Package ‘rTRM’

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Type Package

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

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Author Diego Diez

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       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

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ByteCompile yes

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Description

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

Details
annotateFreq

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(g, graph_list)

Arguments
  g   target graph to annotate.
  graph_list 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 known their frequency in the original list of graphs.

Author(s)
Diego Diez
annotateModule  Annotate a network module with information

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  Annotate a network object with information about clusters.

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

| 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

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biogrid_mm

| 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

Indicates a TRM associated with a target node and one or more query nodes.

Description
This is the main function used to identify TRMs. It takes a graph object and uses 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")
getAnnotations

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

Description

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

Usage

generateAnnotations(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 = generateAnnotations()

generateBiogridData

Downloads network data from BioGRID in TAB2 format.

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

generateBiogridData(release)

Arguments

release release of BioGRID to download.
getConcentricList

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

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

Description

Get the largest connected component

Usage

getLargestComp(g)

Arguments

g an igraph object.

Author(s)

Diego Diez

getMaps

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()
getMotifsFromEntrezgene

getMatrices

Obtain a list of PWMs.

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()

gMotifsFromEntrezgene

Retrieve PWMs associated with genes provided as entrezgene identifiers.

Description

Retrieve PWMs associated with genes provided as entrezgene identifiers.

Usage

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

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

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

**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 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)
getSequencesFromGenome

**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  
*Compute similarity matrix of list of graphs.*

**Description**

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

**Usage**

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

**Arguments**

- `g_list`: list of graph objects.
- `type`: type of similarity, either node or edge (default).

**Author(s)**

Diego Diez

---

getTFclass  
*Return the ontology in the TFclass database associated with an entrezgene identifier*

**Description**

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

**Usage**

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

**Arguments**

- `dbname`: 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

*Initializes mart objects to identify ortholog genes*

**Description**

Initializes mart objects to identify ortholog genes

**Usage**

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

**Arguments**

- `filter` list of supported organisms
- `biomart` (default: "ensembl")
- `host`

**Author(s)**

Diego Diez

layout.arc

*Layouts a graph using arcs.*

**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**

```r
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**

Generates a concentric layout for graphs

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

**Usage**

```r
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**

Plot degree distribution for network nodes

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

**Usage**

```r
plotDegree(g)
```

**Arguments**

- `g` igraph object

**Author(s)**

Diego Diez
Plot an graph in igraph format.

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, vertex.bg, ... = TRUE, label.col, label.cex, label.pos = NULL, label.offset = 1.5, adjust.label.col = FALSE, normalize.layout = TRUE)

Arguments

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

Author(s)

Diego Diez
**plotTRM**

*Plot an annotated TRM.*

---

**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**

```r
plotTRM(g, layout = layout.fruchterman.reingold, mar = .5, vertex.col, vertex.cex, vertex.lwd, edge.col, edge.lwd, edge.lty, label = TRUE, label.cex, label.col, label.pos = NULL, label.offset = 1.5, adjust.label.col = FALSE, normalize.layout = TRUE)
```

**Arguments**

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

**Author(s)**

Diego Diez
plotTRMlegend

Plot the legend of a TRM with information about the cluster families.

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

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

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

Usage
processBiogrid(dblist, 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.
**removeVertices**

**Value**
An igraph object.

**Author(s)**
Diego Diez

---

**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`: (logical) whether to return the largest component or not.
- `keep.hanging`: (logical) whether to return the largest component or not.

**Author(s)**
Diego Diez

---

**writeTRMreport**

**Export a table with TRM nodes and associated information.**

**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
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