Package ‘CBNplot’

May 14, 2024

Type Package

Title plot bayesian network inferred from gene expression data based on enrichment analysis results

Version 1.4.0

Description This package provides the visualization of bayesian network inferred from gene expression data. The networks are based on enrichment analysis results inferred from packages including clusterProfiler and ReactomePA. The networks between pathways and genes inside the pathways can be inferred and visualized.

License Artistic-2.0

Encoding UTF-8

Depends R (>= 4.3.0)

Imports ggplot2, magrittr, graphite, ggraph, igraph, bnlearn (>= 4.7), patchwork, org.Hs.eg.db, clusterProfiler, utils, enrichplot, reshape2, ggforce, dplyr, tidyr, stringr, depmap, ExperimentHub, Rmpfr, graphlayouts, BiocFileCache, ggdist, purrr, pvclust, stats, rlang, oaqc

Suggests knitr, arules, concaveman, ReactomePA, bnviewer, DESeq2, GEOquery, rmarkdown, withr, BiocStyle, testthat (>= 3.0.0)

biocViews Visualization, Bayesian, GeneExpression, NetworkInference, Pathways, Reactome, Network, NetworkEnrichment, GeneSetEnrichment

VignetteBuilder knitr

RoxygenNote 7.2.3

URL https://github.com/noriakis/CBNplot

BugReports https://github.com/noriakis/CBNplot/issues

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CBNplot-package

CBNplot-package

CBNplot: plot bayesian network inferred from gene expression data based on enrichment analysis results

Description

This package provides the visualization of bayesian network inferred from gene expression data. The networks are based on enrichment analysis results inferred from packages including clusterProfiler and ReactomePA. The networks between pathways and genes inside the pathways can be inferred and visualized.

Details

[CBNplot::bngeneplot()] - The main function using gene expression data within the pathway to infer Bayesian network. [CBNplot::bnpathplot()] - The main function using pathway expression data, which is defined by eigengene of the gene expression values to infer Bayesian network. [CBNplot::bngeneplotCustom()] - The function that provides custom visualization for the gene network. [CBNplot::bnpathplotCustom()] - The function that provides custom visualization for the pathway network.
bngeneplot

Author(s)

Maintainer: Noriaki Sato <nori@hgc.jp>

See Also

Useful links:

- https://github.com/noriakis/CBNplot
- Report bugs at https://github.com/noriakis/CBNplot/issues

bngeneplot  bngeneplot

Description

Plot gene relationship within the specified pathway

Usage

bngeneplot(
  results,
  exp,
  expSample = NULL,
  algo = "hc",
  R = 20,
  returnNet = FALSE,
  algorithm.args = NULL,
  bypassConverting = FALSE,
  edgeLink = FALSE,
  pathNum = NULL,
  convertSymbol = TRUE,
  expRow = "ENSEMBL",
  interactive = FALSE,
  cexCategory = 1,
  cl = NULL,
  showDir = FALSE,
  chooseDir = FALSE,
  scoreType = "bic-g",
  labelSize = 4,
  layout = "nicely",
  clusterAlpha = 0.2,
  strType = "normal",
  delZeroDegree = TRUE,
  otherVar = NULL,
  otherVarName = NULL,
  onlyDf = FALSE,
  disc = FALSE,
tr = NULL,
remainCont = NULL,
sp = "hsapiens",
compareRef = FALSE,
compareRefType = "intersection",
pathDb = "reactome",
dep = NULL,
depMeta = NULL,
sizeDep = FALSE,
showDepHist = TRUE,
cellLineName = "5637_URINARY_TRACT",
showLineage = FALSE,
orgDb = org.Hs.eg.db,
shadowText = TRUE,
bgColor = "white",
textColor = "black",
strengthPlot = FALSE,
nStrength = 10,
strThresh = NULL,
hub = NULL,
seed = 1,
useSiGN = FALSE
)

