Package ‘pcalg’
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Title Methods for graphical models and causal inference
Description This package contains several functions for causal structure
learning and causal inference using graphical models. The main algorithms
for causal structure learning are PC (for observational data without hidden
variables), FCI and RFCI (for observational data with hidden vari-
ables),and GIES (for a mix of observational and interventional data without hidden
variables). For causal inference the IDA algorithm and the generalized
backdoor criterion is implemented.
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**backdoor**

Find Set Satisfying the Generalized Backdoor Criterion

**Description**

This function first checks if the total causal effect of one variable (x) onto another variable (y) is identifiable via the generalized backdoor criterion, and if this is the case it explicitly gives a set of variables that satisfies the generalized backdoor criterion with respect to x and y in the given graph.

**Usage**

```r
backdoor(amat, x, y, type = "pag", max.chordal = 10, verbose=FALSE)
```
Arguments

amat  adjacency matrix (see Details for coding) of the given graph specified in type.
x, y  (integer) position of variable x or y in the adjacency matrix.
type  string specifying the type of graph of the adjacency matrix amat. It can be a DAG (type="dag"), a CPDAG (type="cpdag"), a MAG (type="mag"), or a PAG (type="pag").
max.chordal only if type = "mag", is used in pag2magAM to determine paths too large to be checked for chordality.
verbose  logical; if true, some output is produced during computation.

Details

This function is a generalization of Pearl’s backdoor criterion, see Pearl (1993), defined for directed acyclic graphs (DAGs), for single interventions and single outcome variable to more general types of graphs (CPDAGs, MAGs, and PAGs) that describe Markov equivalence classes of DAGs with and without latent variables but without selection variables. For more details see Maathuis and Colombo (2013).

The motivation to find a set W that satisfies the generalized backdoor criterion with respect to x and y in the given graph relies on the result of the generalized backdoor adjustment:

If a set of variables W satisfies the generalized backdoor criterion relative to x and y in the given graph, then the causal effect of x on y is identifiable and is given by

\[ P(Y|do(X = x)) = \sum_{W} P(Y|X, W) \cdot P(W). \]

This result allows to write post-intervention densities (the one written using Pearl’s do-calculus) using only observational densities estimated from the data.

If the input graph is a DAG (type="dag"), this function reduces to Pearl’s backdoor criterion for single interventions and single outcome variable, and the parents of x in the DAG satisfy the backdoor criterion unless y is a parent of x.

If the input graph is a CPDAG C (type="cpdag"), a MAG M (type="mag"), or a PAG P (type="pag") (with both M and P not allowing selection variables), this function first checks if the total causal effect of x on y is identifiable via the generalized backdoor criterion (see Maathuis and Colombo, 2013). If the effect is not identifiable in this way, the output is NA. Otherwise, an explicit set W that satisfies the generalized backdoor criterion with respect to x and y in the given graph is found.

At this moment this function is not able to work with an RFCI-PAG.

It is important to note that there can be pair of nodes x and y for which there is no set W that satisfies the generalized backdoor criterion, but the total causal effect might be identifiable via some other technique.

Coding of adjacency matrix: If type = dag or type = cpdag: coding 0/1 for no edge or tail / arrowhead; e.g. amat[a,b] = 0 and amat[b,a] = 1 implies a -> b. Else: coding 0,1,2,3 for no edge, circle, arrowhead, tail; e.g., amat[a,b] = 2 and amat[b,a] = 3 implies a -> b.
Value

Either NA if the total causal effect is not identifiable via the generalized backdoor criterion, or a set if the effect is identifiable via the generalized backdoor criterion. Note that if the set W is equal to the empty set, the output is NULL.

Author(s)

Diego Colombo and Markus Kalisch (<kalisch@stat.math.ethz.ch>)

References


See Also

pc for estimating a CPDAG, dag2pag and fci for estimating a PAG, and pag2magAM for estimating a MAG.

