Package ‘XINA’

February 22, 2024

Type Package

Title Multiplexes Isobaric Mass Tagged-based Kinetics Data for Network Analysis

Version 1.20.0

biocViews SystemsBiology, Proteomics, RNASeq, Network

Author Lang Ho Lee <lhlee@bwh.harvard.edu> and Sasha A. Singh <sasingh@bwh.harvard.edu>

Maintainer Lang Ho Lee <lhlee@bwh.harvard.edu> and Sasha A. Singh <sasingh@bwh.harvard.edu>

Description The aim of XINA is to determine which proteins exhibit similar patterns within and across experimental conditions, since proteins with co-abundance patterns may have common molecular functions. XINA imports multiple datasets, tags dataset in silico, and combines the data for subsequent subgrouping into multiple clusters. The result is a single output depicting the variation across all conditions. XINA, not only extracts coabundance profiles within and across experiments, but also incorporates protein-protein interaction databases and integrative resources such as KEGG to infer interactors and molecular functions, respectively, and produces intuitive graphical outputs.

Copyright XINA combines multiple quantitative (kinetics) datasets from omics studies into a single input dataset for clustering. Copyright(C)2018 Lang Ho Lee, Arda Halu, Stephanie Morgan, Hiroshi Iwata, Masanori Aikawa, and Sasha A. Singh This program is free software: you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation, either version 3 of the License, any later version. This program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the GNU General Public License for more details. You should have received a copy of the GNU General
Public License along with this program. If not, see <https://www.gnu.org/licenses/>.
Contact emails: L. Lee, LHLEE@BWH.HARVARD.EDU; S. Singh, SASINGH@BWH.HARVARD.EDU; M. Aikawa, MAIKAWA@BWH.HARVARD.EDU
Mailing address: Department of Medicine, Cardiovascular Division Center for Interdisciplinary Cardiovascular Sciences 3 Blackfan Street, 17th Floor Boston, MA 02115 USA

License  GPL-3
Imports  mclust, plyr, alluvial, ggplot2, igraph, gridExtra, tools, grDevices, graphics, utils, STRINGdb
VignetteBuilder  knitr
LazyData  FALSE
RoxygenNote  6.1.1
Encoding  UTF-8
Depends  R (>= 3.5)
Suggests  knitr, rmarkdown
Date  2019-01-31
git_url  https://git.bioconductor.org/packages/XINA
git_branch  RELEASE_3_18
git_last_commit  8ca83bc
git_last_commit_date  2023-10-24
Repository  Bioconductor 3.18
Date/Publication  2024-02-21

R topics documented:

add_legend ......................................................... 3
alluvial_enriched .................................................. 4
alluvial_enrichment_tests ......................................... 5
calculate_centrality_scores ...................................... 6
default_size ....................................................... 7
draw_alluvial_plot ................................................ 7
draw_alluvial_plot ................................................ 7
element_clusters ................................................... 8
extract_data_column ............................................... 9
find_similar_clusters ............................................. 9
genenerate_count_table .......................................... 10
genenerate_superset .............................................. 10
get_colors .......................................................... 11
get_color_for_nodes .............................................. 11
generate_comigrations_by_name .................................. 12
gen_condition_biased_comigrations ................................ 13
gen_layout .......................................................... 14
gen_mTOR_proteins ................................................. 15
Description

Add plot legend and locate it outside of a network plot

Usage

    add_legend(legend_location = "bottomright", ...)

Arguments

    legend_location
        Network centrality score matrix
    ...          Numeric, complex, or logical vectors.

Value

    a legend to a plot
Description

'alluvial_enriched' draws an alluvial plot and finds comigrated proteins. The comigration is a group of proteins that show the same expression pattern, classified and evaluated by XINA clustering, in at least two conditions. XINA can reduce the dataset complexity by filtering based on the number of comigrated proteins (size, 'comigration_size' parameter) and perform an enrichment test (P-value of Fisher's exact test, 'pval_threshold') to determine significance of enriched comigrations. The Fisher's exact test can only be done for two conditions at a time. The following 2x2 table was used to calculate the P-value from the Fisher's exact test. To evaluate significance of co-migrated proteins from cluster #1 in control to cluster #2 in test group,

<table>
<thead>
<tr>
<th></th>
<th>cluster #1 in control</th>
<th>other clusters in control</th>
</tr>
</thead>
<tbody>
<tr>
<td>cluster #2 in test</td>
<td>65 (TP)</td>
<td>175 (FP)</td>
</tr>
<tr>
<td>other clusters in test</td>
<td>35 (FN)</td>
<td>979 (TN)</td>
</tr>
</tbody>
</table>

Usage

```r
alluvial_enriched(clustering_result, selected_conditions,
comigration_size = 0, pval_threshold = 1, pval_method = "fdr",
cex = 0.7, alpha = 0.3)
```

Arguments

- **clustering_result**
  A list containing XINA clustering results. See `xina_clustering`

- **selected_conditions**
  A vector of condition names used in XINA clustering results. The number of selected conditions should be at least two.

- **comigration_size**
  The number of proteins comigrated together in the selected conditions of XINA clustering results. Default is 0

- **pval_threshold**
  This option is available only when you selected two conditions for comigration search.

- **pval_method**
  Method for p-value adjustment. See `p.adjust`

- **cex**
  Scaling of fonts of category labels. Default if 0.7. See `alluvial`

- **alpha**
  Transparency of the stripes. Default if 0.3. See `alluvial`

Value

A data frame containing comigrations and an alluvial plot showing comigrations
Examples

# load XINA example data
data(xina_example)

# Get the experimental conditions in the example data
classes <- as.vector(example_clusters$condition)

# Get comigrations without any thresholds
all_comigrations <- alluvial_enriched(example_clusters, classes)

# Get comigrations that have >= 5 size (the number of comigrated proteins)
all_cor_enriched <- alluvial_enriched(example_clusters, classes, comigration_size=5)

# Get all the comigrations between Control and Stimulus1
comigrations_Control_Stimulus1 <- alluvial_enriched(example_clusters, c(classes[1],classes[2]))

# Get comigrations between Control and Stimulus1, that have >=5 size
comigrations_Control_Stimulus1_over5 <- alluvial_enriched(example_clusters, c(classes[1],classes[2]), comigration_size=5)

# Get comigrations between Control and Stimulus1, that have >= 5 size and enrichment FDR <= 0.01
comigrations_Control_Stimulus1_pval0.01_size5 <- alluvial_enriched(example_clusters, c(classes[1],classes[2]), comigration_size=5, pval_threshold=0.01)

# Get comigrations between Control and Stimulus1, that have >= 5 size and enrichment Benjamini & Yekutieli <= 0.01
comigrations_Control_Stimulus1_BY0.01_size5 <- alluvial_enriched(example_clusters, c(classes[1],classes[2]), comigration_size=5, pval_threshold=0.01, pval_method="BY")

Description

Fisher’s exact test to calculate the significance over all comigrations. The following 2x2 table was used to calculate p-value from Fisher’s exact test. To evaluate significance of comigrated proteins from cluster #1 in control to cluster #2 in test condition,

