## 5 ADDITIONAL PROTEIN INFORMATION

You can get a table that contains all the proteins that are present in our database of the species of interest. The protein table also includes the preferred name, the size and a short description of each protein.

```
> string_proteins <- string_db$get_proteins()
> head(string_proteins)
```

|   | protein_external_id  | preferred_name | protein_size |
|---|----------------------|----------------|--------------|
| 1 | 9606.ENSP00000000233 | ARF5           | 180          |
| 2 | 9606.ENSP00000000412 | M6PR           | 277          |
| 3 | 9606.ENSP00000001008 | FKBP4          | 459          |
| 4 | 9606.ENSP00000001146 | CYP26B1        | 512          |
| 5 | 9606.ENSP00000002125 | NDUFAF7        | 441          |
| 6 | 9606.ENSP00000002165 | FUCA2          | 467          |

```
1
2
3 Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed; Immunophilin protein with PPIase
4 Cytochrome P450 26B1; Involved in the metabolism of retinoic acid (RA), rendering this classical mo
5
6
```

In the following section we will show how to query STRING with R on some specific proteins. In the examples, we will use the famous tumor proteins TP53 and ATM .

First we need to get the STRING identifier of those proteins, using our mp method:

```
> tp53 = string_db$mp( "tp53" )
> atm = string_db$mp( "atm" )
> mdm2 = string_db$mp( "mdm2" )
```

The mp method (i.e. map proteins) is an alternative to our map method, to be used when you need to map only one or few proteins.

It takes in input a vector of protein aliases and returns a vector with the STRING identifiers of those proteins.

## 6 TYPED NETWORK VIEWS AND REGULATORY EDGES

The full functional network, physical network, and regulatory network have different edge semantics. The functional and physical networks are undirected, while the regulatory network is directed from regulator to target. Create a separate **STRINGdb** object for each network type that you need; they can use the same cache directory because their downloaded link files have distinct names. The **string\_db** object created above is the functional network object.

```

> functional_db <- string_db
> physical_db <- STRINGdb$new(
+   version = "12.5", species = 9606, score_threshold = 400,
+   network_type = "physical", link_data = "detailed",
+   input_directory = functional_db$input_directory
+ )
> regulatory_db <- STRINGdb$new(
+   version = "12.5", species = 9606, score_threshold = 400,
+   network_type = "regulatory", link_data = "detailed",
+   input_directory = functional_db$input_directory
+ )

```

Use the typed view on the functional object to overlay the physical and regulatory edge types. The three typed-edge arguments control which edge types and regulatory signs are shown:

```

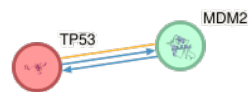
> functional_db$plot_network(
+   c(tp53, mdm2),
+   network_flavor = "typed",
+   typed_physical_edges = TRUE,
+   typed_regulatory_edges = TRUE,
+   show_regulatory_signs = TRUE
+ )

```

proteins: 2

round too large! -- due to technical limitations STRING does not compute PPI enrichment for query and/or background

expected interactions: (p-value: )



For analysis of regulation, use the regulatory object itself. Its interaction table retains direction: **from** is the regulator and **to** is its target. For example, the following retrieves regulatory links within the TP53–MDM2 pair and lists them as **from\_name** -> **to\_name**.

This pair illustrates a well-characterized negative-feedback circuit: TP53 transcriptionally activates MDM2, whereas MDM2 promotes proteasome-dependent degradation of TP53. Both directions are therefore expected in the regulatory graph.

```

> regulatory_edges <- regulatory_db$get_interactions(c(tp53, mdm2))
> regulatory_edges$regulatory_edge <- paste(
+   regulatory_edges$from_name, "->", regulatory_edges$to_name
+ )
> regulatory_edges[, c("regulatory_edge", "combined_score")]

  regulatory_edge combined_score
1      MDM2 -> TP53           997
2      TP53 -> MDM2           996

```

You can retrieve the interactions that connect certain input proteins between each other. The "get\_interactions" method returns a data frame describing the interactions among the queried proteins. The table contains the STRING identifiers in the `from` and `to` columns, the corresponding preferred names in `from_name` and `to_name`, the `combined_score`, and any additional evidence scores available for the current `link_data` setting. This makes it easy to inspect both the interacting proteins and the supporting scores for each interaction.

```

> string_db$get_interactions( c(tp53, atm) )

      from      to combined_score from_name to_name
1 9606.ENSEP00000269305 9606.ENSEP00000278616      999      TP53      ATM
  neighborhood fusion cooccurrence coexpression experimental database textmining
1              0       0             0             0           999      900      954

```

If you want to retrieve the first-shell interaction partners of one or more proteins from the locally loaded graph, you can use the "get\_interaction\_partners" method. The output keeps the same interaction-table structure as "get\_interactions".

```

> string_db$get_interaction_partners( c(tp53, atm), limit=5 )[, c("from", "to", "combined_score", "ex

      from      to combined_score experimental
32004 9606.ENSEP00000269305 9606.ENSEP00000212015      999      999
37406 9606.ENSEP00000269305 9606.ENSEP00000215832      999      999
53636 9606.ENSEP00000269305 9606.ENSEP00000216911      999      999
55816 9606.ENSEP00000269305 9606.ENSEP00000217244      999      999
66287 9606.ENSEP00000269305 9606.ENSEP00000219548      999      999
386993 9606.ENSEP00000278616 9606.ENSEP00000265433      999      999
419128 9606.ENSEP00000278616 9606.ENSEP00000269305      999      999
461927 9606.ENSEP00000278616 9606.ENSEP00000325863      999      992
461988 9606.ENSEP00000278616 9606.ENSEP00000343741      999      972
462088 9606.ENSEP00000278616 9606.ENSEP00000361423      999      999

  from_name to_name
32004      TP53  SIRT1
37406      TP53  MAPK1
53636      TP53  AURKA
55816      TP53 CSNK2A1
66287      TP53  STUB1
386993      ATM   NBN
419128      ATM   TP53

