

# Package ‘CBNplot’

May 14, 2026

**Type** Package

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

**Version** 1.13.0

**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.

**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, pvelust, stats, rlang

**Suggests** knitr, arules, concaveman, ReactomePA, bnviewer, rmarkdown, withr, BiocStyle, testthat (>= 3.0.0)

**biocViews** Visualization, Bayesian, GeneExpression, NetworkInference, Pathways, Reactome, Network, NetworkEnrichment, GeneSetEnrichment

**VignetteBuilder** knitr

**RoxygenNote** 7.3.2

**URL** <https://github.com/noriakis/CBNplot>

**BugReports** <https://github.com/noriakis/CBNplot/issues>

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CBNplot-package	<i>CBNplot: plot bayesian network inferred from gene expression data based on enrichment analysis results</i>
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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.

## 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>

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**bngeneplot***bngeneplot*

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**Description**

Plot gene relationship within the specified pathway

**Usage**

```
bngeneplot(  
  results,  
  exp,  
  expSample = NULL,  
  algo = "hc",  
  R = 20,  
  returnNet = FALSE,  
  algorithm.args = NULL,  
  bypassConverting = FALSE,  
  edgeLink = FALSE,  
  pathNum = NULL,  
  convertSymbol = TRUE,  
  expRow = "ENSEMBL",  
  interactive = FALSE,  
  cexCategory = 1,  
  cl = NULL,  
  showDir = FALSE,  
  chooseDir = FALSE,  
  scoreType = "bic-g",  
  labelSize = 4,  
  layout = "nicely",  
  clusterAlpha = 0.2,  
  strType = "normal",  
  delZeroDegree = TRUE,  
  otherVar = NULL,  
  otherVarName = NULL,  
  onlyDf = FALSE,  
  disc = FALSE,  
  tr = NULL,  
  remainCont = NULL,  
  sp = "hsapiens",  
  compareRef = FALSE,  
  compareRefType = "intersection",  
  pathDb = "reactome",  
  dep = NULL,  
  depMeta = NULL,  
  sizeDep = FALSE,  
  showDepHist = TRUE,  
  cellLineName = "5637_URINARY_TRACT",  
  showLineage = FALSE,  
  orgDb = org.Hs.eg.db,  
  shadowText = TRUE,  
)
```

```

    bgColor = "white",
    textColor = "black",
    strengthPlot = FALSE,
    nStrength = 10,
    strThresh = NULL,
    hub = NULL,
    seed = 1,
    useSiGN = FALSE
)

```

### Arguments

results	the enrichment analysis result
exp	gene expression matrix
expSample	candidate samples to be included in the inference default to all
algo	structure learning method used in boot.strength() default to "hc"
R	the number of bootstrap
returnNet	whether to return the network
algorithm.args	parameters to pass to bnlearn structure learning function
bypassConverting	bypass the symbol converting If you use custom annotation databases that does not have SYMBOL listed in keys. ID of rownames and those listed in EA result must be same.
edgeLink	use geom_edge_link() instead of geom_edge_diagonal()
pathNum	the pathway number (the number of row of the original result, ordered by p-value)
convertSymbol	whether the label of resulting network is converted to symbol, default to TRUE
expRow	the type of the identifier of rows of expression matrix
interactive	whether to use bnviewer (default to FALSE)
cexCategory	scaling factor of size of nodes
cl	cluster object from parallel::makeCluster()
showDir	show the confidence of direction of edges
chooseDir	if undirected edges are present, choose direction of edges (default: FALSE)
scoreType	score type to use on choosing direction
labelSize	the size of label of the nodes
layout	ggraph layout, default to "nicely"
clusterAlpha	if specified multiple pathways, the parameter is passed to geom_mark_hull()
strType	"normal" or "ms" for multiscale implementation
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 <code>graphite::pathways()</code> , default to "hsapiens"
compareRef	whether compare to the reference network
compareRefType	"intersection" or "difference"
pathDb	query to <code>graphite::pathways()</code> , default to "reactome"
dep	the tibble storing dependency score from library <code>depmap</code>
depMeta	<code>depmap::depmap_metadata()</code> , needed for <code>showLineage</code>
sizeDep	whether to reflect <code>DepMap</code> score to the node size
showDepHist	whether to show <code>depmap</code> histogram
cellLineName	the cell line name to be included
showLineage	show the dependency score across the lineage
orgDb	perform <code>clusterProfiler::setReadable</code> based on this organism database
shadowText	whether to use shadow text for the better readability default: TRUE
bgColor	color for text background when <code>shadowText</code> is TRUE
textColor	color for text when <code>shadowText</code> 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 ( <a href="https://sign.hgc.jp/signbn/download.html">https://sign.hgc.jp/signbn/download.html</a> ) 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	<i>bngeneplotCustom</i>
------------------	-------------------------