<table>
<thead>
<tr>
<th></th>
<th>cluster #1 in control</th>
<th>other clusters in control</th>
</tr>
</thead>
<tbody>
<tr>
<td>cluster #2 in test</td>
<td>65 (TP)</td>
<td>175 (FP)</td>
</tr>
<tr>
<td>other clusters in test</td>
<td>35 (FN)</td>
<td>979 (TN)</td>
</tr>
</tbody>
</table>

'alluvial_enrichment_tests' also provides another statistical methods including Hypergeometric test and Chi-square test.
calculate_centrality_scores

Usage
calculate_centrality_scores(net, centrality_type = "Degree")

Arguments
net       protein-protein interaction network of igraph
centrality_type  the maximum number of clusters

Value
A vector of network centrality scores

describe_alluvial_enrichment_tests(count_table, c1, c2, non_cluster = 0,
test_type = "fisher")

Arguments
count_table  A data frame generated by using count.
c1           A selected cluster in the first condition.
c2           A selected cluster in the second condition.
non_cluster  The cluster number for proteins that were not detected in a specific sample. Default is 0.
test_type    Enrichment test type. 'fisher' = Fisher's exact test, 'hyper' = Hypergeometric test, 'chisq' = Chi-square test

Value
P-value of comigration enrichment test and 2x2 table information
default_size

Description
Calculate image size based on the number of clusters

Usage
default_size(max_cluster)

Arguments
max_cluster the maximum number of clusters

Value
A vector of plot width and height

draw_alluvial_plot
draw_alluvial_plot

Description
'draw_alluvial_plot' draw a alluvial plot

Usage
draw_alluvial_plot(clustering_result, selected_conditions, count_table, alluvia_colors = NULL, cex = 0.7, alpha = 0.3)

Arguments
clustering_result A list containing XINA clustering results. See xina_clustering.
selected_conditions A vector of condition names used in XINA clustering results. The number of selected conditions should be at least two.
count_table A data frame generated by using count.
alluvia_colors A vector containing the user-defined colors for each alluvium.
cex Size of cluster number on block axis. Default if 0.7. See alluvial.
alpha Transparency of alluvia colors. Default is 0.3. See alluvial.
example_clusters

Value

An alluvial plot displaying comigrations and the data frame containing the input count_table with colors.

Examples

```r
# load XINA example data
data(xina_example)

# get a vector of experimental conditions analyzed in the clustering results
classes <- as.vector(example_clusters$condition)

comigrations_size_over5 <- alluvial_enriched(example_clusters, classes, comigration_size=5)
draw_alluvial_plot(example_clusters, classes, comigrations_size_over5)
```

example_clusters

Randomly generated example datasets for XINA users. A dataset containing the XINA clustering results.

Description

- aligned. XINA clustering results aligned by conditions
- data_column. Column names for data matrix
- out_dir. Not available in this example dataset
- nClusters. The number of user-desired clusters. It’s 30 in the example.
- max_cluster. The number of clusters found in the dataset. It’s 21 in the example.
- chosen_model. The chosen covariance model for the example dataset. It’s VEI in the example
- optimal_BIC. BIC at the optimized clustering. It’s 29473.57 in the example
- condition. The experimental conditions in the dataset.
- color_for_condition. The default color for the conditions that will be used in XINA plot drawing.
- color_for_clusters. The default color for the clusters that will be used in XINA clustering plot.
- norm_method. The used normalization method to standardize the input data. It’s "sum_normalization" in the example.

Format

A list with the example XINA clustering result
**extract_data_column**

**Description**

Extract data column names from XINA clustering result

**Usage**

```r
evaluate_data_column(col_head_of_clustering)
```

**Arguments**

- `col_head_of_clustering`
  
  Column names of XINA clustering result

**Value**

A vector containing column names of data matrix

---

**find_similar_clusters**

**Description**

Compare clusters and find similar ones

**Usage**

```r
find_similar_clusters(clustering_result, threshold = 0.95)
```

**Arguments**

- `clustering_result`
  
  A list containing XINA clustering results. See `xina_clustering`

- `threshold`
  
  Pearson’s r threshold to find similar ones

**Value**

Write a csv file containing similar clustering information based on the given Pearson’s R threshold
generate_count_table

Description

Count the number of comigrated proteins using count

Usage

generate_count_table(clustering_result, selected_conditions, comigration_size)

Arguments

clustering_result
A list containing XINA clustering results. See xina_clustering

selected_conditions
A vector of condition names used in XINA clustering results.

comigration_size
The number of proteins comigrated together in the selected conditions of XINA clustering results. Default is 0.

Value

A data frame containing comigrations.

generate_superset

Description

Merge input kinetics files

Usage

generate_superset(f_names, data_column, delim = ",", norm = "sum_normalization")

Arguments

f_names
A vector of .csv file paths containing kinetics data

data_column
A vector of column names containing data matrix

delim
The delimiter of input file (default is ",").

norm
The normalization method. It should be one of c('sum_normalization', 'zs-core'). Default is 'sum_normalization'.
**get_colors**

**Value**

A data frame containing kinetics data obtained from files in the f_names vector

**Description**

Generate color series for XINA graphics

**Usage**

```r
get_colors(nClusters, set = "", colorset = NULL)
```

**Arguments**

- `nClusters`: The number of clusters
- `set`: Pre-defined color series set
- `colorset`: manuually defined color codes

**Value**

A vector for color code of XINA graphics

---

**get_color_for_nodes**

**Description**

Pre-defined 30 colors

**Usage**

```r
get_color_for_nodes()
```

**Value**

A vector for color code of XINA graphics
Description

'get_comigrations_by_name' finds proteins comigrated with the given proteins

Usage

get_comigrations_by_name(clustering_result, selected_conditions, protein_list, cex = 0.7, alpha = 0.3)

Arguments

clustering_result
A list containing XINA clustering results. See xina_clustering

selected_conditions
A vector of condition names used in XINA clustering results. The number of selected conditions should be at least two.

protein_list
A vector containing gene names.

cex
Size of cluster number on block axis. Default is 0.7. See alluvial

alpha
Transparency of alluvia colors. Default is 0.3. See alluvial

Value

An alluvial plot displaying comigrations and the data frame containing comigrations of the input proteins

Examples

# load XINA example data
data(xina_example)

# the clustering result table
all_proteins <- as.character(example_clusters$aligned$'Gene name')
# get a vector of experimental conditions analyzed in the clustering results
classes <- as.vector(example_clusters$condition)

comigrated_prots_all <- get_comigrations_by_name(example_clusters, classes, all_proteins[1:3])
get_condition_biased_comigrations

Description

get comigrations that at least one biased cluster is involved in. Biased clusters are defined by

Usage

```
get_condition_biased_comigrations(clustering_result, count_table = NULL,
selected_conditions, condition_composition, threshold_percent = 50,
color_for_null = "gray", color_for_highly_matched = "red4",
cex = 0.7, alpha = 0.3)
```

Arguments

- `clustering_result`  
  A list containing XINA clustering results. See `xina_clustering`
- `count_table`  
  A data frame generated by using `count`. If `count_table` is NULL (by default), XINA will consider all the comigrations.
- `selected_conditions`  
  A vector of condition names used in XINA clustering results. The number of selected conditions should be at least two.
- `condition_composition`  
  The resulting data frame of `plot_condition_compositions`. See `plot_condition_compositions`.
- `threshold_percent`  
  Default is 50. The percentage threshold for finding condition-biased clusters
- `color_for_null`  
  A color for non-condition-biased comigrations. Default is ’gray’
- `color_for_highly_matched`  
  A color for comigrations that are involved with more than two condition-biased clusters. Default is ’red4’
- `cex`  
  Size of cluster number on block axis. Default if 0.7. See `alluvial`.
- `alpha`  
  Transparency of alluvia colors. Default is 0.3. See `alluvial`.

