Package ‘CBNplot’

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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.

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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

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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.
bngeneplot

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 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()
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>showDir</td>
<td>show the confidence of direction of edges</td>
</tr>
<tr>
<td>chooseDir</td>
<td>if undirected edges are present, choose direction of edges (default: FALSE)</td>
</tr>
<tr>
<td>scoreType</td>
<td>score type to use on choosing direction</td>
</tr>
<tr>
<td>labelSize</td>
<td>the size of label of the nodes</td>
</tr>
<tr>
<td>layout</td>
<td>ggraph layout, default to &quot;nicely&quot;</td>
</tr>
<tr>
<td>clusterAlpha</td>
<td>if specified multiple pathways, the parameter is passed to geom_mark_hull()</td>
</tr>
<tr>
<td>strType</td>
<td>&quot;normal&quot; or &quot;ms&quot; for multiscale implementation</td>
</tr>
<tr>
<td>delZeroDegree</td>
<td>delete zero degree nodes</td>
</tr>
<tr>
<td>otherVar</td>
<td>other variables to be included in the inference</td>
</tr>
<tr>
<td>otherVarName</td>
<td>the names of other variables</td>
</tr>
<tr>
<td>onlyDf</td>
<td>return only data.frame used for inference</td>
</tr>
<tr>
<td>disc</td>
<td>discretize the expression data</td>
</tr>
<tr>
<td>tr</td>
<td>Specify data.frame if one needs to discretize as the same parameters as the other dataset</td>
</tr>
<tr>
<td>remainCont</td>
<td>Specify characters when perform discretization, if some columns are to be remain continuous</td>
</tr>
<tr>
<td>sp</td>
<td>query to graphite::pathways(), default to &quot;hsapiens&quot;</td>
</tr>
<tr>
<td>compareRef</td>
<td>whether compare to the reference network</td>
</tr>
<tr>
<td>compareRefType</td>
<td>&quot;intersection&quot; or &quot;difference&quot;</td>
</tr>
<tr>
<td>pathDb</td>
<td>query to graphite::pathways(), default to &quot;reactome&quot;</td>
</tr>
<tr>
<td>dep</td>
<td>the tibble storing dependency score from library depmap</td>
</tr>
<tr>
<td>depMeta</td>
<td>depmap::depmap_metadata(), needed for showLineage</td>
</tr>
<tr>
<td>sizeDep</td>
<td>whether to reflect DepMap score to the node size</td>
</tr>
<tr>
<td>showDepHist</td>
<td>whether to show depmap histogram</td>
</tr>
<tr>
<td>cellLineName</td>
<td>the cell line name to be included</td>
</tr>
<tr>
<td>showLineage</td>
<td>show the dependency score across the lineage</td>
</tr>
<tr>
<td>orgDb</td>
<td>perform clusterProfiler::setReadable based on this organism database</td>
</tr>
<tr>
<td>shadowText</td>
<td>whether to use shadow text for the better readability default: TRUE</td>
</tr>
<tr>
<td>bgColor</td>
<td>color for text background when shadowText is TRUE</td>
</tr>
<tr>
<td>textColor</td>
<td>color for text when shadowText is TRUE</td>
</tr>
<tr>
<td>strengthPlot</td>
<td>append the barplot depicting edges with high strength</td>
</tr>
<tr>
<td>nStrength</td>
<td>specify how many edges are included in the strength plot</td>
</tr>
<tr>
<td>strThresh</td>
<td>the threshold for strength</td>
</tr>
<tr>
<td>hub</td>
<td>visualize the genes with top-n hub scores</td>
</tr>
<tr>
<td>seed</td>
<td>A random seed to make the analysis reproducible, default is 1.</td>
</tr>
<tr>
<td>useSiGN</td>
<td>default to FALSE. For using SiGN-BN in the function in Windows 10/11, 1.</td>
</tr>
</tbody>
</table>

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
data the gene expression matrix
dataSample candidate rows to be included in the inference default to all
dataSet the number of bootstrap
dataNum 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
dataRow 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 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
dgeLink 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.
bngenetest