Examples

```r
# Simulate the true DAG
set.seed(123)
p <- 7
myDAG <- randomDAG(p, prob = 0.2) ## true DAG

## Extract the adjacency matrix of the true DAG
true amat <- (amat <- as(myDAG, "matrix")) != 0 # TRUE/FALSE <--> 1/0
print.table(1*true amat, zero=".") # "visualization"

## Compute the effect using the generalized backdoor criterion
backdoor(true amat, 5, 7, type="dag")
```

```r
# Example not identifiable
## Maathuis and Colombo (2013), Fig. 3, p.14

## create the graph
p <- 5
 amat <- rbind(c(...,1,1),
               c(...,1,1),
               c(...,1,1),
               ., 0
 amat <-...```
```r
c(.,.,1..), 
c(.,.,.), 
c(.,.,.,.)
colnames(amat) <- rownames(amat) <- as.character(1:5)
V <- as.character(1:5)
edL <- vector("list",length=5)
names(edL) <- V
edL[[1]] <- list(edges=c(3,4,5),weights=c(1,1,1))
edL[[2]] <- list(edges=c(3,4,5),weights=c(1,1,1))
edL[[3]] <- list(edges=c(4,weights=c(1)))
edL[[4]] <- list(edges=c(5,weights=c(1)))
g <- new("graphNEL", nodes=V, edgeL=edL, edgemode="directed")

## estimate the true CPDAG
myCPDAG <- dag2cpdag(g)
## Extract the adjacency matrix of the true CPDAG
true.amat <- (as(myCPDAG, "matrix") != 0) # 1/0 ==> TRUE/FALSE

## The effect is not identifiable, in fact:
backdoor(true.amat, 3, 5, type="cpdag")

# Example identifiable
# Maathuis and Colombo (2013), Fig. 4, p.15

## create the graph
p <- 6
amat <- rbind(c(0,0,1,1,0,1), c(0,0,1,1,0,1), c(0,0,0,0,0,1),
               c(0,0,0,0,1,1), c(0,0,0,0,0,0), c(0,0,0,0,0,0))
colnames(amat) <- rownames(amat) <- as.character(1:6)
V <- as.character(1:6)
edL <- vector("list",length=6)
names(edL) <- V
edL[[1]] <- list(edges=c(3,4,6),weights=c(1,1,1))
edL[[2]] <- list(edges=c(3,4,6),weights=c(1,1,1))
edL[[3]] <- list(edges=c(5,weights=c(1)))
edL[[4]] <- list(edges=c(5,6),weights=c(1,1)))
g <- new("graphNEL", nodes=V, edgeL=edL, edgemode="directed")

## estimate the true CPDAG
myCPDAG <- dag2cpdag(g)
## Extract the adjacency matrix of the true CPDAG
true.amat <- as(myCPDAG, "matrix") != 0 # 1/0

## The effect is identifiable and
backdoor(true.amat, 6, 3, type="cpdag")
```

beta.special

---

**beta.special**  
*Compute set of intervention effects*

---

**Description**

This function is DEPRECATED! Use `ida` instead.

**Usage**