Value

An alluvial plot displaying comigrations and the data frame containing condition-biased comigrations.

Examples

```
# load XINA example data
data(xina_example)

# get a vector of experimental conditions analyzed in the clustering results
```
conditions <- as.vector(example_clusters$condition)

# get condition composition information
condition_composition <- plot_condition_compositions(example_clusters)

comigrations_size10 <- alluvial_enriched(example_clusters, conditions, comigration_size=10)
# Finding condition-biased comigrations by 50% threshold
condition_biased_comigrations <-
  get_condition_biased_comigrations(clustering_result=example_clusters,
  count_table=comigrations_size10, selected_conditions=conditions,
  condition_composition=condition_composition)

# Finding condition-biased comigrations by 70% threshold
condition_biased_comigrations <-
  get_condition_biased_comigrations(clustering_result=example_clusters,
  count_table=comigrations_size10, selected_conditions=conditions,
  condition_composition=condition_composition,
  threshold_percent=70)

---

### Description

Get igraph layout by the number of nodes

### Usage

get_layout(subnet_condition)

### Arguments

- **subnet_condition**
  - A igraph sub-network

### Value

igraph network layout
get_mTOR_proteins

Description
Get mTOR pathway genes

Usage
get_mTOR_proteins(time_points, conditions)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>time_points</td>
<td>A vector containing time points of the data matrix</td>
</tr>
<tr>
<td>conditions</td>
<td>A vector containing condition information, for example normal, disease and drug treated disease.</td>
</tr>
</tbody>
</table>

Value
A vector containing mTOR pathway gene names

get_random_data

Description
Get randomized time-series data

Usage
get_random_data(time_points, conditions, num_total, percent.sign = 0.1, equal = TRUE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>time_points</td>
<td>A vector containing time points of the data matrix</td>
</tr>
<tr>
<td>conditions</td>
<td>A vector containing condition information, for example normal, disease and drug treated disease.</td>
</tr>
<tr>
<td>num_total</td>
<td>The number of total proteins to be generated</td>
</tr>
<tr>
<td>percent.sign</td>
<td>Percentage of differentially expressed proteins. Ignored when equal=FALSE.</td>
</tr>
<tr>
<td>equal</td>
<td>If equal is TRUE, all the conditions will have numbers between 0 and 1. If it is FALSE, the first three conditions will have different ranges. First condition will have numbers from 0.3 to 0.4. Second condition will have numbers from 0.6 to 0.8. Third condition will have numbers from 0.3 to 0.5. Other conditions will have numbers from 0 to 1.</td>
</tr>
</tbody>
</table>
**get_stats**

Description

Calculate statistics of the given data for XINA network analysis

Usage

```r
get_stats(centrality_results, na.rm = FALSE)
```

Arguments

- `centrality_results`: Network centrality score data frame calculated by XINA network module
- `na.rm`: If it is FALSE, no exclusion of NA values.

Value

A data frame containing statistics of XINA network centrality scores

---

**get_theme_blank**

Description

Predefined ggplot theme for removing ticks, titles and labels of X and Y axis

Usage

```r
get_theme_blank()
```

Value

A ggplot theme
get_unknown_ppi_nodes

Description
Get proteins with no known interactions within the cluster based on the used protein-protein interaction database source

Usage
get_unknown_ppi_nodes(xina_result, cl)

Arguments
- xina_result: A list containing XINA network analysis results. See xina_analysis
- cl: the clustering number of XINA clustering results. See xina_clustering

Value
A data frame containing proteins with no known interactions within the cluster based on the used protein-protein interaction database source

Examples
# load XINA example data
data(xina_example)

# load the previously processed XINA analysis results
# if you want to learn how to run 'xina_analysis', please see \link[xina_analysis]
data(xina_result_example)

# Extract unknown PPI nodes in the cluster #1
get_unknown_ppi_nodes(xina_result_example, 1)

gn
A character vector containing 19,396 human genes
This is for the random data generation of XINA

Description
- Characters of human genes

Format
A character vector containing 19,396 human genes
<table>
<thead>
<tr>
<th>Data Name</th>
<th>Description</th>
<th>Source</th>
</tr>
</thead>
</table>

**Description**

- Human gene description corresponding to 'gn' vector

**Format**

A character vector containing 19,396 human gene descriptions

**Source**


- gene_symbol_1. Gene name interacting with gene name in 'gene_symbol_2'
- gene_symbol_2. Gene name interacting with gene name in 'gene_symbol_1'
- Experiment_type. Experimental or computational methods supporting the interaction

**Format**

A data frame containing HRPD protein-protein interaction data

**Source**

**length2**

**Description**

Customized function for vector length calculation

**Usage**

```
length2(x, na.rm = FALSE)
```

**Arguments**

- `x` A vector
- `na.rm` If it is FALSE, no exclusion of NA values.

**Value**

A vector length

---

**load_previous_results**

**Description**

Get previous XINA clustering results to R space

**Usage**

```
load_previous_results(clustering_dir = getwd(), data_column = NULL,
                     fp_clusters = "xina_clusters.csv")
```

**Arguments**

- `clustering_dir` The directory path of XINA clustering results
- `data_column` A vector containing column names of data matrix
- `fp_clusters` File path of XINA clustering results

**Value**

Comma-separated file containing aligned XINA clustering results.
**Examples**

```r
# Load XINA's example data
data(xina_example)
write.csv(example_clusters$aligned, "xina_clusters_aligned.csv")
write.csv(example_clusters$clusters, "xina_clusters.csv")

# Reload the clustering result
example_clusters_reloaded <- load_previous_results(".")
```

**Description**

Generate random proteomics dataset for testing XINA. `make_random_xina_data` will make random proteomics data for XINA test. The generated data will have three conditions and seven time points, c("0hr", "2hr", "6hr", "12hr", "24hr", "48hr", "72hr").

**Usage**

```r
make_random_xina_data(n = 500, mtor = TRUE, time_points = c("0hr", "2hr", "6hr", "12hr", "24hr", "48hr", "72hr"),
                    conditions = c("Control", "Stimulus1", "Stimulus2"))
```

**Arguments**

- `n`: The number of proteins for one condition. Default is 500.
- `mtor`: If it is TRUE (default), mTOR pathway genes will be significant. If it is FALSE, randomly selected genes will be significant in first three conditions.
- `time_points`: A vector containing time points of the data matrix.
- `conditions`: A vector containing condition information, for example normal, disease and drug treated disease.