Arguments

results the enrichment analysis result
dep the number of bootstrap
returnNet whether to return the network
algo structure learning method used in boot.strength() default to "hc"
expRow the type of the identifier of rows of expression matrix
interactive whether to use bnviewer (default to FALSE)
cexCategory scaling factor of size of nodes
cl cluster object from parallel::makeCluster()

edgeLink use geom_edge_link() instead of geom_edge_diagonal()
pathNum the pathway number (the number of row of the original result, ordered by p-value)
convertSymbol whether the label of resulting network is converted to symbol, default to TRUE
bypassConverting bypass the symbol converting If you use custom annotation databases that does not have SYMBOL listed in keys. ID of rownames and those listed in EA result must be same.
<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>showDir</td>
<td>show the confidence of direction of edges</td>
</tr>
<tr>
<td>chooseDir</td>
<td>if undirected edges are present, choose direction of edges (default: FALSE)</td>
</tr>
<tr>
<td>scoreType</td>
<td>score type to use on choosing direction</td>
</tr>
<tr>
<td>labelSize</td>
<td>the size of label of the nodes</td>
</tr>
<tr>
<td>layout</td>
<td>ggraph layout, default to &quot;nicely&quot;</td>
</tr>
<tr>
<td>clusterAlpha</td>
<td>if specified multiple pathways, the parameter is passed to geom_mark_hull()</td>
</tr>
<tr>
<td>strType</td>
<td>&quot;normal&quot; or &quot;ms&quot; for multiscale implementation</td>
</tr>
<tr>
<td>delZeroDegree</td>
<td>delete zero degree nodes</td>
</tr>
<tr>
<td>otherVar</td>
<td>other variables to be included in the inference</td>
</tr>
<tr>
<td>otherVarName</td>
<td>the names of other variables</td>
</tr>
<tr>
<td>onlyDf</td>
<td>return only data.frame used for inference</td>
</tr>
<tr>
<td>disc</td>
<td>discretize the expression data</td>
</tr>
<tr>
<td>tr</td>
<td>Specify data.frame if one needs to discretize as the same parameters as the other dataset</td>
</tr>
<tr>
<td>remainCont</td>
<td>Specify characters when perform discretization, if some columns are to be remain continuous</td>
</tr>
<tr>
<td>sp</td>
<td>query to graphite::pathways(), default to &quot;hsapiens&quot;</td>
</tr>
<tr>
<td>compareRef</td>
<td>whether compare to the reference network</td>
</tr>
<tr>
<td>compareRefType</td>
<td>&quot;intersection&quot; or &quot;difference&quot;</td>
</tr>
<tr>
<td>pathDb</td>
<td>query to graphite::pathways(), default to &quot;reactome&quot;</td>
</tr>
<tr>
<td>dep</td>
<td>the tibble storing dependency score from library depmap</td>
</tr>
<tr>
<td>depMeta</td>
<td>depmap::depmap_metadata(), needed for showLineage</td>
</tr>
<tr>
<td>sizeDep</td>
<td>whether to reflect DepMap score to the node size</td>
</tr>
<tr>
<td>showDepHist</td>
<td>whether to show depmap histogram</td>
</tr>
<tr>
<td>cellLineName</td>
<td>the cell line name to be included</td>
</tr>
<tr>
<td>showLineage</td>
<td>show the dependency score across the lineage</td>
</tr>
<tr>
<td>orgDb</td>
<td>perform clusterProfiler::setReadable based on this organism database</td>
</tr>
<tr>
<td>shadowText</td>
<td>whether to use shadow text for the better readability default: TRUE</td>
</tr>
<tr>
<td>bgColor</td>
<td>color for text background when shadowText is TRUE</td>
</tr>
<tr>
<td>textColor</td>
<td>color for text when shadowText is TRUE</td>
</tr>
<tr>
<td>strengthPlot</td>
<td>append the barplot depicting edges with high strength</td>
</tr>
<tr>
<td>nStrength</td>
<td>specify how many edges are included in the strength plot</td>
</tr>
<tr>
<td>strThresh</td>
<td>the threshold for strength</td>
</tr>
<tr>
<td>hub</td>
<td>visualize the genes with top-n hub scores</td>
</tr>
<tr>
<td>seed</td>
<td>A random seed to make the analysis reproducible, default is 1.</td>
</tr>
<tr>
<td>useSiGN</td>
<td>default to FALSE. For using SiGN-BN in the function in Windows 10/11, 1.</td>
</tr>
<tr>
<td></td>
<td>Download the SiGN-BN HC+BS binary in WSL (<a href="https://sign.hgc.jp/signbn/download.html">https://sign.hgc.jp/signbn/download.html</a>)</td>
</tr>
<tr>
<td></td>
<td>2. Set PATH to executable (sign.1.8.3)</td>
</tr>
</tbody>
</table>
Value

