

# Package ‘rTRM’

December 5, 2025

**Type** Package

**Title** Identification of Transcriptional Regulatory Modules from  
Protein-Protein Interaction Networks

**Version** 1.48.0

**Date** 2015-12-25

**Author** Diego Diez

**Depends** R (>= 2.10), igraph (>= 1.0)

**Imports** methods, AnnotationDbi, DBI, RSQLite

**Suggests** RUnit, BiocGenerics, MotifDb, graph, PWMErich, biomaRt,  
Biostrings, BSgenome.Mmusculus.UCSC.mm8.masked, org.Hs.eg.db,  
org.Mm.eg.db, ggplot2, BiocStyle, knitr, rmarkdown

**Maintainer** Diego Diez <diego10ruiz@gmail.com>

**Description** rTRM identifies transcriptional regulatory modules (TRMs)  
from protein-protein interaction networks.

**License** GPL-3

**LazyLoad** yes

**ByteCompile** yes

**VignetteBuilder** knitr

**biocViews** Transcription, Network, GeneRegulation, GraphAndNetwork

**URL** <https://github.com/ddiez/rTRM>

**BugReports** <https://github.com/ddiez/rTRM/issues>

**git\_url** <https://git.bioconductor.org/packages/rTRM>

**git\_branch** RELEASE\_3\_22

**git\_last\_commit** f220f64

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.22

**Date/Publication** 2025-12-04

## Contents

|                          |           |
|--------------------------|-----------|
| rTRM-package             | 2         |
| annotateFreq             | 3         |
| annotateModule           | 4         |
| annotateTRM              | 4         |
| biogrid_hs               | 5         |
| biogrid_mm               | 5         |
| findTRM                  | 6         |
| getAnnotations           | 7         |
| getBiogridData           | 7         |
| getConcentricList        | 8         |
| getLargestComp           | 8         |
| getMaps                  | 9         |
| getMatrices              | 9         |
| getMotifsFromEntrezgene  | 10        |
| getMotifsFromSymbol      | 10        |
| getOrthologFromMatrix    | 11        |
| getOrthologs             | 11        |
| getOrthologsFromBiomart  | 12        |
| getSequencesFromGenome   | 12        |
| getSimilarityMatrix      | 13        |
| getTFclass               | 13        |
| getTFclassFromEntrezgene | 14        |
| getTFterms               | 14        |
| initBiomart              | 15        |
| layout.arc               | 15        |
| layout.concentric        | 16        |
| plotDegree               | 16        |
| plotGraph                | 17        |
| plotTRM                  | 18        |
| plotTRMlegend            | 19        |
| processBiogrid           | 19        |
| removeVertices           | 20        |
| writeTRMreport           | 20        |
| <b>Index</b>             | <b>21</b> |

---

rTRM-package

*Identification transcription regulatory modules (TRMs)*


---

## Description

This package identifies transcriptional regulatory modules (TRMs) from PPI networks.

## Details

Package: rTRM  
 Type: Package  
 Version: 1.0  
 Date: 2013-02-01  
 License: GPL-3

## Author(s)

Diego Diez

Maintainer: Diego Diez <diego10ruiz@gmail.com>

## Examples

```
getAnnotations()
```

---

|              |                                                                        |
|--------------|------------------------------------------------------------------------|
| annotateFreq | <i>Annotate a graph with frequency of nodes/edges in other graphs.</i> |
|--------------|------------------------------------------------------------------------|

---

## Description

Returns an annotated graph with node size and edge width proportional at the number of occurrences of nodes/edges in a supplied list of graphs.

## Usage

```
annotateFreq(g, graph_list)
```

## Arguments

|                         |                                            |
|-------------------------|--------------------------------------------|
| <code>g</code>          | target graph to annotate.                  |
| <code>graph_list</code> | list of graph to extract information from. |

## Details

Commonly `graph_list` refers to a list of predicted TRMs (with `findTRM`) and `g` is the combined TRM. This function annotates the nodes/edges in `g` to know their frequency in the original list of graphs.