```r
beta.special(dat=NA, x.pos, y.pos, verbose=0, a=0.01, myDAG=NA, myplot=FALSE, perfect=FALSE, method="local", collTest=TRUE, pcObj=NA, all.dags=NA, u2pd="rand")
```
Arguments

dat Data matrix
x.pos, y.pos integer column positions of x and y in dat.
verbose 0=no comments, 2=detail on estimates
a Significance level of tests for finding CPDAG
myDAG Needed if true correlation matrix shall be computed
myplot Plot estimated graph
perfect True cor matrix is calculated from myDAG
method "local" - local (all combinations of parents in regr.); "global" - all DAGs
collTest True - Exclude orientations of undirected edges that introduce a new collider
pcObj Fit of PC Algorithm (CPDAG); if this is available, no new fit is done
all.dags All DAGs in the format of function allDags; if this is available, no new function
u2pd function for converting a UDAG to a PDAG; "rand": udag2pdag; "relaxed": udag2pdagRelaxed; "retry": udag2pdagSpecial.

Value
estimates of intervention effects

Author(s)
Markus Kalisch (<kalisch@stat.math.ethz.ch>)

See Also
pcAlgo, dag2cpdag; beta.special.pcObj for a fast version of beta.special(), using a precomputed pc-object.

beta.special.pcObj Compute set of intervention effects in a fast way

Description
This function is DEPRECATED! Use ida or idafast instead.

Usage
beta.special.pcObj(x.pos, y.pos, pcObj, mcov=NA, amat=NA, amatSkel=NA, t.amat=NA)
Arguments

x.pos Column of x in dat
y.pos Column of y in dat
pcObj Precomputed pc-object
mcov Covariance that was used in the pc-object fit
amat, amatSkel, t amat Matrices that can be precomputed, if needed (see code for details on how to precompute)

Value

estimates of intervention effects

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>)

See Also

pcAlgo, dag2cpdag, beta.special

Description

$G^2$ test for (conditional) independence of binary variables $X$ and $Y$ given the (possibly empty) set of binary variables $S$.

binCItest() is a wrapper of gSquareBin(), to be easily used in skeleton, pc and fci.

Usage

gSquareBin(x, y, S, dm, adaptDF = FALSE, verbose = FALSE)
binCItest (x, y, S, suffStat)

Arguments

x, y (integer) position of variable $X$ and $Y$, respectively, in the adjacency matrix.
S (integer) positions of zero or more conditioning variables in the adjacency matrix.
dm data matrix (with {0, 1} entries).
adaptDF logical specifying if the degrees of freedom should be lowered by one for each zero count. The value for the degrees of freedom cannot go below 1.
suffStat a list with two elements, "dm", and "adaptDF" corresponding to the above two arguments of gSquareBin().
verbose logical indicating if detailed output is to be provided.
Details

The $G^2$ statistic is used to test for (conditional) independence of $X$ and $Y$ given a set $S$ (can be NULL). This function is a specialized version of `gsquaredis` which is for discrete variables with more than two levels.

Value

The p-value of the test.

Author(s)

Nicoletta Andri and Markus Kalisch (<kalisch@stat.math.ethz.ch>)

References


See Also

`gsquaredis` for a (conditional) independence test for discrete variables with more than two levels.

`dsepTest`, `gaussCitest` and `disCitest` for similar functions for a d-separation oracle, a conditional independence test for Gaussian variables and a conditional independence test for discrete variables, respectively.

`skeleton`, `pc` or `fci` which need a testing function such as `binCitest`.

Examples

```r
n <- 100
set.seed(123)
## Simulate independent data of {0,1}-variables:
x <- rbinom(n, 1, pr=1/2)
y <- rbinom(n, 1, pr=1/2)
z <- rbinom(n, 1, pr=1/2)
dat <- cbind(x,y,z)

binCitest(1,3,2, list(dm = dat, adaptDF = FALSE)) # 0.36, not signif.
binCitest(1,3,2, list(dm = dat, adaptDF = TRUE )) # the same, here

## Simulate data from a chain of 3 variables: x1 -> x2 -> x3
set.seed(12)
b0 <- 0
b1 <- 1
b2 <- 1
n <- 10000
x1 <- rbinom(n, size=1, prob=1/2) # sample(c(0,1), n, replace=TRUE)

## NB: plogis(u) := "expit(u)" := exp(u) / (1 + exp(u))
p2 <- plogis(b0 + b1*x1) ; x2 <- rbinom(n, 1, prob = p2) # {0,1}
p3 <- plogis(b0 + b2*x2) ; x3 <- rbinom(n, 1, prob = p2) # {0,1}
```
checkTriple

Description

For each subset of nbrsA and nbrsC where a and c are conditionally independent, it is checked if b is in the conditioning set.

Usage

checkTriple(a, b, c, nbrsA, nbrsC,
            sepsetA, sepsetC,
            suffStat, indepTest, alpha, version.unf = c(NA, NA),
            maj.rule = FALSE, verbose = FALSE)

Arguments

a, b, c  (integer) positions in adjacency matrix for nodes a, b, and c, respectively.
nbrsA, nbrsC  neighbors of a and c, respectively.
sepsetA  vector containing Sepset(a,c).
sepsetC  vector containing Sepset(c,a).
suffStat  a list of sufficient statistics for independent tests; see, e.g., pc.
indepTest  a function for the independence test, see, e.g., pc.
alpha  significance level of test.
version.unf  (integer) vector of length two:

version.unf[1]: 1 - check for all separating subsets of nbrsA and nbrsC if b is in that set,
                2 - it also checks if there at all exists any sepset which is a subset of the
                neighbours (there might be none, although b is in the sepset, which indicates
                an ambiguous situation);
version.unf[2]: 1 - do not consider the initial sepsets sepsetA and sepsetC (same as Tetrad),
                2 - consider if b is in sepsetA or sepsetC.
checkTriple

major rule logical indicating that the following majority rule is applied: if b is in less than 50% of the checked sepsets, we say that b is in no sepset. If b is in more than 50% of the checked sepsets, we say that b is in all sepsets. If b is in exactly 50% of the checked sepsets, the triple is considered ‘ambiguous’.

verbose Logical asking for detailed output of intermediate steps.

Details

This function is used in the conservative versions of structure learning algorithms.

Value

decision Decision on possibly ambiguous triple, an integer code.
1 b is in NO sepset (make v-structure);
2 b is in ALL sepsets (make no v-structure);
3 b is in SOME but not all sepsets (ambiguous triple)

vers Version (1 or 2) of the ambiguous triple (1=normal ambiguous triple that is b is in some sepsets; 2=triple coming from version.unf[1]==2, that is, a and c are indep given the initial sepset but there doesn’t exist a subset of the neighbours that d-separates them.)

sepsetA Updated version of sepsetA
sepsetC Updated version of sepsetC

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Diego Colombo.

References


Examples