**Value**

Three comma-separated files containing time-series data for XINA.

**Examples**

```r
make_random_xina_data()
g1 <- read.csv("Control.csv", check.names=FALSE,
               stringsAsFactors = FALSE)
g2 <- read.csv("Stimulus1.csv", check.names=FALSE,
               stringsAsFactors = FALSE)
g3 <- read.csv("Stimulus2.csv", check.names=FALSE,
               stringsAsFactors = FALSE)
```
**mutate_colors**

\[
\begin{align*}
\text{head}(g1) \\
\text{head}(g2) \\
\text{head}(g3)
\end{align*}
\]

---

### Description

'mutate_colors' generates new color scheme for XINA clustering plot based on condition composition results (\texttt{plot_condition_compositions}). If any clusters have higher percentage than the 'threshold_percent', XINA will assign new colors in accordance to 'color_for_condition'. If not, XINA will give 'gray' color or user-defined color via 'null_color' parameter.

### Usage

\[
\text{mutate_colors}(\text{condition_composition}, \text{color_for_condition}, \\
\text{null_color = "gray"}, \text{threshold_percent = 50})
\]

### Arguments

- \textit{condition_composition} 
  A data frame generated by \texttt{plot_condition_compositions}
- \textit{color_for_condition} 
  A vector like 'color_for_condition' of \texttt{xina_clustering}
- \textit{null_color} 
  Default is 'gray'. This color is for clusters that are not biased to any of experimental conditions
- \textit{threshold_percent} 
  Default is 50. The percentage threshold for giving new colors

### Value

A data frame containing statistics of XINA network centrality scores

### Examples

# load XINA example data
data(xina_example)

# Plot condition composition pie-chart with default option
condition_composition <- plot_condition_compositions(example_clusters)
example_clusters$color_for_clusters <- mutate_colors(condition_composition,
example_clusters$color_for_condition)
plot_clusters(example_clusters, xval=c(0,2,6,12,24,48,72), xylab=FALSE)
organize_clusters  

**Description**  
Organize XINA clustering information by gene name

**Usage**  
organize_clusters(clustering_dir = getwd(), super_ds, file_out = TRUE)

**Arguments**  
- *clustering_dir* The directory path of XINA clustering results  
- *super_ds* XINA clusters  
- *file_out* If it is TRUE, it writes the aligned clustering information to "xina_clusters_aligned.csv" file.

**Value**  
Comma-separated file containing aligned XINA clustering results.

plot_clusters  

**Description**  
Draw all the clustering results. 'plot_clusters' draws two plots, scaled and unscaled line graphs. Scaled graphs have same y limits that are 0 to 1 by default, but can be changed via 'y_lim' parameter.

**Usage**  
plot_clusters(clustering_result, y_lim = NULL, xval = NULL, xtickmark = NULL, xylab = TRUE, ggplot_theme = NULL)

**Arguments**  
- *clustering_result* A list containing XINA clustering results. See `xina_clustering`  
- *y_lim* Y axis limit. If you set y_lim=c(0,1), 'plot_clusters' will plot line graphs scaled from 0 to 1 in y-axis. Default is NULL, which means unscaled line graphs.  
- *xval* XINA basically considers time points as an ordinary variable, like 1,2,3,4...n. You can make the time points as a continuous variable using xval.  
- *xtickmark* Change X axis tick marks. Default is data_column of the clustering result list.  
- *xylab* If it is FALSE, x and y labels will be blank. If it is TRUE (default), x and y labels will be shown.  
- *ggplot_theme* This is ggplot theme to modify XINA clustering plot.
Value

Line graphs of all the clusters

Examples

```r
library(ggplot2)

# load XINA example data
data(xina_example)

# Draw clustering plots
plot_clusters(example_clusters)

# Apply theme to the clustering plot
theme1 <- theme(title=element_text(size=8, face='bold'),
                axis.text.x = element_text(size=7),
                axis.text.y = element_blank(),
                axis.ticks.x = element_blank(),
                axis.ticks.y = element_blank(),
                axis.title.x = element_blank(),
                axis.title.y = element_blank())
plot_clusters(example_clusters, ggplot_theme=theme1)
```

Description

Draw line graphs of all the proteins in the given dataset

Usage

```r
plot_clusters_all(clustering_result, selected_condition = NULL)
```

Arguments

- `clustering_result`:
  A list containing XINA clustering results. See `xina_clustering`

- `selected_condition`:
  A condition name to draw the kinetics plot

Value

A list containing clustering results and pdf file containing a BIC plot in current working directory.
Examples

```r
# load XINA example data
data(xina_example)

# Plot kinetics of all the proteins in Control
plot_clusters_all(example_clusters, selected_condition="Control")

# Plot kinetics of all the proteins in Stimulus1
plot_clusters_all(example_clusters, selected_condition="Stimulus1")

# Plot kinetics of all the proteins in Stimulus2
plot_clusters_all(example_clusters, selected_condition="Stimulus2")

# Plot kinetics of all the proteins in three data
plot_clusters_all(example_clusters)
```

Description

computes condition composition of the XINA clustering results and draws pie-charts.

Usage

```r
plot_condition_compositions(clustering_result, bullseye = FALSE, ggplot_theme = NULL)
```

Arguments

- `clustering_result`:
  A list containing XINA clustering results. See `xina_clustering`
- `bullseye`:
  If it is TRUE, draw bullseye plot instead of the pie-chart. Default is FALSE
- `ggplot_theme`:
  This is ggplot theme to modify condition composition pie-chart and bullseye plots.

Value

A condition composition plot and a data frame containing condition compositions of the clusters
plot_enrichment_results

Examples

# load XINA example data
data(xina_example)

# Plot condition composition pie-chart with default option
plot_condition_compositions(example_clusters)

# Make a new color code for conditions
condition_colors <- c("tomato","steelblue1","gold")
names(condition_colors) <- example_clusters$condition
example_clusters$color_for_condition <- condition_colors

# Draw condition composition pie-chart with the new color code
plot_condition_compositions(example_clusters)

# Draw condition composition bullseye plot
plot_condition_compositions(example_clusters, bullseye = TRUE)

plot_enrichment_results

plot_enrichment_results

Description

Plot GO and KEGG enrichment results

Usage

plot_enrichment_results(enriched_results,
  term_description = "term_description", sig_score = "pvalue",
  num_terms = 0, get_log = TRUE, fill_color = "darkgray")

Arguments

enriched_results
  GO or KEGG enrichment results. See xina_enrichment and xina_enrichment

term_description
  Description of terms to be drawn on Y axis. Default is "term_description" of
  XINA enrichment results.

sig_score
  significant score to plot on X axis. Default is "pvalue".

num_terms
  The number of terms to be plotted. Default is 0, which means no limit.

get_log
  If this is TRUE, 'plot_enrichment_results' will take -log10 of p-values.

fill_color
  Default is 'darkgray'. You can change color of bars.