ggplot2 object

Examples

data("exampleEaRes");data("exampleGeneExp")
res <- bngeneplot(results = exampleEaRes, exp = exampleGeneExp, pathNum = 1,
R = 10, convertSymbol = TRUE, expRow = "ENSEMBL")

Description

Plot gene relationship within the specified pathway using customized theme

Usage

bngeneplotCustom(
  results,
  exp,
  expSample = NULL,
  algo = "hc",
  R = 20,
  pathNum = NULL,
  convertSymbol = TRUE,
  expRow = "ENSEMBL",
  interactive = FALSE,
  cexCategory = 1,
  cl = NULL,
  showDir = FALSE,
  chooseDir = FALSE,
  algorithm.args = NULL,
  labelSize = 4,
  layout = "nicely",
  strType = "normal",
  returnNet = FALSE,
  otherVar = NULL,
  otherVarName = NULL,
  onlyDf = FALSE,
  disc = FALSE,
  tr = NULL,
  remainCont = NULL,
  dep = NULL,
  sizeDep = FALSE,
  orgDb = org.Hs.eg.db,
bngeneplotCustom

bypassConverting = FALSE,
edgeLink = FALSE,
cellLineName = "5637_URINARY_TRACT",
fontFamily = "sans",
strengthPlot = FALSE,
nStrength = 10,
strThresh = NULL,
hub = NULL,
glowEdgeNum = NULL,
nodePal = c("blue", "red"),
edgePal = c("blue", "red"),
textCol = "black",
titleCol = "black",
backCol = "white",
barTextCol = "black",
barPal = c("red", "blue"),
barBackCol = "white",
scoreType = "bic-g",
barLegendKeyCol = "white",
barAxisCol = "black",
bg.colour = NULL,
bg.r = 0.1,
barPanelGridCol = "black",
titleSize = 24,
seed = 1
)

Arguments

results the enrichment analysis result
exp gene expression matrix
expSample candidate rows to be included in the inference default to all
algo structure learning method used in boot.strength() default to "hc"
R the number of bootstrap
pathNum the pathway number (the number of row of the original result, ordered by p-value)
convertSymbol whether the label of resulting network is converted to symbol, default to TRUE
expRow the type of the identifier of rows of expression matrix
interactive whether to use bnviewer (default to FALSE)
cexCategory scaling factor of size of nodes
c1 cluster object from parallel::makeCluster()
showDir show the confidence of direction of edges
chooseDir if undirected edges are present, choose direction of edges
algorithm.args parameters to pass to bnlearn structure learning function
labelSize the size of label of the nodes
**bngeneplotCustom**

