Package ‘CBNplot’

May 29, 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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CBNplot-package

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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.
Author(s)

Maintainer: Noriaki Sato <nori@hgc.jp>

See Also

Useful links:

- [https://github.com/noriakis/CBNplot](https://github.com/noriakis/CBNplot)
- Report bugs at [https://github.com/noriakis/CBNplot/issues](https://github.com/noriakis/CBNplot/issues)

Description

Plot gene relationship within the specified pathway

Usage

```r
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
c1 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

**delZeroDegree** 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 expressoin 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
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
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>layout</td>
<td>ggraph layout, default to &quot;nicely&quot;</td>
</tr>
<tr>
<td>strType</td>
<td>&quot;normal&quot; or &quot;ms&quot; for multiscale implementation</td>
</tr>
<tr>
<td>returnNet</td>
<td>whether to return the network</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>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 ID of rownames and those listed in EA result must be same</td>
</tr>
<tr>
<td>edgeLink</td>
<td>use geom_edge_link() instead of geom_edge_diagonal()</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>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>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>titleCol</td>
<td>color of title 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>barAxisCol</td>
<td>axis color in barplot</td>
</tr>
<tr>
<td>bg.colour</td>
<td>parameter to pass to geom_node_text</td>
</tr>
<tr>
<td>bg.r</td>
<td>parameter to pass to geom_node_text</td>
</tr>
<tr>
<td>barPanelGridCol</td>
<td>panel grid color in barplot</td>
</tr>
<tr>
<td>titleSize</td>
<td>the size of title</td>
</tr>
<tr>
<td>seed</td>
<td>A random seed to make the analysis reproducible, default is 1.</td>
</tr>
</tbody>
</table>
bngenetest

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", 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)

corvertSymbol
- 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,
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
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.
bnpathplotCustom

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,  
onlyDf = FALSE,  
algoArgs = NULL,  
nStrength = 10,  
edgeLink = FALSE,  
strThresh = NULL,  
hub = NULL,  
glowEdgeNum = NULL,  
nodePal = c("blue", "red"),  
edgePal = c("blue", "red"),  
backCol = "white",  
textCol = "black",  
backTextCol = "black",  
barPal = c("red", "blue"),  
barBackCol = "white",  
scoreType = "bic-g",  
barLegendKeyCol = "white",  
orgDb = org.Hs.eg.db,  
barAxisCol = "black",  
bg.colour = NULL,  
unit = 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
cl 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
discretize the expression data

Specify data.frame if one needs to discretize as the same parameters as the other dataset

Specify characters when perform discretization, if some columns are to be remain continuous

the cutoff value for qvalue

the cutoff value for adjusted pvalues

the number of pathways to be included

scaling factor of width of edges

whether to return the network

the tibble storing dependency score from library depmap

whether to reflect DepMap score to the node size

the cell line name to be included

font family name to be used for plotting

other variables to be included in the inference

the names of other variables

return only data.frame used for inference

parameters to pass to bnlearn structure learning function

append the barplot depicting edges with high strength

specify how many edges are included in the strength plot

use geom_edge_link() instead of geom_edge_diagonal()

threshold for strength, automatically determined if NULL

change the shape of node according to hub scores (default NULL)

edges with top-n confidence of direction are highlighted

vector of coloring of nodes (low, high)

vector of coloring of edges (low, high)

color of texts in network plot

color of background in network plot

text color in barplot

bar color

background color in barplot

score type to use on inference

legend key color in barplot

perform clusterProfiler::setReadable based on this organism database

axis color in barplot

panel grid color in barplot
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**

```r
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**

```r
cmpareBNs(listOfNets)
```

**Arguments**

- listOfNets: list of networks
**exampleGeneExp**

**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

---

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)

---

**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)
```

queryCpDistLw

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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