Value

ggplot2 object

Examples

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

Description

Testing various R for bayesian network between genes

Usage

bngenetest(
  results,
  exp,
  expSample = NULL,
  algo = "hc",
  Rrange = seq(2, 40, 2),
  cl = NULL,
  algorithm.args = NULL,
  pathNum = NULL,
  convertSymbol = TRUE,
  expRow = "ENSEMBL",
  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")
```

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,
)```

bnpathplot

cexLine = 0.5,
chooseDir = FALSE,
showDir = FALSE,
delZeroDegree = TRUE,
labelSize = 4,
layout = "nicely",
onlyDf = FALSE,
disc = FALSE,
tr = NULL,
remainCont = NULL,
shadowText = TRUE,
bgColor = "white",
textColor = "black",
compareRef = FALSE,
strThresh = NULL,
strType = "normal",
hub = NULL,
scoreType = "bic-g",
databasePal = "Set2",
dep = NULL,
sizeDep = FALSE,
orgDb = org.Hs.eg.db,
bypassConverting = FALSE,
useSiGN = FALSE,
edgeLink = TRUE,
cellLineName = "5637_URINARY_TRACT",
strengthPlot = FALSE,
nStrength = 10,
seed = 1
)

Arguments

results the enrichment analysis result
exp gene expression matrix
expSample candidate rows to be included in the inference default to all
algo structure learning method used in boot.strength() default to "hc"
algorithm.args parameters to pass to bnlearn structure learning function
expRow the type of the identifier of rows of expression matrix
cl cluster object from parallel::makeCluster()
returnNet whether to return the network
otherVar other variables to be included in the inference
otherVarName the names of other variables
qvalueCutOff the cutoff value for qvalue
adjpCutOff the cutoff value for adjusted pvalues
nCategory  the number of pathways to be included
R  the number of bootstrap
interactive  whether to use bnviewer (default to FALSE)
color  color of node, default to adjusted p-value
cexCategory  scaling factor of size of nodes
cexLine  scaling factor of width of edges
chooseDir  if undirected edges are present, choose direction of edges
showDir  show the confidence of direction of edges
delZeroDegree  delete zero degree nodes
labelSize  the size of label of the nodes
layout  ggraph layout, default to "nicely"
onlyDf  return only data.frame used for inference
disc  discretize the expression data
tr  Specify data.frame if one needs to discretize as the same parameters as the other dataset
remainCont  Specify characters when perform discretization, if some columns are to be remain continuous
shadowText  whether to use shadow text for the better readability (default: TRUE)
bgColor  color for text background when shadowText is TRUE
textColor  color for text when shadowText is TRUE
compareRef  whether compare to the reference network between pathway
strThresh  threshold for strength, automatically determined if NULL
strType  "normal" or "ms" for multiscale implementation
hub  change the shape of node according to hub scores (default NULL)
scoreType  score type to use on choosing edge direction
databasePal  palette to be used in scale_color_brewer when the multiple results are to be shown
dep  the tibble storing dependency score from library depmap
sizeDep  whether to reflect DepMap score to the node size
orgDb  perform clusterProfiler::setReadable based on this organism database
bypassConverting  bypass the symbol converting If you use custom annotation databases that does not have SYMBOL listed in keys. ID of rownames and those listed in EA result must be same.
useSiGN  default to FALSE. For using SiGN-BN in the function in Windows 10/11, 1. Download the SiGN-BN HC+BS binary in WSL (https://sign.hgc.jp/signbn/download.html) 2. Set PATH to executable (sign.1.8.3)
edgeLink  whether to set edge to geom_edge_link() FALSE to use geom_edge_diagonal()
cellLineColor  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.
### Description

Plot pathway relationship using customized theme

### Usage

```r
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_TRAC",
  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
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
F-measures of each combination of network

Examples

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

---

exampleEaRes  
**Example enrichment analysis result**

Description

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

Usage

data(exampleEaRes)

Format

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

Value

example enrichment analysis result

---

exampleGeneExp  
**Example gene expression data**

Description

An example gene expression data to be used for testing purpose made by runif() for ERCC genes and 100 samples. No biological meanings can be obtained from the data.

Usage

data(exampleGeneExp)
**inferMS**

**Format**

An object of class `data.frame` with 7 rows and 100 columns.

**Value**

example gene expression

---

**Description**

multiscale bootstrap-based inference of Bayesian network

**Usage**

```r
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**

```r
loadSign(fileName)
```

**Arguments**

- `fileName`: the result of SiGN-BN
**Value**

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

---

**obtainPath**

**Description**

obtain the analysis results including the queried gene symbol

**Usage**

`obtainPath(res, geneSymbol)`

**Arguments**

- `res` enrichment analysis result
- `geneSymbol` the candidate gene

**Value**

subset of enrichment results

**Examples**

```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**

`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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