- **layout**: ggraph layout, default to "nicely"
- **strType**: "normal" or "ms" for multiscale implementation
- **returnNet**: whether to return the network
- **otherVar**: other variables to be included in the inference
- **otherVarName**: the names of other variables
- **onlyDf**: return only data.frame used for inference
- **disc**: discretize the expression data
- **tr**: Specify data.frame if one needs to discretize as the same parameters as the other dataset
- **remainCont**: Specify characters when perform discretization, if some columns are to be remain continuous
- **dep**: the tibble storing dependency score from library depmap
- **sizeDep**: whether to reflect DepMap score to the node size
- **orgDb**: perform clusterProfiler::setReadable based on this organism database
- **bypassConverting**: bypass the symbol converting ID of rownames and those listed in EA result must be same
- **edgeLink**: use geom_edge_link() instead of geom_edge_diagonal()
- **cellLineName**: the cell line name to be included
- **fontFamily**: font family name to be used for plotting
- **strengthPlot**: append the barplot depicting edges with high strength
- **nStrength**: specify how many edges are included in the strength plot
- **strThresh**: the threshold for strength
- **hub**: visualize the genes with top-n hub scores
- **glowEdgeNum**: edges with top-n confidence of direction are highlighted
- **nodePal**: vector of coloring of nodes (low, high)
- **edgePal**: vector of coloring of edges (low, high)
- **textCol**: color of texts in network plot
- **titleCol**: color of title in network plot
- **backCol**: color of background in network plot
- **barTextCol**: text color in barplot
- **barPal**: bar color
- **barBackCol**: background color in barplot
- **scoreType**: score type to use on inference
- **barLegendKeyCol**: legend key color in barplot
- **barAxisCol**: axis color in barplot
- **bg.colour**: parameter to pass to geom_node_text
- **bg.r**: parameter to pass to geom_node_text
- **barPanelGridCol**: panel grid color in barplot
- **titleSize**: the size of title
- **seed**: A random seed to make the analysis reproducible, default is 1.
Value

ggplot2 object

Examples

data("exampleEaRes");data("exampleGeneExp")
res <- bngeneplotCustom(results=exampleEaRes, exp=exampleGeneExp,
    pathNum=1, glowEdgeNum=NULL, hub=3, R=40,
    fontFamily="sans")

Description

Testing various R for bayesian network between genes

Usage

bngenetest(
    results,
    exp,
    expSample = NULL,
    algo = "hc",
    Rrange = seq(2, 40, 2),
    cl = NULL,
    algorithm.args = NULL,
    pathNum = NULL,
    convertSymbol = TRUE,
    expRow = "ENSEMBL",
    scoreType = "aic-g",
    orgDb = org.Hs.eg.db,
    bypassConverting = FALSE
)

Arguments

results the enrichment analysis result
exp gene expression matrix
expSample candidate rows to be included in the inference default to all
algo structure learning method used in boot.strength() default to "hc"
Rrange the sequence of R values to be tested
cl cluster object from parallel::makeCluster()
algorithm.args parameters to pass to bnlearn structure learning function
pathNum: the pathway number (the number of row of the original result, ordered by p-value)

collSymbol: whether the label of resulting network is converted to symbol, default to TRUE

expRow: the type of the identifier of rows of expression matrix

scoreType: return the specified scores

orgDb: perform clusterProfiler::setReadable based on this organism database

bypassConverting: bypass symbol converting

Value

list of graphs and scores

Examples

data("exampleEaRes"); data("exampleGeneExp")
res <- bngenetest(results = exampleEaRes, exp = exampleGeneExp,
algo="hc", Rrange=seq(10, 30, 10), pathNum=1, scoreType="bge")

bnpathplot

Description

Plot pathway relationship

Usage

bnpathplot(
results,
exp,
expSample = NULL,
algo = "hc",
algorithm.args = NULL,
expRow = "ENSEMBL",
cl = NULL,
returnNet = FALSE,
otherVar = NULL,
otherVarName = NULL,
qvalueCutOff = 0.05,
adjpCutOff = 0.05,
nCategory = 15,
R = 20,
interactive = FALSE,
color = "p.adjust",
cexCategory = 1,
bnpathplot