```
# Using Gaussian Data
#
# Load predefined data
data(gmG)
n <- nrow(gmG$x)
Y <- colnames(gmG$x)

# define independence test (partial correlations), and test level
indepTest <- gaussCItest
alpha <- 0.01
# define sufficient statistics
suffStat <- list(C = cor(gmG$x), n = n)
```
### Description

Compares the true undirected graph with an estimated undirected graph in terms of True Positive Rate (TPR), False Positive Rate (FPR) and True Discovery Rate (TDR).

### Usage

```r
compareGraphs(gl, gt)
```
compareGraphs

Arguments

- `gl` Estimated graph (graph object)
- `gt` True graph (graph object)

Details

If the input graph is directed, the directions are omitted. Special cases:

- If the true graph contains no edges, the tpr is defined to be zero.
- Similarly, if the true graph contains no gaps, the fpr is defined to be one.
- If there are no edges in the true graph and there are none in the estimated graph, tdr is one. If there are none in the true graph but there are some in the estimated graph, tdr is zero.

Value

A named numeric vector with three numbers:

- `tpr` True Positive Rate: Number of correctly found edges (in estimated graph) divided by number of true edges (in true graph)
- `fpr` False Positive Rate: Number of incorrectly found edges divided by number of true gaps (in true graph)
- `tdr` True Discovery Rate: Number of correctly found edges divided by number of found edges (both in estimated graph)

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Martin Maechler

See Also

randomDAG for generating a random DAG.

Examples

```r
## generate a graph with 4 nodes
V <- LETTERS[1:4]
edL2 <- vector("list", length=4)
names(edL2) <- V
edL2[[1]] <- list(edges= 2)
edL2[[2]] <- list(edges= c(1,3,4))
edL2[[3]] <- list(edges= c(2,4))
edL2[[4]] <- list(edges= c(2,3))
gt <- new("graphNEL", nodes=V, edgeL=edL2, edgemode="undirected")