## Author(s)

Diego Diez

---

|                |                                                   |
|----------------|---------------------------------------------------|
| annotateModule | <i>Annotate a network module with information</i> |
|----------------|---------------------------------------------------|

---

**Description**

Uses information about expression, enrichment and parent PPI network to annotate a subgraph.

**Usage**

```
annotateModule(g, enrich, trm, targets, ppi, exprs, tfs)
```

**Arguments**

|         |                                                                            |
|---------|----------------------------------------------------------------------------|
| g       | graph to annotate in igraph format.                                        |
| enrich  | list of enriched transcription factors (or motifs).                        |
| trm     | TRM to compare with (to identify bridges).                                 |
| targets | list of target transcription factors (typically those with ChIP-seq data). |
| ppi     | parent PPI network (to check membership of nodes).                         |
| exprs   | list of entrezgene ids representing expressed genes.                       |
| tfs     |                                                                            |

**Author(s)**

Diego Diez

---

|             |                                                                   |
|-------------|-------------------------------------------------------------------|
| annotateTRM | <i>Annotate a network object with information about clusters.</i> |
|-------------|-------------------------------------------------------------------|

---

**Description**

This function takes a network object and includes cluster information as piecolor attribute, suitable to be plotted with plotTRM()

**Usage**

```
annotateTRM(g, target)
```

**Arguments**

|        |                              |
|--------|------------------------------|
| g      | a network object.            |
| target | target node (from findTRM()) |

**Author(s)**

Diego Diez

---

`biogrid_hs`*Network dataset of class 'igraph'*

---

**Description**

Human protein-protein interaction (PPI) dataset from the BioGRID database release .

**Usage**

```
data(biogrid_hs)
```

**Format**

An igraph object.

**Author(s)**

Diego Diez

---

`biogrid_mm`*Network dataset of class 'igraph'*

---

**Description**

Mouse protein-protein interaction (PPI) dataset from the BioGRID database .

**Usage**

```
data(biogrid_mm)
```

**Format**

An igraph object.

**Author(s)**

Diego Diez

---

|         |                                                                                    |
|---------|------------------------------------------------------------------------------------|
| findTRM | <i>Identifies a TRM associated with a target node and one or more query nodes.</i> |
|---------|------------------------------------------------------------------------------------|

---

### Description

This the main function used to identify TRMs. It takes a graph object and use it to search in the neighborhood of a target node for query nodes that are separated a maximum distance (controlled by max.bridge parameter).

### Usage

```
findTRM(g, target, query, method = "nsa", max.bridge = 1, extended = FALSE, strict = FALSE, type = "igraph")
```

### Arguments

|            |                                                                                  |
|------------|----------------------------------------------------------------------------------|
| g          | the network used to identify TRMs (typically a PPI network)                      |
| target     | character variable with the name of a target node.                               |
| query      | character vector with the list of query nodes.                                   |
| method     | method to use.                                                                   |
| max.bridge | maximum number of nodes allowed between the target and query nodes.              |
| extended   | whether to allow distance restrictions to include both target and query nodes.   |
| strict     | whether to return a single component (using decompose.graph())                   |
| type       | type of graph object to return, either an "igraph" (the default) or a "graphNEL" |

### Details

Currently only "first" and "nsa" methods are available. First is used for tests and returns the first neighborhood of the target node. Method "nsa" implements the TRM finding algorithm.

### Value

A network in igraph format or NULL.

### Author(s)

Diego Diez

### Examples

```
# load example network.
load(system.file(package = "rTRM", "extra/example.rda"))

# define target and query nodes.
target = "N6"
query = c("N7", "N12", "N28")

# find TRM:
s = findTRM(g, target = target, query = query, method = "nsa", max.bridge = 1)
```

---

|                |                                                                                 |
|----------------|---------------------------------------------------------------------------------|
| getAnnotations | <i>Obtain the 'pwm' table fromt the database, containing PWM's annotations.</i> |
|----------------|---------------------------------------------------------------------------------|

---

**Description**

Obtain the 'pwm' table fromt the database, containing PWM's annotations.

