Package ‘CBNplot’

March 6, 2024

Type  Package

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

Version 1.2.1

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, 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

Config/testthat/edition 3

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

git_branch RELEASE_3_18

git_last_commit ccccb66

git_last_commit_date 2023-12-21
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)

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See Also

Useful links:

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

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
exp gene expression matrix
expSample candidate samples 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
returnNet whether to return the network
algorithm.args 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.
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
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()
```
showDir  
  show the confidence of direction of edges
chooseDir  
  if undirected edges are present, choose direction of edges (default: FALSE)
scoreType  
  score type to use on choosing direction
labelSize  
  the size of label of the nodes
layout  
  ggraph layout, default to "nicely"
clusterAlpha  
  if specified multiple pathways, the parameter is passed to geom_mark_hull()
strType  
  "normal" or "ms" for multiscale implementation
deXZeroDegree  
  delete zero degree nodes
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
sp  
  query to graphite::pathways(), default to "hsapiens"
compareRef  
  whether compare to the reference network
compareRefType  
  "intersection" or "difference"
pathDb  
  query to graphite::pathways(), default to "reactome"
dep  
  the tibble storing dependency score from library depmap
depMeta  
  depmap::depmap_metadata(), needed for showLineage
sizeDep  
  whether to reflect DepMap score to the node size
showDepHist  
  whether to show depmap histogram
cellLineName  
  the cell line name to be included
showLineage  
  show the dependency score across the lineage
orgDb  
  perform clusterProfiler::setReadable based on this organism database
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
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
seed  
  A random seed to make the analysis reproducible, default is 1.
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)
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
cl 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

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

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

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,
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,
cllLineName = "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
compareRef: 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")

bnpathplotCustom

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,
onlyIf = 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
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"
)

Value

ggplot2 object

Examples

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

```r
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
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**
example 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

---

**Description**

multiscale bootstrap-based inference of Bayesian network

**Usage**

```r
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**

```r
loadSign(fileName)
```

**Arguments**

- `fileName` : the result of SiGN-BN
queryCpDistLs

Value

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

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")

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

```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
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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