cexLine = 0.5,
chooseDir = FALSE,
showDir = FALSE,
delZeroDegree = TRUE,
labelSize = 4,
layout = "nicely",
onlyDf = FALSE,
disc = FALSE,
tr = NULL,
remainCont = NULL,
shadowText = TRUE,
bgColor = "white",
textColor = "black",
compareRef = FALSE,
strThresh = NULL,
strType = "normal",
hub = NULL,
scoreType = "bic-g",
databasePal = "Set2",
dep = NULL,
sizeDep = FALSE,
orgDb = org.Hs.eg.db,
bypassConverting = FALSE,
useSiGN = FALSE,
edgeLink = TRUE,
cell_lineName = "5637_URINARY_TRACT",
strengthPlot = FALSE,
nStrength = 10,
seed = 1
}

Arguments

results the enrichment analysis result
exp gene expression matrix
expSample candidate rows to be included in the inference default to all
algo structure learning method used in boot.strength() default to "hc"
algorithm.args parameters to pass to bnlearn structure learning function
expRow the type of the identifier of rows of expression matrix
cl cluster object from parallel::makeCluster()
returnNet whether to return the network
otherVar other variables to be included in the inference
otherVarName the names of other variables
qvalueCutOff the cutoff value for qvalue
adjpCutOff the cutoff value for adjusted pvalues
nCategory: the number of pathways to be included
R: the number of bootstrap
interactive: whether to use bnviewer (default to FALSE)
color: color of node, default to adjusted p-value
cexCategory: scaling factor of size of nodes
cexLine: scaling factor of width of edges
chooseDir: if undirected edges are present, choose direction of edges
showDir: show the confidence of direction of edges
delZeroDegree: delete zero degree nodes
labelSize: the size of label of the nodes
layout: ggraph layout, default to "nicely"
onlyDf: return only data.frame used for inference
disc: discretize the expression data
tr: Specify data.frame if one needs to discretize as the same parameters as the other dataset
remainCont: Specify characters when perform discretization, if some columns are to be remain continuous
shadowText: whether to use shadow text for the better readability (default: TRUE)
bgColor: color for text background when shadowText is TRUE
textColor: color for text when shadowText is TRUE
cmpareRef: whether compare to the reference network between pathway
strThresh: threshold for strength, automatically determined if NULL
strType: "normal" or "ms" for multiscale implementation
hub: change the shape of node according to hub scores (default NULL)
scoreType: score type to use on choosing edge direction
databasePal: palette to be used in scale_color_brewer when the multiple results are to be shown
dep: the tibble storing dependency score from library depmap
sizeDep: whether to reflect DepMap score to the node size
orgDb: perform clusterProfiler::setReadable based on this organism database
bypassConverting: bypass the symbol converting If you use custom annotation databases that does not have SYMBOL listed in keys. ID of rownames and those listed in EA result must be same.
useSiGN: default to FALSE. For using SiGN-BN in the function in Windows 10/11, 1. Download the SiGN-BN HC+BS binary in WSL (https://sign.hgc.jp/signbn/download.html) 2. Set PATH to executable (sign.1.8.3)
edgeLink: whether to set edge to geom_edge_link() FALSE to use geom_edge_diagonal()
cellLineName: the cell line name to be included
strengthPlot: append the barplot depicting edges with high strength
nStrength: specify how many edges are included in the strength plot
seed: A random seed to make the analysis reproducible, default is 1.
Value

ggplot2 object

Examples

data("exampleEaRes"); data("exampleGeneExp")

res <- bnpathplot(results = exampleEaRes, exp = exampleGeneExp,
  R = 10, expRow = "ENSEMBL")