```

|        |     |       |
|--------|-----|-------|
| 461927 | ATM | MRE11 |
| 461988 | ATM | ATR   |
| 462088 | ATM | ABL1  |

You can also output only interactions supported by a particular type of evidence. Here we retrieve only experimentally supported interactions, keeping only the protein names together with the experimental score:

```
> interaction_partners <- string_db$get_interaction_partners( c(tp53, atm), limit=5 )
> interaction_partners_exp <- subset(interaction_partners, experimental > 0,
+                                   select = c("from_name", "to_name", "experimental"))
> interaction_partners_exp
```

|        | from_name | to_name | experimental |
|--------|-----------|---------|--------------|
| 32004  | TP53      | SIRT1   | 999          |
| 37406  | TP53      | MAPK1   | 999          |
| 53636  | TP53      | AURKA   | 999          |
| 55816  | TP53      | CSNK2A1 | 999          |
| 66287  | TP53      | STUB1   | 999          |
| 386993 | ATM       | NBN     | 999          |
| 419128 | ATM       | TP53    | 999          |
| 461927 | ATM       | MRE11   | 992          |
| 461988 | ATM       | ATR     | 972          |
| 462088 | ATM       | ABL1    | 999          |

STRING provides a way to get homologous proteins: in our database we store ALL-AGAINST-ALL alignments within species. You can retrieve all paralogs of the protein using "get\_paralogs" method.

```
> # Get all homologs of TP53 in human.
> string_db$get_paralogs(tp53)
```

|   | ncbiTaxonId_A | stringId_A            | ncbiTaxonId_B | stringId_B            |
|---|---------------|-----------------------|---------------|-----------------------|
| 1 | 9606          | 9606.ENSEP00000269305 | 9606          | 9606.ENSEP00000269305 |
|   | bitscore      |                       |               |                       |
| 1 | 815.8         |                       |               |                       |

STRING also stores best hits (as measured by bitscore) between proteins from different species. "get\_homologs\_bests" lets you retrieve these homologs.

```
> # get the best hits of TP53 in all STRING species
> tp53_bests <- string_db$get_homologs_bests(tp53)
> tp53_bests_100 <- subset(tp53_bests, bitscore > 100)
> nrow(tp53_bests_100)
```

```
[1] 318
```

```
> head(tp53_besthits_100, n=10)
```

|    | ncbiTaxonId_A | stringId_A               | ncbiTaxonId_B | stringId_B                |
|----|---------------|--------------------------|---------------|---------------------------|
| 1  | 9606          | 9606.ENSPPAP000000269305 | 9597          | 9597.ENSPPAP00000011040   |
| 2  | 9606          | 9606.ENSPPAP000000269305 | 9598          | 9598.ENSPPAP00000014836   |
| 3  | 9606          | 9606.ENSPPAP000000269305 | 9606          | 9606.ENSPPAP000000269305  |
| 4  | 9606          | 9606.ENSPPAP000000269305 | 9601          | 9601.ENSPPAP00000008923   |
| 5  | 9606          | 9606.ENSPPAP000000269305 | 61621         | 61621.ENSPPAP00000028632  |
| 6  | 9606          | 9606.ENSPPAP000000269305 | 61622         | 61622.ENSPPAP00000026843  |
| 7  | 9606          | 9606.ENSPPAP000000269305 | 591936        | 591936.ENSPPAP00000010553 |
| 8  | 9606          | 9606.ENSPPAP000000269305 | 60711         | 60711.ENSPPAP00000007551  |
| 9  | 9606          | 9606.ENSPPAP000000269305 | 9541          | 9541.ENSPPAP00000038526   |
| 10 | 9606          | 9606.ENSPPAP000000269305 | 9544          | 9544.ENSPPAP00000011334   |

|    | bitscore |
|----|----------|
| 1  | 815.8    |
| 2  | 815.8    |
| 3  | 815.8    |
| 4  | 799.3    |
| 5  | 786.6    |
| 6  | 786.6    |
| 7  | 785.8    |
| 8  | 785.0    |
| 9  | 783.9    |
| 10 | 783.9    |

... or you can specify the species of interest:

```
> # get the homologs of the following two proteins in the mouse (i.e. species_id=10090)
> string_db$get_homologs_besthits(c(tp53, atm), target_species_id=10090)
```

|   | ncbiTaxonId_A | stringId_A               | ncbiTaxonId_B | stringId_B                |
|---|---------------|--------------------------|---------------|---------------------------|
| 1 | 9606          | 9606.ENSPPAP000000269305 | 10090         | 10090.ENSPPAP000000104298 |
| 2 | 9606          | 9606.ENSPPAP000000278616 | 10090         | 10090.ENSPPAP000000156344 |

|   | bitscore |
|---|----------|
| 1 | 598.2    |
| 2 | 5328.8   |

## 7 CITATION

Please cite:

Szklarczyk D, Nastou K, Koutrouli M, Kirsch R, Mehryary F, Hachilif R, Hu D, Peluso ME, Huang Q, Fang T, Doncheva NT, Pyysalo S, Bork P, Jensen LJ, von Mering C. The STRING database in 2025: protein networks with directionality of regulation. *Nucleic Acids Res.* 2025 Jan 6;53(D1):D730-D737. doi: 10.1093/nar/gkaf1113.