Value

ggplot bar graph
Examples

```r
# Not run:
library(STRINGdb)

# load XINA example data
data(xina_example)

# Get STRING database for protein-protein interaction information
string_db <- STRINGdb$new( version="10", species=9606, score_threshold=0, input_directory="" )
string_db

# XINA analysis with STRING DB
xina_result <- xina_analysis(example_clusters, string_db)

# Select proteins that showed cluster #1 in the Stimulus2 condition
subgroup <- subset(example_clusters$aligned, Stimulus2==1)
protein_list <- as.vector(subgroup$Gene name)

# Enrichment test and get significantly enriched functional terms that have adjusted p-value less than 0.1
kegg_enriched <- xina_enrichment(string_db, protein_list, enrichment_type = "KEGG", pval_threshold=0.1)
plot_enrichment_results(kegg_enriched$KEGG, num_terms=10)

# End(Not run)
```

Description

Draw NULL plot

Usage

```r
plot_NA()
```

Value

a empty plot
**Description**

Give ranks based on network centrality scores

**Usage**

`rank_centrality(centrality_score, type, num_breaks = 5)`

**Arguments**

- `centrality_score`: Network centrality score matrix
- `type`: Network centrality score type, such as 'Eigenvector'
- `num_breaks`: The number of ranks

**Value**

A vector containing ranks

---

**string_example**

*Protein-protein interaction resource downloaded from STRING DB for XINA's example dataset A data frame containing protein-protein interactions*

**Description**

- `gene_symbol_1`. Gene name interacting with gene name in `gene_symbol_2`
- `gene_symbol_2`. Gene name interacting with gene name in `gene_symbol_1`
- `PPI_Source`. Data original source

**Format**

A data frame containing STRING protein-protein interaction data

**Source**

[https://string-db.org/](https://string-db.org/)
Description

xina_analysis is to analyze protein-protein interaction (PPI) networks using STRINGdb and igraph R package. This module computes PPI networks within each XINA clusters.

Usage

```r
xina_analysis(clustering_result, ppi_db, is_stringdb = TRUE, 
               flag_simplify = TRUE, node_shape = "sphere", 
               num_clusters_in_row = 5, img_size = NULL, img_qual = 300)
```

Arguments

- **clustering_result**: A list containing XINA clustering results. See `xina_clustering`
- **ppi_db**: STRINGdb object
- **is_stringdb**: If it is TRUE (default), XINA will process `ppi_db` as STRINGdb, but it is FALSE, XINA will accepts your `ppi_db` as it is. You can make your own igraph network using customized PPI information instead of STRINGdb.
- **flag_simplify**: If it is TRUE (default), XINA will exclude unconnected proteins
- **node_shape**: You can choose node shape. Default is "sphere". See `shapes`
- **num_clusters_in_row**: The number of clusters in a row on the XINA network plot. Default is 5.
- **img_size**: Set the image size. For width=1000 and height=1500, it is `img_size=c(1000,1500)`.
- **img_qual**: Set the image resolution. Default is 300.

Value

A PNG file (XINA_Cluster_Networks.png) displaying PPI network plots of all the clusters and a list containing XINA network analysis results.

<table>
<thead>
<tr>
<th>Item</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>All_network</td>
<td>PPI network of all the input proteins</td>
</tr>
<tr>
<td>Sub_network</td>
<td>A list containing PPI networks of each clusters</td>
</tr>
<tr>
<td>Data</td>
<td>XINA clustering results. See <code>xina_clustering</code></td>
</tr>
<tr>
<td>Nodes</td>
<td>A list of proteins in each cluster</td>
</tr>
<tr>
<td>Conditions</td>
<td>A list of experimental condition of proteins in each cluster</td>
</tr>
<tr>
<td>Titles</td>
<td>A list of plot titles for XINA plotting</td>
</tr>
<tr>
<td>out_dir</td>
<td>A directory path storing XINA network analysis results</td>
</tr>
<tr>
<td>is_stringdb</td>
<td>False = different PPI DB and TRUE = STRING DB</td>
</tr>
</tbody>
</table>
### Examples

```r
# Not run:
data(xina_example)

# use the following code for utilizing up-to-date STRING DB
tax_id <- 9606  # for human
tax_id <- 10090  # for mouse
library(STRINGdb)
library(igraph)
string_db <- STRINGdb$new(version='10', species=tax_id, score_threshold=0, input_directory='')
xina_result <- xina_analysis(example_clusters, string_db, flag_simplify=FALSE)

# Run XINA with a protein-protein interaction edgelist
data(HPRD)
net_all <- simplify(graph_from_data_frame(d=hprd_ppi, directed=FALSE), remove.multiple = FALSE, remove.loops = TRUE)
xina_result <- xina_analysis(example_clusters, net_all, is_stringdb=FALSE, flag_simplify=FALSE)
```

```r
# End(Not run)
```

### Description

Clustering multiplexed time-series omics data to find co-abundance profiles

### Usage

```r
xina_clustering(f_names, data_column, out_dir = getwd(), nClusters = 20, norm = "sum_normalization", chosen_model = "")
```

### Arguments

- **f_names**: A vector containing input file (.csv) paths
- **data_column**: A vector containing column names (1st row of the input file) of data matrix
- **out_dir**: A directory path for saving clustering results. (default: out_dir=getwd())
- **nClusters**: The number of desired maximum clusters
- **norm**: Default is "sum_normalization". Sum-normalization is to divide the data matrix by row sum. If you want to know more about sum-normalization, see https://www.ncbi.nlm.nih.gov/pubmed/19861354. "zscore" is to calculate Z score for each protein. See `scale`.
- **chosen_model**: You can choose a specific model rather than testing all the models that are available in mclust. `mclustModelNames` If you want k-means clustering instead of the model-based clustering, use "kmeans" here.
Value

- A plot containing a BIC plot in current working directory and a list containing the following information:

<table>
<thead>
<tr>
<th>Item</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>clusters</td>
<td>XINA clustering results</td>
</tr>
<tr>
<td>aligned</td>
<td>XINA clustering results aligned by ID</td>
</tr>
<tr>
<td>data_column</td>
<td>Data matrix column names</td>
</tr>
<tr>
<td>out_dir</td>
<td>The directory path containing XINA results</td>
</tr>
<tr>
<td>nClusters</td>
<td>The number of clusters desired by user</td>
</tr>
<tr>
<td>max_cluster</td>
<td>The number of clusters optimized by BIC</td>
</tr>
<tr>
<td>chosen_model</td>
<td>The used covariance model for model-based clustering</td>
</tr>
<tr>
<td>optimal_BIC</td>
<td>BIC of the optimized covariance model</td>
</tr>
<tr>
<td>condition</td>
<td>Experimental conditions of the user input data</td>
</tr>
<tr>
<td>color_for_condition</td>
<td>Colors assigned to each experimental conditions which is used for condition composition plot</td>
</tr>
<tr>
<td>color_for_clusters</td>
<td>Colors assigned to each clusters which is used for XINA clustering plot</td>
</tr>
<tr>
<td>norm_method</td>
<td>Used normalization method</td>
</tr>
</tbody>
</table>