Description

Plot pathway relationship using customized theme

Usage

bnpathplotCustom(
  results,
  exp,
  expSample = NULL,
  algo = "hc",
  R = 20,
  expRow = "ENSEMBL",
  color = "p.adjust",
  cexCategory = 1,
  cl = NULL,
  showDir = FALSE,
  chooseDir = FALSE,
  labelSize = 4,
  layout = "nicely",
  strType = "normal",
  compareRef = FALSE,
  disc = FALSE,
  tr = NULL,
  remainCont = NULL,
  qvalueCutOff = 0.05,
  adjpCutOff = 0.05,
  nCategory = 15,
  cexLine = 1,
  returnNet = FALSE,
  dep = NULL,
  sizeDep = FALSE,
  cellLineName = "5637_URINARY_TRACT",
  fontFamily = "sans",
otherVar = NULL,
otherVarName = NULL,
onlyDf = FALSE,
algorithm.args = NULL,
strengthPlot = FALSE,
nStrength = 10,
edgeLink = FALSE,
strThresh = NULL,
hub = NULL,
glowEdgeNum = NULL,
nodePal = c("blue", "red"),
edgePal = c("blue", "red"),
textCol = "black",
backCol = "white",
barTextCol = "black",
barPal = c("red", "blue"),
barBackCol = "white",
scoreType = "bic-g",
barLegendKeyCol = "white",
orgDb = org.Hs.eg.db,
barAxisCol = "black",
barPanelGridCol = "black",
bg.colour = NULL,
bg.r = 0.1,
seed = 1,
bypassConverting = FALSE
)

Arguments

results the enrichment analysis result
exp gene expression matrix
expSample candidate rows to be included in the inference default to all
algo structure learning method used in boot.strength() default to "hc"
R the number of bootstrap
expRow the type of the identifier of rows of expression matrix
color color of node, default to adjusted p-value
cexCategory scaling factor of size of nodes
c1 cluster object from parallel::makeCluster()
showDir show the confidence of direction of edges
chooseDir if undirected edges are present, choose direction of edges
labelSize the size of label of the nodes
layout ggraph layout, default to "nicely"
strType "normal" or "ms" for multiscale implementation
compareRef whether compare to the reference network between pathway
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>disc</td>
<td>discretize the expression data</td>
</tr>
<tr>
<td>tr</td>
<td>Specify data.frame if one needs to discretize as the same parameters as the other dataset</td>
</tr>
<tr>
<td>remainCont</td>
<td>Specify characters when perform discretization, if some columns are to be remain continuous</td>
</tr>
<tr>
<td>qvalueCutOff</td>
<td>the cutoff value for qvalue</td>
</tr>
<tr>
<td>adjpCutOff</td>
<td>the cutoff value for adjusted pvalues</td>
</tr>
<tr>
<td>nCategory</td>
<td>the number of pathways to be included</td>
</tr>
<tr>
<td>cexLine</td>
<td>scaling factor of width of edges</td>
</tr>
<tr>
<td>returnNet</td>
<td>whether to return the network</td>
</tr>
<tr>
<td>dep</td>
<td>the tibble storing dependency score from library depmap</td>
</tr>
<tr>
<td>sizeDep</td>
<td>whether to reflect DepMap score to the node size</td>
</tr>
<tr>
<td>cellLineName</td>
<td>the cell line name to be included</td>
</tr>
<tr>
<td>fontFamily</td>
<td>font family name to be used for plotting</td>
</tr>
<tr>
<td>otherVar</td>
<td>other variables to be included in the inference</td>
</tr>
<tr>
<td>otherVarName</td>
<td>the names of other variables</td>
</tr>
<tr>
<td>onlyDf</td>
<td>return only data.frame used for inference</td>
</tr>
<tr>
<td>algorithm.args</td>
<td>parameters to pass to bnlearn structure learning function</td>
</tr>
<tr>
<td>strengthPlot</td>
<td>append the barplot depicting edges with high strength</td>
</tr>
<tr>
<td>nStrength</td>
<td>specify how many edges are included in the strength plot</td>
</tr>
<tr>
<td>edgeLink</td>
<td>use geom_edge_link() instead of geom_edge_diagonal()</td>
</tr>
<tr>
<td>strThresh</td>
<td>threshold for strength, automatically determined if NULL</td>
</tr>
<tr>
<td>hub</td>
<td>change the shape of node according to hub scores (default NULL)</td>
</tr>
<tr>
<td>glowEdgeNum</td>
<td>edges with top-n confidence of direction are highlighted</td>
</tr>
<tr>
<td>nodePal</td>
<td>vector of coloring of nodes (low, high)</td>
</tr>
<tr>
<td>edgePal</td>
<td>vector of coloring of edges (low, high)</td>
</tr>
<tr>
<td>textCol</td>
<td>color of texts in network plot</td>
</tr>
<tr>
<td>backCol</td>
<td>color of background in network plot</td>
</tr>
<tr>
<td>barTextCol</td>
<td>text color in barplot</td>
</tr>
<tr>
<td>barPal</td>
<td>bar color</td>
</tr>
<tr>
<td>barBackCol</td>
<td>background color in barplot</td>
</tr>
<tr>
<td>scoreType</td>
<td>score type to use on inference</td>
</tr>
<tr>
<td>barLegendKeyCol</td>
<td>legend key color in barplot</td>
</tr>
<tr>
<td>orgDb</td>
<td>perform clusterProfiler::setReadable based on this organism database</td>
</tr>
<tr>
<td>barAxisCol</td>
<td>axis color in barplot</td>
</tr>
<tr>
<td>barPanelGridCol</td>
<td>panel grid color in barplot</td>
</tr>
</tbody>
</table>
bg.colour parameter to pass to geom_node_text
bg.r parameter to pass to geom_node_text
seed A random seed to make the analysis reproducible, default is 1.
bypassConverting bypass the symbol converting ID of rownames and those listed in EA result must be same

