Package ‘CBNplot’

May 3, 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.

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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, pvcust, stats, rlang, oaqc

Suggests knitr, arules, concaveman, ReactomePA, bnviewer, DESeq2, GEOquery, markdown, 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

Config/testthat/edition 3

git_url https://git.bioconductor.org/packages/CBNplot

git_branch RELEASE_3_19

git_last_commit 1bd1558

git_last_commit_date 2024-04-30
CBNplot-package

Repository Bioconductor 3.19
Date/Publication 2024-05-03
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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

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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
gene expression matrix
candidate samples to be included in the inference default to all
structure learning method used in boot.strength() default to "hc"
the number of bootstrap
whether to return the network
parameters to pass to bnlearn structure learning function
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.
use geom_edge_link() instead of geom_edge_diagonal()
the pathway number (the number of row of the original result, ordered by p-value)
whether the label of resulting network is converted to symbol, default to TRUE
the type of the identifier of rows of expression matrix
whether to use bnviewer (default to FALSE)
scaling factor of size of nodes
cluster object from parallel::makeCluster()
showDir  
chooseDir  
scoreType  
labelSize  
layout  
clusterAlpha  
strType  
delZeroDegree  
otherVar  
otherVarName  
onlyDf  
disc  
tr  
remainCont  
sp  
compareRef  
compareRefType  
pathDb  
dep  
depMeta  
sizeDep  
showDepHist  
cellLineName  
showLineage  
orgDb  
shadowText  
bgColor  
textColor  
strengthPlot  
nStrength  
strThresh  
hub  
seed  
useSiGN  

show the confidence of direction of edges
if undirected edges are present, choose direction of edges (default: FALSE)
score type to use on choosing direction
the size of label of the nodes
ggraph layout, default to "nicely"
if specified multiple pathways, the parameter is passed to geom_mark_hull()
"normal" or "ms" for multiscale implementation
delete zero degree nodes
other variables to be included in the inference
the names of other variables
return only data.frame used for inference
discretize the expression data
Specify data.frame if one needs to discretize as the same parametersas the other dataset
Specify characters when perform discretization, if some columns are to be remain continuous
query to graphite::pathways(), default to "hsapiens"
whether compare to the reference network
"intersection" or "difference"
query to graphite::pathways(), default to "reactome"
the tibble storing dependency score from library depmap
depmap::depmap_metadata(), needed for showLineage
whether to reflect DepMap score to the node size
whether to show depmap histogram
the cell line name to be included
show the dependency score across the lineage
perform clusterProfiler::setReadable based on this organism database
whether to use shadow text for the better readability default: TRUE
color for text background when shadowText is TRUE
color for text when shadowText is TRUE
append the barplot depicting edges with high strength
specify how many edges are included in the strength plot
the threshold for strength
visualize the genes with top-n hub scores
A random seed to make the analysis reproducible, default is 1.
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)
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
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
dgeLink: 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**

```r
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**

```r
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**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>results</code></td>
<td>the enrichment analysis result</td>
</tr>
<tr>
<td><code>exp</code></td>
<td>gene expression matrix</td>
</tr>
<tr>
<td><code>expSample</code></td>
<td>candidate rows to be included in the inference default to all</td>
</tr>
<tr>
<td><code>algo</code></td>
<td>structure learning method used in boot.strength() default to &quot;hc&quot;</td>
</tr>
<tr>
<td><code>Rrange</code></td>
<td>the sequence of R values to be tested</td>
</tr>
<tr>
<td><code>cl</code></td>
<td>cluster object from parallel::makeCluster()</td>
</tr>
<tr>
<td><code>algorithm.args</code></td>
<td>parameters to pass to bnlearn structure learning function</td>
</tr>
</tbody>
</table>
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
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")