---

## 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 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 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

<code>bypassConverting</code>	bypass the symbol converting ID of rownames and those listed in EA result must be same
<code>edgeLink</code>	use <code>geom_edge_link()</code> instead of <code>geom_edge_diagonal()</code>
<code>cellLineName</code>	the cell line name to be included
<code>fontFamily</code>	font family name to be used for plotting
<code>strengthPlot</code>	append the barplot depicting edges with high strength
<code>nStrength</code>	specify how many edges are included in the strength plot
<code>strThresh</code>	the threshold for strength
<code>hub</code>	visualize the genes with top-n hub scores
<code>glowEdgeNum</code>	edges with top-n confidence of direction are highlighted
<code>nodePal</code>	vector of coloring of nodes (low, high)
<code>edgePal</code>	vector of coloring of edges (low, high)
<code>textCol</code>	color of texts in network plot
<code>titleCol</code>	color of title in network plot
<code>backCol</code>	color of background in network plot
<code>barTextCol</code>	text color in barplot
<code>barPal</code>	bar color
<code>barBackCol</code>	background color in barplot
<code>scoreType</code>	score type to use on inference
<code>barLegendKeyCol</code>	legend key color in barplot
<code>barAxisCol</code>	axis color in barplot
<code>bg.colour</code>	parameter to pass to <code>geom_node_text</code>
<code>bg.r</code>	parameter to pass to <code>geom_node_text</code>
<code>barPanelGridCol</code>	panel grid color in barplot
<code>titleSize</code>	the size of title
<code>seed</code>	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 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

```
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 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)

<code>bgColor</code>	color for text background when <code>shadowText</code> is TRUE
<code>textColor</code>	color for text when <code>shadowText</code> is TRUE
<code>compareRef</code>	whether compare to the reference network between pathway
<code>strThresh</code>	threshold for strength, automatically determined if NULL
<code>strType</code>	"normal" or "ms" for multiscale implementation
<code>hub</code>	change the shape of node according to hub scores (default NULL)
<code>scoreType</code>	score type to use on choosing edge direction
<code>databasePal</code>	palette to be used in <code>scale_color_brewer</code> when the multiple results are to be shown
<code>dep</code>	the tibble storing dependency score from library <code>depmap</code>
<code>sizeDep</code>	whether to reflect <code>DepMap</code> score to the node size
<code>orgDb</code>	perform <code>clusterProfiler::setReadable</code> based on this organism database
<code>bypassConverting</code>	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.
<code>useSiGN</code>	default to FALSE. For using SiGN-BN in the function in Windows 10/11, 1. Download the SiGN-BN HC+BS binary in WSL ( <a href="https://sign.hgc.jp/signbn/download.html">https://sign.hgc.jp/signbn/download.html</a> ) 2. Set PATH to executable (sign.1.8.3)
<code>edgeLink</code>	whether to set edge to <code>geom_edge_link()</code> FALSE to use <code>geom_edge_diagonal()</code>
<code>cellLineName</code>	the cell line name to be included
<code>strengthPlot</code>	append the barplot depicting edges with high strength
<code>nStrength</code>	specify how many edges are included in the strength plot
<code>seed</code>	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 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)
```

---

 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 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")

```

---

`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	<i>Example gene expression data</i>
----------------	-------------------------------------

---

**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	<i>inferMS</i>
---------	----------------

---

**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**

<code>data</code>	data.frame to perform inference
<code>algo</code>	structure learning method used in <code>boot.strength()</code>
<code>algorithm.args</code>	parameters to pass to bnlearn structure learning function
<code>R</code>	the number of bootstrap
<code>cl</code>	cluster object from <code>parallel::makeCluster()</code>
<code>r</code>	vector for size of each bootstrap replicate

**Value**

object of class `bn.strength`

---

loadSign	<i>loadSign</i>
----------	-----------------

---

**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	<i>obtainPath</i>
------------	-------------------

---

**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	<i>queryCpDistLs</i>
---------------	----------------------

---

### 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

<code>fitted</code>	<code>bn.fit</code> object
<code>candidate</code>	name of node
<code>evidences</code>	the evidences
<code>discPalette</code>	palette to be used for plotting if the event is discrete
<code>...</code>	other parameters passed to <code>bnlearn cpdist</code>

### 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	<i>queryCpDistLw</i>
---------------	----------------------

---

### 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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