**Usage**

```
getAnnotations(filter, dbname = NULL)
```

**Arguments**

|        |                                                          |
|--------|----------------------------------------------------------|
| filter | one or more PWM ids.                                     |
| dbname | the location of the database (to load custom databases). |

**Author(s)**

Diego Diez

**Examples**

```
ann = getAnnotations()
```

---

|                |                                                            |
|----------------|------------------------------------------------------------|
| getBiogridData | <i>Downloads network data from BioGRID in TAB2 format.</i> |
|----------------|------------------------------------------------------------|

---

**Description**

This function is used to generate igraph network objects from BioGRID data. It downloads the database into a data.frame object that can be used later with processBiogrid()

**Usage**

```
getBiogridData(release)
```

**Arguments**

|         |                                 |
|---------|---------------------------------|
| release | release of BioGRID to download. |
|---------|---------------------------------|

**Details**

The release to download must be specified as currently there is no way to download automatically the latests release.

**Value**

An data.frame object.

**Author(s)**

Diego Diez

---

|                   |                                                                                            |
|-------------------|--------------------------------------------------------------------------------------------|
| getConcentricList | <i>Returns a list with nodes membership to be used in a graph with a concentric layout</i> |
|-------------------|--------------------------------------------------------------------------------------------|

---

### Description

Specify target and enriched motifs and returns a list with circle membership. This information is used by layout.concentric to position the nodes in plots.

### Usage

```
getConcentricList(g, t, e, max.size = 60, order.by = "label")
```

### Arguments

|          |                                                    |
|----------|----------------------------------------------------|
| g        | graph to layout (extract the nodes).               |
| t        | list of target nodes (will go in the center).      |
| e        | list of enriched nodes (will go in the periphery). |
| max.size | maximum number of nodes per layer.                 |
| order.by | ordering attribute for list before split.          |

### Author(s)

Diego Diez

---

|                |                                             |
|----------------|---------------------------------------------|
| getLargestComp | <i>Gets the largest connected component</i> |
|----------------|---------------------------------------------|

---

### Description

Returns the largest connected component from a graph.

### Usage

```
getLargestComp(g)
```

### Arguments

|   |                   |
|---|-------------------|
| g | an igraph object. |
|---|-------------------|

### Author(s)

Diego Diez

---

|         |                                                                    |
|---------|--------------------------------------------------------------------|
| getMaps | <i>Obtain the mapping between PWM and Entrez Gene identifiers.</i> |
|---------|--------------------------------------------------------------------|

---

**Description**

Obtain the mapping between PWM and Entrez Gene identifiers.

**Usage**

```
getMaps(filter, dbname = NULL)
```

**Arguments**

|        |                                   |
|--------|-----------------------------------|
| filter | vector of PWMs to filter results. |
| dbname |                                   |

**Author(s)**

Diego Diez

**Examples**

```
getMaps()
```

---

|             |                               |
|-------------|-------------------------------|
| getMatrices | <i>Obtain a list of PWMs.</i> |
|-------------|-------------------------------|

---

**Description**

Returns a list of PWMs, by default all the PWMs in the database. Alternatively, filtered by the ids provided by filter.

**Usage**

```
getMatrices(filter, dbname = NULL)
```

**Arguments**

|        |                                 |
|--------|---------------------------------|
| filter | list of PWMs to filter results. |
| dbname |                                 |

**Author(s)**

Diego Diez

**Examples**

```
pwms = getMatrices()
```

---

getMotifsFromEntrezgene

*Retrieve PWMs associated with genes provided as entrezgene identifiers.*

---

**Description**

Retrieve PWMs associated with genes provided as entrezgene identifiers.

**Usage**

```
getMotifsFromEntrezgene(e, organism)
```

**Arguments**

|          |                                                            |
|----------|------------------------------------------------------------|
| e        | vector of entrezgene identifiers to retrieve exiting PWMs. |
| organism | target organism.                                           |

**Author(s)**

Diego Diez

---

getMotifsFromSymbol

*Retrieve PWMs associated with genes provided as symbol.*

---

**Description**

Retrieve PWMs associated with genes provided as symbol.