Value
ggplot2 object

Examples
data("exampleEaRes");data("exampleGeneExp")
res <- bnpathplotCustom(results=exampleEaRes, exp=exampleGeneExp, fontFamily="sans", glowEdgeNum=3, hub=3)

Description
Testing various R for bayesian network between pathways

Usage
bnpathtest(
  results,
  exp,
  expSample = NULL,
  algo = "hc",
  algorithm.args = NULL,
  expRow = "ENSEMBL",
  cl = NULL,
  orgDb = org.Hs.eg.db,
  bypassConverting = FALSE,
  qvalueCutOff = 0.05,
  adjpCutOff = 0.05,
  nCategory = 15,
  Rrange = seq(2, 40, 2),
  scoreType = "aic-g"
)
Arguments

results  the enrichment analysis result
exp      gene expression matrix
expSample candidate rows to be included in the inference default to all
algo     structure learning method used in boot.strength() default to "hc"
algorithm.args parameters to pass to bnlearn structure learning function
expRow   the type of the identifier of rows of expression matrix
cl       cluster object from parallel::makeCluster()
orgDb    perform clusterProfiler::setReadable based on this organism database
bypassConverting bypass symbol converting
qvalueCutOff the cutoff value for qvalue
adjpCutOff the cutoff value for adjusted pvalues
nCategory the number of pathways to be included
Rrange   the sequence of R values to be tested
scoreType return the specified scores

Value

list of graphs and scores

Examples

data("exampleEaRes");data("exampleGeneExp"
res <- bnpathtest(results = exampleEaRes, exp = exampleGeneExp,
    algo="hc", Rrange=seq(10, 30, 10), expRow = "ENSEMBL",
    scoreType="bge")

Description

Take the list of networks and returns the F-measures

Usage

compareBNs(listOfNets)

Arguments

listOfNets list of networks
Value

F-measures of each combination of network

Examples

data("exampleEaRes"); data("exampleGeneExp")

net1 <- bngeneplot(results = exampleEaRes, exp = exampleGeneExp, pathNum = 1, R = 10, returnNet=TRUE)
net2 <- bngeneplot(results = exampleEaRes, exp = exampleGeneExp, pathNum = 1, R = 10, returnNet=TRUE)
res <- compareBNs(list(net1$av, net2$av))

exampleEaRes    Example enrichment analysis result

Description

An example enrichment analysis result to be used for testing purpose. The result was produced by running ReactomePA::enrichPathway() and subsequent clusterProfiler::setReadable() on 'exampleGeneExp'.