Examples

```r
# Generate random multiplexed time-series data
random_data_info <- make_random_xina_data()

# Data files
data_files <- paste(random_data_info$conditions, ".csv", sep='')

# time points of the data matrix
data_column <- random_data_info$time_points

# mclust requires the fixed random seed to get reproduce the clustering results
set.seed(0)

# Run the model-based clustering to find co-abundance profiles
exaple_clusters <- xina_clustering(data_files, data_column=data_column, nClusters=30)

# Run k-means clustering to find co-abundance profiles
example_clusters <- xina_clustering(data_files, data_column=data_column, nClusters=30, chosen_model="kmeans")
```

---

**Description**

*xina_enrichment* conducts functional enrichment tests using gene ontology or KEGG pathway terms for a given protein list.
**Usage**

```r
xina_enrichment(string_db, protein_list, enrichment_type = "GO",
               pval_threshold = 0.05, methodMT = "fdr")
```

**Arguments**

- `string_db` STRINGdb object
- `protein_list` A vector of gene names to draw protein-protein interaction network.
- `enrichment_type` A functional annotation for the enrichment test. 'enrichment_type' should be one of 'GO' and 'KEGG'.
- `pval_threshold` P-value threshold to get significantly enriched terms from the given proteins
- `methodMT` Method for p-value adjustment. See `get_enrichment`. Default is 'fdr'.

**Value**

A list of data frames containing enrichment results

**Examples**

```r
## Not run:
library(STRINGdb)
library(Biobase)

# load XINA example data
data(xina_example)

# Get STRING database for protein-protein interaction information
string_db <- STRINGdb$new(version="10", species=9606, score_threshold=0, input_directory="")

# XINA analysis with STRING DB
xina_result <- xina_analysis(example_clusters, string_db)

# Select proteins that showed cluster #1 in the Stimulus2 condition
subgroup <- subset(example_clusters$aligned, Stimulus2==1)
protein_list <- as.vector(subgroup$`Gene name`)

# Enrichment test using KEGG pathway terms that have adjusted p-value less than 0.1
kegg_enriched <- xina_enrichment(string_db, protein_list,
enrichment_type = "KEGG", pval_threshold=0.1)
plot_enrichment_results(kegg_enriched$KEGG, num_terms=10)

# Enrichment test using GO terms that have adjusted p-value less than 0.1
go_enriched <- xina_enrichment(string_db, protein_list,
enrichment_type = "GO", pval_threshold=0.1)
plot_enrichment_results(go_enriched$Component, num_terms=10)

## End(Not run)
```
xina_plot_all is to draw protein-protein interaction network plots of all the clusters

Usage

xina_plot_all(xina_result, clustering_result, condition = "all", centrality_type = NULL, flag_simplify = TRUE, num_breaks = 5, layout_specified = "", vertex_label_flag = FALSE, vertex.label.color = "black", vertex.color = "", edge.color = NULL, vertex.label.dist = 0.6, vertex.label.cex = 0.8, edge.arrow.size = 0.4, vertex.size = 10, vertex.shape = "sphere", legend_location = "bottom", num_clusters_in_row = 5, flag_unknown_only = FALSE, img_size = NULL, img_qual = 300)

Arguments

xina_result A list containing XINA network analysis results. See xina_analysis
clustering_result A list containing XINA clustering results. See xina_clustering
condition Default is 'all', which means use all the proteins to draw graphs. If you specify the experimental condition name used for XINA clustering, xina_plot_all will draw graphs using specific condition's proteins.

centrality_type 'centrality_type' should be one of c('Degree', 'Eigenvector', 'Hub', 'Authority', 'Closeness', 'Betweenness')

<table>
<thead>
<tr>
<th>Centrality score</th>
<th>igraph function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Degree</td>
<td>degree</td>
</tr>
<tr>
<td>Eigenvector</td>
<td>eigen_centrality</td>
</tr>
<tr>
<td>Hub</td>
<td>hub_score</td>
</tr>
<tr>
<td>Authority</td>
<td>authority_score</td>
</tr>
<tr>
<td>Closeness</td>
<td>closeness</td>
</tr>
<tr>
<td>Betweenness</td>
<td>betweenness</td>
</tr>
</tbody>
</table>

flag_simplify If it is TRUE (default), XINA will exclude unconnected proteins
num_breaks 'num_breaks' is the number of ranks based on network centrality. Default is 5.
layout_specified This can change network layout. 'layout_specified' should be one of c('sphere', 'star', 'gem', 'tree', 'circle', 'random', 'nicely'). XINA's layouts are based on igraph's layout. See layout_
xina_plot_all

**Layout**

<table>
<thead>
<tr>
<th>Layout</th>
<th>igraph layout name</th>
</tr>
</thead>
<tbody>
<tr>
<td>sphere</td>
<td>layout_on_sphere</td>
</tr>
<tr>
<td>star</td>
<td>layout_as_star</td>
</tr>
<tr>
<td>gem</td>
<td>layout_with_gem</td>
</tr>
<tr>
<td>tree</td>
<td>layout_as_tree</td>
</tr>
<tr>
<td>circle</td>
<td>layout_in_circle</td>
</tr>
<tr>
<td>random</td>
<td>layout_randomly</td>
</tr>
<tr>
<td>nicely</td>
<td>layout_nicely</td>
</tr>
</tbody>
</table>

Default is 'layout_nicely' of igraph

**vertex_label_flag**

If vertex_label_flag is TRUE (default), igraph network graphs will be labeled by gene names. If vertex_label_flag is FALSE, igraph network graphs will be drawn without labels.

**vertex.label.color**

Color of labels. Default is black.

**vertex.color**

Color of nodes. Default is pink.

**edge.color**

Color of edges. Default is pink.

**vertex.label.dist**

Distance between node and label. Default is 0.6.

**vertex.label.cex**

Size of labels. Default is 0.8.

**edge.arrow.size**

Size of edges. Default is 0.4.

**vertex.size**

Size of nodes. Default is 10.

**vertex.shape**

You can choose node shape. Default is 'sphere'. See shapes.

**legend_location**

If centrality_type is chosen, xina_plot_single adds the color legend guiding rank of nodes based on the centrality score. Default is 'bottomright', but you can choose one of these: 'bottomright', 'bottom', 'bottomleft', 'left', 'topleft', 'top', 'topright', 'right' and 'center'.

**num_clusters_in_row**

The number of clusters in a row on the XINA network plot. Default is 5.

**flag_unknown_only**

If this is TRUE, 'xina_plot_all' will plot proteins that do not have any protein-protein interaction in the given database.

**img_size**

Set the image size. For width=1000 and height=1500, it is img_size=c(1000,1500). Default is c(3000,3000).

**img_qual**

Set the image resolution. Default is 300.

**Value**

PNG images of PPI network plots of all the clusters.
Examples

```r
## the following code is to show how it works quickly
## load XINA example data
data(xina_example)

## load the previously processed XINA analysis results
# if you want to learn how to run 'xina_analysis', please see \link[xina]{xina_analysis}
data(xina_result_example)

# XINA network plots
xina_plot_all(xina_result_example, example_clusters)

# XINA network plots for Control condition
xina_plot_all(xina_result_example, example_clusters, condition='Control')
```

Description

`xina_plot_bycluster` is to draw protein-protein interaction network plots of each cluster.