**Usage**

```
getMotifsFromSymbol(s, organism)
```

**Arguments**

|          |                         |
|----------|-------------------------|
| s        | vector of gene symbols. |
| organism | target organism.        |

**Author(s)**

Diego Diez

---

|                       |                                                                                      |
|-----------------------|--------------------------------------------------------------------------------------|
| getOrthologFromMatrix | <i>Obtain gene identifiers for a target organism associated with a list of PWMs.</i> |
|-----------------------|--------------------------------------------------------------------------------------|

---

**Description**

Obtain gene identifiers for a target organism associated with a list of PWMs.

**Usage**

```
getOrthologFromMatrix(filter, organism = "human", dbname = NULL)
```

**Arguments**

|          |                                        |
|----------|----------------------------------------|
| filter   | vector of matrices to filter results.  |
| organism | target organism.                       |
| dbname   | database- usually not need to specify. |

**Author(s)**

Diego Diez

---

|              |                                                                             |
|--------------|-----------------------------------------------------------------------------|
| getOrthologs | <i>Obtain the mapping to Entrez Gene identifiers in the given organism.</i> |
|--------------|-----------------------------------------------------------------------------|

---

**Description**

Obtain the mapping to Entrez Gene identifiers in the given organism.

**Usage**

```
getOrthologs(filter, organism, dbname = NULL)
```

**Arguments**

|          |                                                                                                                                                                                |
|----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| filter   | entrezgene identifiers for the original mapping (PWM to gene). These can belong to diverse species and correspond to the "entrezgene" column obtained with getMaps() function. |
| organism | target organisms, currently supported "human" and "mouse"                                                                                                                      |
| dbname   |                                                                                                                                                                                |

**Details**

If organism is not specified the entire table of orthologs (with all supported species) is returned.

**Value**

A data.frame object with ortholog information.

**Author(s)**

Diego Diez

**Examples**

```
getOrthologs(organism = "human")
```

---

```
getOrthologsFromBiomart
```

*Returns ortholog genes for a target organism*

---

**Description**

Returns ortholog genes for a target organism

**Usage**

```
getOrthologsFromBiomart(eg, target_org, mart)
```

**Arguments**

|            |                                             |
|------------|---------------------------------------------|
| eg         | list of entrezgene ids to obtain orthologs. |
| target_org | target organism.                            |
| mart       | mart object.                                |

**Author(s)**

Diego Diez

---

```
getSequencesFromGenome
```

*Retrieves a set of sequences from a BSgenome object and optionally appends a label to each sequence id.*

---

**Description**

This is just a wrapper to getSeq() in package Biostrings that facilitates adding a label to each sequence.

**Usage**

```
getSequencesFromGenome(BED, genome, append.id)
```

**Arguments**

|           |                                               |
|-----------|-----------------------------------------------|
| BED       | file with peak locations in BED format.       |
| genome    | a BSgenome object (e.g. Mmusculus)            |
| append.id | optional label to append to each sequence id. |

**Author(s)**

Diego Diez

---

|                     |                                                     |
|---------------------|-----------------------------------------------------|
| getSimilarityMatrix | <i>Compute similarity matrix of list of graphs.</i> |
|---------------------|-----------------------------------------------------|

---

**Description**

This function computes pair-wise similarity based on common nodes (default) or edges between the graphs passed as a list.

**Usage**

```
getSimilarityMatrix(g_list, type = "edges")
```

**Arguments**

|                     |                                                    |
|---------------------|----------------------------------------------------|
| <code>g_list</code> | list of graph objects.                             |
| <code>type</code>   | type of similarity, either node or edge (default). |

**Author(s)**

Diego Diez

---

|            |                                                                                             |
|------------|---------------------------------------------------------------------------------------------|
| getTFclass | <i>Return the ontology in the TFclass database associated with an entrezgene identifier</i> |
|------------|---------------------------------------------------------------------------------------------|

---

**Description**

Return the ontology in the TFclass database associated with an entrezgene identifier.