## change graph
gl <- graph::addEdge("A","C", gt,1)

## compare the two graphs
if (require(Rgraphviz)) {
```
condIndFisherZ

Test Conditional Independence of Gaussians via Fisher’s Z

Description

Using Fisher’s z-transformation of the partial correlation, test for zero partial correlation of sets of normally / Gaussian distributed random variables.

The gaussCItest() function, using zStat() to test for (conditional) independence between gaussian random variables, with an interface that can easily be used in skeleton, pc and fci.

Usage

condIndFisherZ(x, y, S, C, n, cutoff, verbose= )
zStat (x, y, S, C, n)
gaussCItest (x, y, S, suffStat)

Arguments

x, y, S
It is tested, whether x and y are conditionally independent given the subset S of the remaining nodes. x, y, S all are integers, corresponding to variable or node numbers.

C
Correlation matrix of nodes

n
Integer specifying the number of observations (“samples”) used to estimate the correlation matrix C.

cutoff
Numeric cutoff for significance level of individual partial correlation tests. Must be set to qnorm(1 - alpha/2) for a test significance level of alpha.

verbose
Logical indicating whether some intermediate output should be shown; currently not used.

suffStat
A list with two elements, ”C” and ”n”, corresponding to the above arguments with the same name.

Details

For gaussian random variables and after performing Fisher’s z-transformation of the partial correlation, the test statistic zStat() is (asymptotically for large enough n) standard normally distributed.

Partial correlation is tested in a two-sided hypothesis test, i.e., basically, condIndFisherZ(*) == abs(zStat(*)) > qnorm(1 - alpha/2)

In a multivariate normal distribution, zero partial correlation is equivalent to conditional independence.
Value

\( zStat() \) gives a number

\[
Z = \sqrt{n - |S| - 3 \cdot \log((1 + r)/(1 - r))}/2
\]

which is asymptotically normally distributed under the null hypothesis of correlation 0.

condIndFisherZ() returns a logical \( L \) indicating whether the “partial correlation of \( x \) and \( y \) given \( S \) is zero” could not be rejected on the given significance level. More intuitively and for multivariate normal data, this means: If \( \text{TRUE} \) then it seems plausible, that \( x \) and \( y \) are conditionally independent given \( S \). If \( \text{FALSE} \) then there was strong evidence found against this conditional independence statement.

gaussCItest() returns the p-value of the test.

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Martin Maechler

References

Markus Kalisch and Peter Bühlmann (2005) Estimating high-dimensional directed acyclic graphs with the PC-algorithm; Research Report Nr.-130, ETH Zurich; http://stat.ethz.ch/research/research_reports/2005

See Also

pcorOrder for computing a partial correlation given the correlation matrix in a recursive way.
dsepTest, discItest and binItest for similar functions for a d-separation oracle, a conditional independence test for discrete variables and a conditional independence test for binary variables, respectively.

Examples

```r
set.seed(42)
  ## Generate four independent normal random variables
  n <- 20
  data <- matrix(rnorm(n*4), n, 4)
  ## Compute corresponding correlation matrix
  corMatrix <- cor(data)
  ## Test, whether variable 1 (col 1) and variable 2 (col 2) are
  ## independent given variable 3 (col 3) and variable 4 (col 4) on 0.05
  ## significance level
  x <- 1
  y <- 2
  S <- c(3, 4)
  n <- 20
  alpha <- 0.05
  cutoff <- 1-qnorm(alpha/2)
  (bl <- condIndFisherZ(x, y, S, corMatrix, n, cutoff))
  # -> 1 and 2 seem to be conditionally independent given 3, 4
```
Now an example with conditional dependence

data <- matrix(rnorm(n*3),n,3)
data[,3] <- 2*data[,1]
corMatrix <- cor(data)
(b2 <- condIndFisherZ(1,3,2,corMatrix,n,cutoff))

# R and S seem to be conditionally dependent given Z

set.seed(29)
x <- rnorm(100)
y <- 3*x + rnorm(100)
z <- 2*y + rnorm(100)
dat <- cbind(x,y,z)

suffStat <- list(C = cor(dat), n = nrow(dat))
gaussCltest(1,3,NULL, suffStat) # dependent [highly signif.]
gaussCltest(1,3, 2, suffStat) # independent | Z

---

**corGraph**

## Computing the correlation graph

### Description

Computes the correlation graph. This is the graph in which an edge is drawn between node i and node j, if the null hypothesis “Correlation between \(X_i\) and \(X_j\) is zero” can be rejected at the given significance level \(\alpha\) (alpha).

### Usage

```
corGraph(dm, alpha=0.05, Cmethod="pearson")
```

### Arguments

- **dm**: Numeric matrix with rows as samples and columns as variables.
- **alpha**: Significance level for correlation test (numeric)
- **Cmethod**: A character string indicating which correlation coefficient is to be used for the test. One of "pearson", "kendall", or "spearman", can be abbreviated. (string)

### Value

Undirected correlation graph (graph object)

### Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Martin Maechler
Examples

```r
## create correlated samples
x1 <- rnorm(100)
x2 <- rnorm(100)
mat <- cbind(x1, x2, x3 = x1*x2)

if (require(Rgraphviz)) {
  ## analyze the data'
  (g <- corGraph(mat)) # a 'graphNEL' graph, undirected
  plot(g) # => (1) and (2) are each linked to (3)