Usage

```r
xina_plot_bycluster(xina_result, clustering_result, cl = NULL, condition = "all", flag_legend = TRUE, centrality_type = NULL, flag_simplify = TRUE, layout_specified = "", vertex_label_flag = TRUE, vertex.label.dist = 0.6, vertex.label.cex = 0.8, edge.arrow.size = 0.4, vertex.size = 10, vertex.shape = "sphere", vertex.color = "", edge.color = "darkgray", legend_location = "bottom", flag_unknown_only = FALSE)
```

Arguments

- `xina_result`: A list containing XINA network analysis results. See `xina_analysis`
- `clustering_result`: A list containing XINA clustering results. See `xina_clustering`
- `cl`: Cluster number in the XINA clustering results
- `condition`: Default is 'all', which means use all the proteins to draw graphs. If you specify the experimental condition name used for XINA clustering.
- `flag_legend`: If it is TRUE, a legend will be printed out together.
- `centrality_type`: 'centrality_type' should be one of c('Degree', 'Eigenvector', 'Hub', 'Authority', 'Closeness', 'Betweenness')
**Centrality score**

- **Degree**
- **Eigenvector**
- **Hub**
- **Authority**
- **Closeness**
- **Betweenness**

**igraph function**

- `degree`
- `eigen_centrality`
- `hub_score`
- `authority_score`
- `closeness`
- `betweenness`

**flag_simplify**

If it is TRUE (default), XINA will exclude unconnected proteins.

**layout_specified**

This can change network layout. 'layout_specified' should be one of c('sphere', 'star', 'gem', 'tree', 'circle', 'random', 'nicely'). XINA's layouts are based on igraph's layout. See `layout_`

**Layout**

<table>
<thead>
<tr>
<th>Layout</th>
<th>igraph layout name</th>
</tr>
</thead>
<tbody>
<tr>
<td>sphere</td>
<td><code>layout_on_sphere</code></td>
</tr>
<tr>
<td>star</td>
<td><code>layout_as_star</code></td>
</tr>
<tr>
<td>gem</td>
<td><code>layout_with_gem</code></td>
</tr>
<tr>
<td>tree</td>
<td><code>layout_as_tree</code></td>
</tr>
<tr>
<td>circle</td>
<td><code>layout_in_circle</code></td>
</tr>
<tr>
<td>random</td>
<td><code>layout_randomly</code></td>
</tr>
<tr>
<td>nicely</td>
<td><code>layout Nicely</code></td>
</tr>
</tbody>
</table>

Default is 'layout nicely' of igraph.

**vertex_label_flag**

- If `vertex_label_flag` is TRUE (default), igraph network graphs will be labeled by gene names.
- If `vertex_label_flag` is FALSE, igraph network graphs will be drawn without labels.

**vertex.label.dist**

Distance between node and label. Default is 0.6.

**vertex.label.cex**

Size of labels. Default is 0.8.

**edge.arrow.size**

Size of labels. Default is 0.8.

**vertex.size**

Size of nodes. Default is 10.

**vertex.shape**

You can choose node shape. Default is 'sphere'. See `shapes`

**vertex.color**

Color of nodes. Default is pink.

**edge.color**

Color of edges. Default is pink.

**legend_location**

If centrality_type is chosen, xina_plot_single adds the color legend guiding rank of nodes based on the centrality score. Default is 'bottomright', but you can choose one of these 'bottomright', 'bottom', 'bottomleft', 'left', 'topleft', 'top', 'topright', 'right' and 'center'.

**flag_unknown_only**

If this is TRUE, 'xina_plot_bycluster' will plot proteins that do not have any protein-protein interaction in the given database.
Value

A PNG file (XINA_Cluster_Networks.png) displaying protein-protein interaction network plots of all the clusters and a list containing XINA network analysis results

PNG images of PPI network plots of all the clusters

Examples

## the following code is to show how it works quickly
## load XINA example data
data(xina_example)

## load the previously processed XINA analysis results
# if you want to learn how to run `xina_analysis`, please see \link[^1]{xina_analysis}
data(xina_result_example)

# plot cluster #1
xina_plot_bycluster(xina_result_example, example_clusters, cl=1)

# plot PPI network of Control condition in cluster #1
xina_plot_bycluster(xina_result_example, example_clusters, cl=1, condition='Control')

---

**xina_plot_single**  

**xina_plot_single**

### Description

**xina_plot_single** draws protein-protein interaction network plot for given 'protein_list'.

### Usage

```r
xina_plot_single(xina_result, protein_list, centrality_type = NULL,
                  layout_specified = "", vertex_label_flag = TRUE, main = NULL,
                  vertex.label.color = "black", vertex.color = NA,
                  edge.color = "darkgray", vertex.label.dist = 0.6,
                  vertex.label.cex = 0.8, edge.arrow.size = 0.4, vertex.size = 10,
                  vertex.shape = "sphere", legend_location = "bottom",
                  num_breaks = 5, digits_round_up = 5, flag_simplify = TRUE,
                  flag_legend = TRUE)
```

### Arguments

- **xina_result**  A list containing XINA network analysis results. See [xina_analysis](xina_analysis)
- **protein_list**  A vector of gene names to draw a protein-protein interaction network graph.
centrality_type

'centrality_type' should be one of c('Degree', 'Eigenvector', 'Hub', 'Authority', 'Closeness', 'Betweenness')

<table>
<thead>
<tr>
<th>Centrality score</th>
<th>igraph function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Degree</td>
<td>degree</td>
</tr>
<tr>
<td>Eigenvector</td>
<td>eigen_centrality</td>
</tr>
<tr>
<td>Hub</td>
<td>hub_score</td>
</tr>
<tr>
<td>Authority</td>
<td>authority_score</td>
</tr>
<tr>
<td>Closeness</td>
<td>closeness</td>
</tr>
<tr>
<td>Betweenness</td>
<td>betweenness</td>
</tr>
</tbody>
</table>

layout_specified

This can change network layout. 'layout_specified' should be one of c('sphere', 'star', 'gem', 'tree', 'circle', 'random', 'nicely'). XINA's layouts are based on igraph's layout. See layout_

<table>
<thead>
<tr>
<th>Layout</th>
<th>igraph layout name</th>
</tr>
</thead>
<tbody>
<tr>
<td>sphere</td>
<td>layout_on_sphere</td>
</tr>
<tr>
<td>star</td>
<td>layout_as_star</td>
</tr>
<tr>
<td>gem</td>
<td>layout_with_gem</td>
</tr>
<tr>
<td>tree</td>
<td>layout_as_tree</td>
</tr>
<tr>
<td>circle</td>
<td>layout_in_circle</td>
</tr>
<tr>
<td>random</td>
<td>layout_randomly</td>
</tr>
<tr>
<td>nicely</td>
<td>layout_nicely</td>
</tr>
</tbody>
</table>

Default is 'layout_nicely' of igraph

vertex_label_flag

If vertex_label_flag is TRUE (default), igraph network graphs will be labeled by gene names. If vertex_label_flag is FALSE, igraph network graphs will be drawn without labels.