**Usage**

```
getTFclass(dbname = NULL)
```

**Arguments**

|                     |                                 |
|---------------------|---------------------------------|
| <code>dbname</code> | SQLite file to use as database. |
|---------------------|---------------------------------|

**Author(s)**

Diego Diez

getTFclassFromEntrezgene

*Applies getTFclass sequentially to a vector of entrezgene identifiers.*

---

### Description

Applies getTFclass sequentially to a vector of entrezgene identifiers.

### Usage

```
getTFclassFromEntrezgene(x, subset = "Class", tfclass, dbname = NULL)
```

### Arguments

|         |                                                                           |
|---------|---------------------------------------------------------------------------|
| x       | vector of entrezgene identifiers.                                         |
| subset  | level in the ontology (subset in TFclass terminology. By default "Class") |
| tfclass | data.frame with tfclass data to pass to the recursive function.           |
| dbname  | SQLite file to use as database.                                           |

### Author(s)

Diego Diez

---

getTFterms

*Get terms associated with a specified TFclass subset.*

---

### Description

Returns a vector of names (not ids) with the members of a particular subset in the TFclass database.  
By default it returns the Class subset.

### Usage

```
getTFterms(subset = "Class", dbname = NULL)
```

### Arguments

|        |                                      |
|--------|--------------------------------------|
| subset | a subset in TFclass (default Class). |
| dbname | SQLite file to use as database.      |

### Author(s)

Diego Diez

---

|             |                                                            |
|-------------|------------------------------------------------------------|
| initBiomart | <i>Initializes mart objects to identify ortholog genes</i> |
|-------------|------------------------------------------------------------|

---

**Description**

Initializes mart objects to identify ortholog genes

**Usage**

```
initBiomart(filter, biomart = "ensembl", host)
```

**Arguments**

|         |                             |
|---------|-----------------------------|
| filter  | list of supported organisms |
| biomart |                             |
| host    |                             |

**Author(s)**

Diego Diez

---

|            |                                    |
|------------|------------------------------------|
| layout.arc | <i>Layouts a graph using arcs.</i> |
|------------|------------------------------------|

---

**Description**

Generates a layout for graphs that places in the center the target transcription factors, in the sides the enriched transcription factors and in between of them the bridge proteins.

**Usage**

```
layout.arc(g, target, query)
```

**Arguments**

|        |                                                                 |
|--------|-----------------------------------------------------------------|
| g      | the graph object to layout.                                     |
| target | list of target nodes (typically target transcription factors.)  |
| query  | list of query nodes (typically enriched transcription factors.) |

**Value**

A matrix with the x and y locations of each node in the target graph.

**Author(s)**

Diego Diez

---

|                   |                                                 |
|-------------------|-------------------------------------------------|
| layout.concentric | <i>Generates a concentric layout for graphs</i> |
|-------------------|-------------------------------------------------|

---

**Description**

Generates a matrix with x,y coordinates for each node in a target graph, which layouts the nodes using concentric circles.

**Usage**

```
layout.concentric(g, concentric = NULL, radius = NULL, order.by)
```

**Arguments**

|            |                                         |
|------------|-----------------------------------------|
| g          | graph (igraph) to layout.               |
| concentric | list with the components of each layer. |
| radius     | radius of each layer.                   |
| order.by   | graph attributes to order nodes by.     |

**Author(s)**

Diego Diez

---

|            |                                                   |
|------------|---------------------------------------------------|
| plotDegree | <i>Plot degree distribution for network nodes</i> |
|------------|---------------------------------------------------|

---

**Description**

Plots the degree distribution and fits a power law, returning in the legend the values of the fitted parameters.

**Usage**

```
plotDegree(g)
```

**Arguments**

|   |               |
|---|---------------|
| g | igraph object |
|---|---------------|

**Author(s)**

Diego Diez

---

|           |                                        |
|-----------|----------------------------------------|
| plotGraph | <i>Plot an graph in igraph format.</i> |
|-----------|----------------------------------------|

---

**Description**

This function plots graphs of the class igraph.

