Package ‘CBNplot’
February 20, 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

Repository Bioconductor 3.18
Date/Publication 2024-02-20
Author Noriaki Sato [cre, aut]
Maintainer Noriaki Sato <nori@hgc.jp>

R topics documented:

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>CBNplot-package</td>
<td>2</td>
</tr>
<tr>
<td>bngeneplot</td>
<td>3</td>
</tr>
<tr>
<td>bngeneplotCustom</td>
<td>6</td>
</tr>
<tr>
<td>bngenetest</td>
<td>9</td>
</tr>
<tr>
<td>bnpathplot</td>
<td>10</td>
</tr>
<tr>
<td>bnpathplotCustom</td>
<td>13</td>
</tr>
<tr>
<td>bnpathtest</td>
<td>16</td>
</tr>
<tr>
<td>compareBNs</td>
<td>17</td>
</tr>
<tr>
<td>exampleEaRes</td>
<td>18</td>
</tr>
<tr>
<td>exampleGeneExp</td>
<td>18</td>
</tr>
<tr>
<td>inferMS</td>
<td>19</td>
</tr>
<tr>
<td>loadSign</td>
<td>19</td>
</tr>
<tr>
<td>obtainPath</td>
<td>20</td>
</tr>
<tr>
<td>queryCpDistLs</td>
<td>20</td>
</tr>
<tr>
<td>queryCpDistLw</td>
<td>21</td>
</tr>
</tbody>
</table>

Index 23

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](https://github.com/noriakis/CBNplot)
- Report bugs at [https://github.com/noriakis/CBNplot/issues](https://github.com/noriakis/CBNplot/issues)

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
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"
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
gColor 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
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
barAxisCol   axis color in barplot
bg.colour    parameter to pass to geom_node_text
bg.r         parameter to pass to geom_node_text
barPanelGridCol
barPanelGridCol
barPanelGridCol
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
The `bnpathplot` function plots pathway relationships. It takes several arguments:

- **results**: A data frame containing the results of a biological network analysis.
- **exp**: A data frame containing expression data.
- **algo**: An algorithm name (default: "hc").
- **Rrange**: A range of values for a parameter (default: `seq(10, 30, 10)`).
- **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**

A 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")
```

**Description**

Plot pathway relationship.

**Usage**

```r
bnpathplot(results, exp, expSample = NULL, algo = "hc",
algorithm.args = NULL, expRow = "ENSEMBL",
c1 = 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,
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
de1ZeroDegree  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,
b.g.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 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
bnpathtest

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"
)
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"
algo.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

```r
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

```r
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

```r
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
queryCpDistLs

Value

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

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

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$nAv, net$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

```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