Package 'CBNplot'

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Type Package

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

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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` *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
- 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
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 learnng 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
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 parametersas 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")
```

---

bngeneplotCustom *bngeneplotCustom*

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,
```

```
  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 learnng 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 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
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")
```

---

bngenetest *bngenetest*

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 learnng function

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 *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 = NULL,
  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 learnng 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 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
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 *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 = NULL,
  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
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

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
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 learnng 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

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)
```

---

bnpathtest *bnpathtest*

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 learnng 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")
```

---

compareBNs *compareBNs*

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)
```

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 learnng 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

Value

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

`obtainPath` *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` *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

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 *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

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 <- queryCpDistLw(fitted, candidate="ERCC4", evidence="ERCC2",
                     levels=c(0.1, 0.5, 0.8), n=500)
```

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