**Usage**

```
plotGraph(g, layout = layout.fruchterman.reingold, mar = .5, vertex.pch = 21, vertex.cex, vertex.col)
```

**Arguments**

|                               |                                                                                               |
|-------------------------------|-----------------------------------------------------------------------------------------------|
| <code>g</code>                | a network object.                                                                             |
| <code>layout</code>           | graph layout, either a function or the output of a layout function.                           |
| <code>mar</code>              | plot margin.                                                                                  |
| <code>vertex.pch</code>       | node size.                                                                                    |
| <code>vertex.cex</code>       | node size.                                                                                    |
| <code>vertex.col</code>       | node line color.                                                                              |
| <code>vertex.bg</code>        | node background color.                                                                        |
| <code>vertex.lwd</code>       | node line width.                                                                              |
| <code>edge.col</code>         | edge color.                                                                                   |
| <code>edge.lwd</code>         | edge line width.                                                                              |
| <code>edge.lty</code>         | edge line type.                                                                               |
| <code>label</code>            | logical; whether to plot labels.                                                              |
| <code>label.col</code>        | label color.                                                                                  |
| <code>label.cex</code>        | label expansion.                                                                              |
| <code>label.pos</code>        | label position.                                                                               |
| <code>label.offset</code>     | label offset.                                                                                 |
| <code>adjust.label.col</code> | whether to automatically adjust label color depending on the luminance of the node's color/s. |
| <code>normalize.layout</code> | whether to apply layout.norm (with limits xmin=-1, xmax=1, ymin=-1, ymax=1) to the layout.    |

**Author(s)**

Diego Diez

---

|         |                               |
|---------|-------------------------------|
| plotTRM | <i>Plot an annotated TRM.</i> |
|---------|-------------------------------|

---

### Description

This function plots the output `findTRM()` after it has been annotated with cluster information with `annotateTRM()` function. Cluster membership is plotted using a pie plot.

### Usage

```
plotTRM(g, layout = layout.fruchterman.reingold, mar = .5, vertex.col, vertex.cex, vertex.lwd, edge
```

### Arguments

|                               |                                                                                                                                                                 |
|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>g</code>                | a network object with cluster information (attribute <code>piecolor</code> ).                                                                                   |
| <code>layout</code>           | graph layout, either a function or the output of a layout function.                                                                                             |
| <code>mar</code>              | plot margin.                                                                                                                                                    |
| <code>vertex.col</code>       | node color.                                                                                                                                                     |
| <code>vertex.cex</code>       | node size.                                                                                                                                                      |
| <code>vertex.lwd</code>       | node border line width.                                                                                                                                         |
| <code>edge.col</code>         | edge color.                                                                                                                                                     |
| <code>edge.lwd</code>         | edge line width.                                                                                                                                                |
| <code>edge.lty</code>         | edge line type.                                                                                                                                                 |
| <code>label</code>            | logical; whether to plot labels.                                                                                                                                |
| <code>label.cex</code>        | label expansion.                                                                                                                                                |
| <code>label.col</code>        | label color.                                                                                                                                                    |
| <code>label.pos</code>        | label position.                                                                                                                                                 |
| <code>label.offset</code>     | label offset.                                                                                                                                                   |
| <code>adjust.label.col</code> | whether to automatically adjust label color depending on the luminance of the node's color.                                                                     |
| <code>normalize.layout</code> | whether to apply <code>layout.norm</code> (with limits <code>xmin=-1</code> , <code>xmax=1</code> , <code>ymin=-1</code> , <code>ymax=1</code> ) to the layout. |

### Author(s)

Diego Diez

---

|               |                                                                              |
|---------------|------------------------------------------------------------------------------|
| plotTRMlegend | <i>Plot the legend of a TRM with information about the cluster families.</i> |
|---------------|------------------------------------------------------------------------------|

---

**Description**

This function just plots a legend with the cluster membership of the provided list of genes. The legend includes the most prominent families of each cluster and there is some name polishing as well.

