Package 'mDAG'

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| Type Package |
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| Title Inferring Causal Network from Mixed Observational Data Using a Directed Acyclic Graph |
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| Description Learning a mixed directed acyclic graph based on both continuous and categorical data. |
| LazyData true |
| Encoding UTF-8 |
| License GPL (>= 2) |
| Imports Rcpp (>= 0.12.14), pcalg, mgm, bnlearn, methods, nnet |
| Depends R (\geq 2.10), logistf |
| LinkingTo Rcpp, RcppArmadillo |
| RoxygenNote 6.1.1 |
| NeedsCompilation yes |
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R topics documented:

| Index | mDAG | | • | • | • • | • | • | ••• | • | • | ••• | • | • | • | • • | • | • | • | • | • | • | • | • | | 2 |
|-------|--------------|------|---|-------|-----|-------|---|-----|---|---|-----|---|---|---|-----|---|---|-------|---|-------|---|---|---|--|---|
| | example_data | | | | | | | | | | | | | | | | | | | | | | | | |

example_data

Description

An example data, including 5 variables (4 continuous variables and 1 binary variable) and 100 samples.

Usage

data(example_data)

mDAG

Inferring Causal Network from Mixed Observational Data Using a Directed Acyclic Graph

Description

This function learns a mixed directed acyclic graph based on both continuous and categorical data.

Usage

```
mDAG(data, type, level, SNP = rep(0, ncol(data)), lambdaGam = 0.25,
ruleReg = "OR", threshold = "LW", weights = rep(1, nrow(data)),
alpha = 0.05, nperm = 10000)
```

Arguments

| data | A n x p matrix. Each row is a sample; each column is a variable. |
|-----------|--|
| type | A string vector of length p, indicating the type of variable for each column in data. 'g' for Gaussian, 'c' for categorical. |
| level | A vector of length p, indicating the number of categories of each variable. For continuous variables, set it to 1. |
| SNP | A vector of length p, indicating which variable is a SNP. |
| lambdaGam | Hyperparameter γ in the EBIC if lambdaSel = 'EBIC'. Defaults is lambdaGam = 0.25. |
| ruleReg | Default is 'OR'. Rule used to combine two estimates from nodewise regression (one from regressing A on B and the other from B on A). ruleReg = 'AND' requires both estimates to be nonzero in order to set the edge to be present. ruleReg = 'OR' requires at least one estiamte to be nonzero in order to set the edge to be present. |

mDAG

| threshold | Default is 'LW'. A threshold below which the combined estimates from node- wise regression are put to zero. threshold = 'LW' refers to the threshold in Loh and Wainwright (2012). threshold = 'HW' refers to the threshold in Haslbeck and Waldorp (2016). If threshold = 'none' no thresholding is applied. |
|-----------|--|
| weights | A vector of length n, indicating weights for observations. |
| alpha | Significance level for permutation test of conditional independece. Default is 0.05. |
| nperm | The number of permutations in the permutation test of conditional independece. Default is 10000. |

Value

A list of the following components:

- arcs: A two-column matrix, indicating arcs of the DAG.
- nodes: A list. Each element is named after a node and contains the following elements.
 - nbr: a string vector indicating the neighbourhood of the node.
 - parents: a string vector indicating the parents of the node.
 - children: a string vector indicating the children of the node.
- skeleton: A p x p adjacency matrix. If there is an edge from node i to node j, its (i, j) th entry = 1; otherwise = 0.

Author(s)

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References

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Min Jin Ha (2013). PenPC: A Two-step Approach to Estimate the Skeletons of High Dimensional Directed Acyclic Graphs. R package version 0.99.1.

Examples

```
# load package
library(mDAG)
type=c("g","g","g","g","g","c")
level=c(1,1,1,1,2)
# To save time for running example, we set nperm as 150.
# Use default nperm=10000 to generate a more reliable DAG for your own data.
dag=mDAG(data=example_data, type=type, level=level, nperm=150)
print(dag$skeleton)
# draw the DAG
# library(bnlearn)
# bnlearn:::graphviz.backend(nodes=names(dag$nodes),arcs=dag$arcs,shape="rectangle")
```

4

Index

 $\texttt{example_data, 2}$

mDAG, 2