  ## use different significance level and different method
  (g2 <- corGraph(mat, alpha=0.01, Cmethod="kendall")
  plot(g2) ## same edges as 'g'
}
```

`dag2cpdag` *Convert a DAG to a CPDAG*

Description

Convert a DAG (Directed Acyclic Graph) to a Completed Partially Directed Acyclic Graph (CPDAG).

Usage

`dag2cpdag(g)`

Arguments

- `g` an R object of class "graph" (package `graph`), representing a DAG.

Details

This function converts a DAG into its corresponding (unique) CPDAG as follows. Because every DAG in the Markov equivalence class described by a CPDAG shares the same skeleton and the same v-structures, this function takes the skeleton and the v-structures of the given DAG `g`. Afterwards it simply uses the 3 orientation rules of the PC algorithm (see references) to orient as many of the remaining undirected edges as possible.

The output of this function is exactly the same as the one using

`pc(suffStat, indepTest, alpha, labels)`

using the true correlation matrix in the function `gaussCITest` with a large virtual sample size and a large alpha, but it is much faster.

Value

A graph object containing the CPDAG.
Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Diego Colombo

References


See Also

randomDAG, pc

Examples

```r
p <- 10  # number of random variables
s <- 0.4  # sparseness of the graph

## generate a random DAG
set.seed(42)
g <- randomDAG(p, s)
g01 <- l*(as(g,"matrix") > 0)  # 0/1-version of adjacency matrix
print.table(g01, zero=".")

## compute its unique CPDAG
system.time(
  res <- dag2cpdag(g)
)
## res has some bidirected edges
## ==> adj.matrix: no longer upper triangular, but {0,1}
print.table(as(res, "matrix"), zero=".")
dm <- as(res, "matrix") - g01  # difference: 2 entries in lower tri.
print.table(dm, zero=".")
stopifnot(all(dm %in% 0:1), sum(dm == 1) == 2)

## Find CPDAG with PC algorithm:
## As dependence oracle, we use the true correlation matrix in
## gaussCITest() with a large "virtual sample size" and a large alpha:
system.time(
  rpc <- pc(suffStat = list(C = cov2cor(trueCov(g)), n = 10^9),
             indepTest = gaussCITest, alpha = 0.9999, p = p)
)
## confirm that it coincides with dag2cpdag()'s result:
stopifnot(all.equal(as(res, "matrix"),
                     as(rpc@graph,"matrix"), tol=0))
```
Convert a DAG to an Essential Graph

Description

Convert a DAG to an (interventional or observational) essential graph.

Usage

dag2essgraph(dag, targets = list(integer(0)))

Arguments

dag
  The DAG whose essential graph has to be calculated, represented as an instance of a class derived from Score.

targets
  List of intervention targets with respect to which the essential graph has to be calculated. An observational setting is represented by one single empty target (list(integer(0))).

Details

This function converts a DAG to its corresponding (interventional or observational) essential graph, using the algorithm of Hauser and Bühlmann (2012).

The essential graph is a partially directed graph that represents the (interventional or observational) Markov equivalence class of a DAG. It has the same skeleton as the DAG; a directed edge represents an arrow that has a common orientation in all representatives of the (interventional or observational) Markov equivalence class, whereas an undirected edge represents an arrow that has different orientations in different representatives of the equivalence class. In the observational case, the essential graph is also known as “CPDAG” (Spirtes et al., 2000).

In a purely observational setting (i.e., if targets = list(integer(0))), the function yields the same graph as dag2cpdag, although it uses different classes for parameters and return value.

Value

An instance of EssGraph representing the essential graph.

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

References


See Also
dag2cpdag, Score, EssGraph

Examples

```r
p <- 10  # Number of random variables
s <- 0.4  # Sparseness of the DAG

## Generate a random DAG
set.seed(42)
dag <- as(randomDAG(p, s), "GaussParDAG")

## Calculate observational essential graph
res.obs <- dag2essgraph(dag)

## Calculate interventional essential graph for intervention targets
## {Q} and {S}
res.int <- dag2essgraph(dag, as.list(c(1, 3)))
```

---

**dag2pag**

Convert a DAG with latent variables into a PAG

**Description**

Convert a DAG with latent variables into its corresponding (unique) Partial Ancestral Graph (PAG).

**Usage**