**Usage**

```
plotTRMlegend(x, title = NULL, cex = 1)
```

**Arguments**

|       |                                                          |
|-------|----------------------------------------------------------|
| x     | list of family names or igraph object.                   |
| title | title for the legend.                                    |
| cex   | numeric value controlling the size of the legend's text. |

**Author(s)**

Diego Diez

---

|                |                                                                                    |
|----------------|------------------------------------------------------------------------------------|
| processBiogrid | <i>Process a data.frame with BioGRID data into a network for a target organism</i> |
|----------------|------------------------------------------------------------------------------------|

---

**Description**

Process a data.frame with BioGRID data into a network for a target organism.

**Usage**

```
processBiogrid(dblast, org = "human", simplify = TRUE, type = "physical", mimic.old = FALSE)
```

**Arguments**

|           |                                                                                                                          |
|-----------|--------------------------------------------------------------------------------------------------------------------------|
| dblist    | data.frame containing the BioGRID data.                                                                                  |
| org       | target organism (default: "human")                                                                                       |
| simplify  | whether to eliminate redundant edges (default TRUE)                                                                      |
| type      | type of interaction (physical or genetic) to include (default: "physical")                                               |
| mimic.old | mimic old behavior of processBiogrid() when interactions for multiple species could be retrieved. Used only for testing. |

**Value**

An igraph object.

**Author(s)**

Diego Diez

---

|                |                                                                    |
|----------------|--------------------------------------------------------------------|
| removeVertices | <i>Remove nodes from a graph and returns the largest component</i> |
|----------------|--------------------------------------------------------------------|

---

**Description**

Remove nodes from a graph and returns the largest component

**Usage**

```
removeVertices(g, filter, keep.hanging = FALSE)
```

**Arguments**

|              |                                                           |
|--------------|-----------------------------------------------------------|
| g            | graph to remove nodes.                                    |
| filter       |                                                           |
| keep.hanging | (logical) whether to return the largest component or not. |

**Author(s)**

Diego Diez

---

|                |                                                                  |
|----------------|------------------------------------------------------------------|
| writeTRMreport | <i>Export a table with TRM nodes and associated information.</i> |
|----------------|------------------------------------------------------------------|

---

**Description**

This function generates a data.frame with the nodes in the provided graph and associated annotations.

**Usage**

```
writeTRMreport(graph, file, organism, target, query, sort.by = "symbol")
```

**Arguments**

|          |                                                             |
|----------|-------------------------------------------------------------|
| graph    | a graph object.                                             |
| file     | file name.                                                  |
| organism | organisms for the annotations.                              |
| target   | target transcription factor.                                |
| query    | query transcription factors.                                |
| sort.by  | order the columns of the data.frame by (default: "symbol"). |

**Author(s)**

Diego Diez

# Index

- \* **datasets**
  - biogrid\_hs, [5](#)
  - biogrid\_mm, [5](#)
- \* **package**
  - rTRM-package, [2](#)
- annotateFreq, [3](#)
- annotateModule, [4](#)
- annotateTRM, [4](#)
- biogrid\_hs, [5](#)
- biogrid\_mm, [5](#)
- findTRM, [6](#)
- getAnnotations, [7](#)
- getBiogridData, [7](#)
- getConcentricList, [8](#)
- getLargestComp, [8](#)
- getMaps, [9](#)
- getMatrices, [9](#)
- getMotifsFromEntrezgene, [10](#)
- getMotifsFromSymbol, [10](#)
- getOrthologFromMatrix, [11](#)
- getOrthologs, [11](#)
- getOrthologsFromBiomart, [12](#)
- getSequencesFromGenome, [12](#)
- getSimilarityMatrix, [13](#)
- getTFclass, [13](#)
- getTFclassFromEntrezgene, [14](#)
- getTFterms, [14](#)
- initBiomart, [15](#)
- layout.arc, [15](#)
- layout.concentric, [16](#)
- plotDegree, [16](#)
- plotGraph, [17](#)
- plotTRM, [18](#)
- plotTRMlegend, [19](#)
- processBiogrid, [19](#)
- removeVertices, [20](#)
- rTRM (rTRM-package), [2](#)
- rTRM-package, [2](#)
- writeTRMreport, [20](#)