Package ‘CBNplot’

January 26, 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.
License  Artistic-2.0
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-package

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

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
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 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"
dergMeta  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
textSize 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

g.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
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
```r
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
```r
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 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")

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
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
dgeLink 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**

```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**

`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

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

Description

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

Usage

loadSign(fileName)

Arguments

fileName the result of SiGN-BN
### queryCpDistLs

**Description**

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

**Usage**

```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`

---

### 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`

---

### Value

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

* datasets
  exampleEaRes, 18
  exampleGeneExp, 18

* internal
  CBNplot-package, 2
  bngeneplot, 3
  bngeneplotCustom, 6
  bngenetest, 9
  bnpathplot, 10
  bnpathplotCustom, 13
  bnpathtest, 16
  CBNplot (CBNplot-package), 2
  CBNplot-package, 2
  compareBNs, 17
  exampleEaRes, 18
  exampleGeneExp, 18
  inferMS, 19
  loadSign, 19
  obtainPath, 20
  queryCpDistLs, 20
  queryCpDistLw, 21