Package ‘CBNplot’

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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)

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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)

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**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
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
de1ZeroDegree  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
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
edgeLink  use geom_edge_link() instead of geom_edge_diagonal()
cellLineName  the cell line name to be included
fontFamily  font family name to be used for plotting
strengthPlot  append the barplot depicting edges with high strength
nStrength  specify how many edges are included in the strength plot
strThresh  the threshold for strength
hub  visualize the genes with top-n hub scores
glowEdgeNum  edges with top-n confidence of direction are highlighted
nodePal  vector of coloring of nodes (low, high)
edgePal  vector of coloring of edges (low, high)
textCol  color of texts in network plot
titleCol  color of title in network plot
backCol  color of background in network plot
barTextCol  text color in barplot
barPal  bar color
barBackCol  background color in barplot
scoreType  score type to use on inference
barLegendKeyCol  legend key color in barplot
barAxisCol  axis color in barplot
bg.colour  parameter to pass to geom_node_text
bg.r  parameter to pass to geom_node_text
barPanelGridCol  panel grid color in barplot
titleSize  the size of title
seed  A random seed to make the analysis reproducible, default is 1.
Value

ggplot2 object

Examples

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

Description

Testing various R for bayesian network between genes

Usage

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

Arguments

results the enrichment analysis result
exp gene expression matrix
expSample candidate rows to be included in the inference default to all
algo structure learning method used in boot.strength() default to "hc"
Rrange the sequence of R values to be tested
cl cluster object from parallel::makeCluster()
algorithm.args parameters to pass to bnlearn structure learning function
**bnpathplot**

*bnpathplot*

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

return the specified scores

perform clusterProfiler::setReadable based on this organism database

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,  
de1ZeroDegree = 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 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")

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

Description

Take the list of networks and returns the F-measures

Usage

compareBNs(listOfNets)

Arguments

listOfNets  list of networks
Value

F-measures of each combination of network

Examples

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

exampleEaRes  
Example enrichment analysis result

Description

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

Usage

data(exampleEaRes)

Format

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

Value

example enrichment analysis result

table.

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**
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
### obtainPath

**Description**

obtain the analysis results including the queried gene symbol

**Usage**

```r
obtainPath(res, geneSymbol)
```

**Arguments**

- **res**: enrichment analysis result
- **geneSymbol**: the candidate gene

**Value**

subset of enrichment results

**Examples**

```r
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**

```r
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
queryCpDistLw

Value

list of dataframe containing raw values

Examples

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