main

Title of network figure. IF it is NULL (default), it will be the number of plotted proteins.

vertex.label.color

Color of labels. Default is black.

vertex.color

Color of nodes. Default is pink.

draw.pbq.color

Color of edges. Default is pink.

vertex.label.dist

Distance between node and label. Default is 0.6

vertex.label.cex

Size of labels. Default is 0.8

draw.pbq.size

Size of edges. Default is 0.4

vertex.size

Size of nodes. Default is 10

vertex.shape

You can choose node shape. Default is 'sphere'. See shapes
If centrality_type is chosen, 'xina_plot_single' adds the color legend guiding rank of nodes based on the centrality score. Default is 'bottomright', but you can choose one of these 'bottomright', 'bottom', 'bottomleft', 'left', 'topleft', 'top', 'topright', 'right' and 'center'.

num_breaks 'num_breaks' is the number of ranks based on network centrality. Default is 5.

digits_round_up See Round flag_simplify If it is TRUE (default), XINA will exclude unconnected proteins flag_legend If it is TRUE, a legend will be printed out together.

Value
A PNG file (XINA_Cluster_Networks.png) displaying protein-protein interaction network plots of all the clusters and a list containing XINA network analysis results

Examples
## the following code is to show how it works quickly
## load XINA example data
data(xina_example)

## load the previously processed XINA analysis results
# if you want to learn how to run 'xina_analysis', please see \link[XINA]{xina_analysis}
data(xina_result_example)

# get gene names that are clustered to #21 in "Stimulus2" condition
subgroup <- subset(example_clusters$aligned, Stimulus2==21)
protein_list <- subgroup$`Gene name`

# Calculate protein-protein interaction network
xina_plot_single(xina_result_example, protein_list)

# Calculate protein-protein interaction network and Eigenvector centrality
eigen_info <- xina_plot_single(xina_result_example, protein_list, centrality_type='Eigenvector')

---

xina_result_example Previously processed xina analysis using XINA’s random example data
A list containing 'xina_analysis' results

Description
- All_network. PPI network of all the input proteins
- Sub_network. A list containing PPI networks of each clusters
- Data. XINA clustering results. See xina_clustering
- Nodes. A list of proteins in each cluster
• Conditions. A list of experimental condition of proteins in each cluster
• Titles. A list of plot titles for XINA plotting
• out_dir. A directory path storing XINA network analysis results
• is_stringdb. False = different PPI DB and TRUE = STRING DB

**Format**

A data frame containing STRING protein-protein interaction data

**Source**

XINA
## Index

<table>
<thead>
<tr>
<th>Function</th>
<th>Pages</th>
</tr>
</thead>
<tbody>
<tr>
<td>add_legend</td>
<td>3</td>
</tr>
<tr>
<td>alluvial, alluvial_enriched, alluvial_enrichment_tests</td>
<td>4, 7, 12, 13</td>
</tr>
<tr>
<td>authority_score</td>
<td>32, 35, 37</td>
</tr>
<tr>
<td>betweenness</td>
<td>32, 35, 37</td>
</tr>
<tr>
<td>calculate_centrality_scores, closeness, degree, count</td>
<td>6, 32, 35, 37</td>
</tr>
<tr>
<td>default_size</td>
<td>7</td>
</tr>
<tr>
<td>draw_alluvial_plot</td>
<td>7</td>
</tr>
<tr>
<td>eigen_centrality</td>
<td>32, 35, 37</td>
</tr>
<tr>
<td>example_clusters, extract_data_column</td>
<td>8, 9</td>
</tr>
<tr>
<td>find_similar_clusters</td>
<td>9</td>
</tr>
<tr>
<td>generate_count_table</td>
<td>10</td>
</tr>
<tr>
<td>generate_superset</td>
<td>10</td>
</tr>
<tr>
<td>get_color_for_nodes</td>
<td>11</td>
</tr>
<tr>
<td>get_colors</td>
<td>11</td>
</tr>
<tr>
<td>get_comigrations_by_name</td>
<td>12</td>
</tr>
<tr>
<td>get_condition_biased_comigrations</td>
<td>13</td>
</tr>
<tr>
<td>get_enrichment</td>
<td>31</td>
</tr>
<tr>
<td>get_layout</td>
<td>14</td>
</tr>
<tr>
<td>get_mTOR_proteins</td>
<td>15</td>
</tr>
<tr>
<td>get_random_data</td>
<td>15</td>
</tr>
<tr>
<td>get_stats</td>
<td>16</td>
</tr>
<tr>
<td>get_theme_blank</td>
<td>16</td>
</tr>
<tr>
<td>get_unknown_ppi_nodes</td>
<td>17</td>
</tr>
<tr>
<td>gn, gn_desc</td>
<td>17, 18</td>
</tr>
<tr>
<td>hprd_ppi</td>
<td>18</td>
</tr>
<tr>
<td>hub_score</td>
<td>32, 35, 37</td>
</tr>
<tr>
<td>layout_, layout_as_star, layout_as_tree, layout_in_circle, layout_nicely, layout_on_sphere, layout_randomly, layout_with_gem</td>
<td>32, 35, 37</td>
</tr>
<tr>
<td>length2</td>
<td>19</td>
</tr>
<tr>
<td>load_previous_results</td>
<td>19</td>
</tr>
<tr>
<td>make_random_xina_data</td>
<td>20</td>
</tr>
<tr>
<td>mclustModelNames</td>
<td>29</td>
</tr>
<tr>
<td>mutate_colors</td>
<td>21</td>
</tr>
<tr>
<td>organize_clusters</td>
<td>22</td>
</tr>
<tr>
<td>p.adjust</td>
<td>4</td>
</tr>
<tr>
<td>plot_clusters</td>
<td>22</td>
</tr>
<tr>
<td>plot_clusters_all</td>
<td>23</td>
</tr>
<tr>
<td>plot_condition_compositions, plot_enrichment_results</td>
<td>13, 21, 24, 25</td>
</tr>
<tr>
<td>plot_NA</td>
<td>26</td>
</tr>
<tr>
<td>rank_centrality</td>
<td>27</td>
</tr>
<tr>
<td>Round</td>
<td>38</td>
</tr>
<tr>
<td>scale</td>
<td>29</td>
</tr>
<tr>
<td>shapes</td>
<td>28, 33, 35, 37</td>
</tr>
<tr>
<td>string_example</td>
<td>27</td>
</tr>
<tr>
<td>xina_analysis</td>
<td>17, 28, 32, 34, 36</td>
</tr>
<tr>
<td>xina_clustering</td>
<td>4, 7, 9, 10, 12, 13, 17, 21–24, 28, 29, 32, 34, 38</td>
</tr>
<tr>
<td>xina_enrichment</td>
<td>25, 30</td>
</tr>
<tr>
<td>xina_plot_all</td>
<td>32</td>
</tr>
<tr>
<td>xina_plot_bycluster</td>
<td>34</td>
</tr>
<tr>
<td>xina_plot_single</td>
<td>36</td>
</tr>
<tr>
<td>xina_result_example</td>
<td>38</td>
</tr>
</tbody>
</table>