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,  
cellLineName = "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
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>nCategory</td>
<td>the number of pathways to be included</td>
</tr>
<tr>
<td>R</td>
<td>the number of bootstrap</td>
</tr>
<tr>
<td>interactive</td>
<td>whether to use bnviewer (default to FALSE)</td>
</tr>
<tr>
<td>color</td>
<td>color of node, default to adjusted p-value</td>
</tr>
<tr>
<td>cexCategory</td>
<td>scaling factor of size of nodes</td>
</tr>
<tr>
<td>cexLine</td>
<td>scaling factor of width of edges</td>
</tr>
<tr>
<td>chooseDir</td>
<td>if undirected edges are present, choose direction of edges</td>
</tr>
<tr>
<td>showDir</td>
<td>show the confidence of direction of edges</td>
</tr>
<tr>
<td>delZeroDegree</td>
<td>delete zero degree nodes</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>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>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>compareRef</td>
<td>whether compare to the reference network between pathway</td>
</tr>
<tr>
<td>strThresh</td>
<td>threshold for strength, automatically determined if NULL</td>
</tr>
<tr>
<td>strType</td>
<td>&quot;normal&quot; or &quot;ms&quot; for multiscale implementation</td>
</tr>
<tr>
<td>hub</td>
<td>change the shape of node according to hub scores (default NULL)</td>
</tr>
<tr>
<td>scoreType</td>
<td>score type to use on choosing edge direction</td>
</tr>
<tr>
<td>databasePal</td>
<td>palette to be used in scale_color_brewer when the multiple results are to be shown</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>orgDb</td>
<td>perform clusterProfiler::setReadable based on this organism database</td>
</tr>
<tr>
<td>bypassConverting</td>
<td>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.</td>
</tr>
<tr>
<td>useSiGN</td>
<td>default to FALSE. For using SiGN-BN in the function in Windows 10/11, 1. 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>) 2. Set PATH to executable (sign.1.8.3)</td>
</tr>
<tr>
<td>edgeLink</td>
<td>whether to set edge to geom_edge_link() FALSE to use geom_edge_diagonal()</td>
</tr>
<tr>
<td>cellLineName</td>
<td>the cell line name to be included</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>seed</td>
<td>A random seed to make the analysis reproducible, default is 1.</td>
</tr>
</tbody>
</table>
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
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
qvalueCutOff  the cutoff value for qvalue
adjpCutOff  the cutoff value for adjusted pvalues
nCategory  the number of pathways to be included
cexLine  scaling factor of width of edges
returnNet  whether to return the network
dep  the tibble storing dependency score from library depmap
sizeDep  whether to reflect DepMap score to the node size
cellLineName  the cell line name to be included
fontFamily  font family name to be used for plotting
otherVar  other variables to be included in the inference
otherVarName  the names of other variables
onlyDf  return only data.frame used for inference
algorithm.args  parameters to pass to bnlearn structure learning function
strengthPlot  append the barplot depicting edges with high strength
nStrength  specify how many edges are included in the strength plot
edgeLink  use geom_edge_link() instead of geom_edge_diagonal()
strThresh  threshold for strength, automatically determined if NULL
hub  change the shape of node according to hub scores (default NULL)
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
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
orgDb  perform clusterProfiler::setReadable based on this organism database
barAxisCol  axis color in barplot
barPanelGridCol  panel grid color in barplot
bnpathtest

- 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"
)

compareBNs

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 <- bnpathest(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
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))

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

example enrichment analysis result

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

Value
example gene expression

data.frame

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

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

Usage
loadSign(fileName)

Arguments
fileName the result of SiGN-BN
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

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

Value
subset of enrichment results

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

obtainPath

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")

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

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

Value
subset of enrichment results

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

Value
list of edges, nodes, strength, and bn (bnlearn)
**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 <- queryCpDistLs(fitted, candidate="ERCC4",
                     evidences=c("ERCC2<0.1","ERCC2>0.5","ERCC2>0.8"), n=500)
```

**Description**

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

**Usage**

```r
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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