Usage

data(exampleEaRes)

Format

An object of class enrichResult with 47 rows and 9 columns.

Value

eample enrichment analysis result

exampleGeneExp    Example gene expression data

Description

An example gene expression data to be used for testing purpose made by runif() for ERCC genes and 100 samples. No biological meanings can be obtained from the data.

Usage

data(exampleGeneExp)
inferMS

Format
An object of class data.frame with 7 rows and 100 columns.

Value
example gene expression

inferMS inferMS

Description
multiscale bootstrap-based inference of Bayesian network

Usage
inferMS(data, algo, algorithm.args, R, cl = NULL, r = seq(0.5, 1.5, 0.1))

Arguments
data
data.frame to perform inference
algo
structure learning method used in boot.strength()
algorithm.args
parameters to pass to bnlearn structure learning function
R
the number of bootstrap
cl
cluster object from parallel::makeCluster()
r
vector for size of each bootstrap replicate

Value
object of class bn.strength

loadSign loadSign

Description
Load the output of SiGN-BN (HC+BS)

Usage
loadSign(fileName)

Arguments
fileName
the result of SiGN-BN
queryCpDistLs

Value

list of edges, nodes, strength, and bn (bnlearn)

descPath

Description

obtain the analysis results including the queried gene symbol

Usage

obtainPath(res, geneSymbol)

Arguments

res enrichment analysis result
geneSymbol the candidate gene

Value

subset of enrichment results

Examples

data("exampleEaRes")
obtainPath(res = exampleEaRes, geneSymbol="ERCC7")

queryCpDistLs

Description

produce a plot of bnlearn::cpdist by performing bnlearn::cpdist on specified node, evidence and level.

Usage

queryCpDistLs(fitted, candidate, evidences, discPalette = "Set2", ...)

Arguments

fitted bn.fit object
candidate name of node
evidences the evidences
discPalette palette to be used for plotting if the event is discrete
... other parameters passed to bnlearn cpdist
queryCpDistLw

Value

list of dataframe containing raw values

Examples

library(bnlearn)
data("exampleEaRes")
data("exampleGeneExp")
net <- bngeneplot(exampleEaRes, exampleGeneExp, 
  pathNum=1, returnNet=TRUE)
fitted <- bn.fit(net$av, net$df)
res <- queryCpDistLs(fitted, candidate="ERCC4", 
  evidences=c("ERCC2<0.1","ERCC2>0.5","ERCC2>0.8"), n=500)

queryCpDistLw

Description

produce a plot of bnlearn::cpdist by performing bnlearn::cpdist on specified node, evidence and 
level.

Usage

queryCpDistLw(
  fitted, 
  candidate, 
  evidence, 
  levels, 
  point = FALSE, 
  pointSize = 5, 
  alpha = TRUE, 
  ...
)

Arguments

  fitted        bn.fit object
  candidate     name of node
  evidence      evidence variable name
  levels        level to be listed
  point         geom_point the weighted mean
  pointSize     point size for geom_point
  alpha         whether to reflect the weights by alpha (TRUE) or color (FALSE)
  ...           other parameters passed to bnlearn cpdist
queryCpDistLw

Value

list of dataframe containing raw values

Examples

```r
library(bnlearn)
data("exampleEaRes")
data("exampleGeneExp")
net <- bngeneplot(exampleEaRes, exampleGeneExp,
                   pathNum=1, returnNet=TRUE)
fitted <- bn.fit(net$av, net$df)
res <- queryCpDistLw(fitted, candidate="ERCC4", evidence="ERCC2",
                     levels=c(0.1, 0.5, 0.8), n=500)
```
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