```r
dag2pag(suffStat, indepTest, graph, L, alpha, rules = rep(TRUE, 10),
         verbose = FALSE)
```

**Arguments**

- `suffStat` The sufficient statistics, a **list** containing all necessary elements for the conditional independence decisions in the function `indepTest`.
- `indepTest` A **function** for testing conditional independence. The function is internally called as `indepTest(x, y, S, suffStat)`, and tests conditional independence of `x` and `y` given `S`. Here, `x` and `y` are variables, and `S` is a (possibly empty) vector of variables (all variables are denoted by their column numbers in the adjacency matrix). `suffStat` is a list containing all relevant elements for the conditional independence decisions. The return value of `indepTest()` is the p-value of the test for conditional independence.
- `graph` A DAG with `p` nodes, a **graph** object. The graph must be topological sorted (for example produced using `randomDAG`).
- `L` Array containing the labels of the nodes in the `graph` corresponding to the latent variables.
- `alpha` Significance level for the individual conditional independence tests.
rules Logical vector of length 10 indicating which rules should be used when directing edges. The order of the rules is taken from Zhang (2009).

verbose Logical; if TRUE, detailed output is provided.

Details
This function converts a DAG (graph object) with latent variables into its corresponding (unique) PAG, an fciAlgo class object, using the ancestor information and conditional independence tests entailed in the true DAG. The output of this function is exactly the same as the one using

\[ \text{fci(suffStat, gaussCItest, p, alpha, rules = rep(TRUE, 10))} \]

using the true correlation matrix in gaussCItest() with a large “virtual sample size” and a large alpha, but it is much faster, see the example.

Value
An object of class fciAlgo, containing the estimated graph (in the form of an adjacency matrix with various possible edge marks), the conditioning sets that lead to edge removals (sepset) and several other parameters.

Author(s)
Diego Colombo and Markus Kalisch <kalisch@stat.math.ethz.ch>.

References

See Also
fci, pc

Examples
```r
## create the graph
set.seed(78)
g <- randomDAG(10, prob = 0.25)
graph::nodes(g) # "1" "2" ... "10" % FIXME: should be kept in result!

## define nodes 2 and 6 to be latent variables
L <- c(2, 6)

## compute the true covariance matrix of g
cov.mat <- trueCov(g)
## transform covariance matrix into a correlation matrix
true.corr <- cov2cor(cov.mat)

## Find PAG
## as dependence "oracle", we use the true correlation matrix in
```
### G square Test for (conditional) Independence for Discrete Data

**Description**

$G^2$ test for (conditional) independence of discrete variables $X$ and $Y$ given the (possibly empty) set of discrete variables $S$.

`disCItest()` is a wrapper of `gsquareDis()`, to be easily used in `skeleton, pc` and `fci`.

**Usage**

```r
gsquareDis(x, y, S, dm, nlev, adaptDF = FALSE, verbose = FALSE)
```

```r
disCItest (x, y, S, suffStat)
```

**Arguments**

- `x`: Position of variable X in the adjacency matrix
- `y`: Position of variable Y in the adjacency matrix
- `S`: Position of conditioning variables in the adjacency matrix
- `dm`: Data matrix (rows: samples, columns: variables) with binary entries
- `nlev`: Vector with numbers of levels for each variable
- `adaptDF`: Lower the degrees of freedom by one for each zero count. The value for the degrees of freedom cannot go below 1.
verbose Logical indicating if detailed output is to be provided.
suffStat A list with three elements: "dm", "nlev", "adaptDF"; each corresponding to the above arguments of gSquareDis().

Details

The $G^2$ statistic is used to test for (conditional) independence of X and Y given a set S (can be NULL). If only binary variables are involved, gSquareBin is a specialized (a bit more efficient) alternative to gSquareDis().

Value

The p-value of the test.

Author(s)

Nicoletta Andri and Markus Kalisch (<kalisch@stat.math.ethz.ch>).

References


See Also

gSquareBin for a (conditional) independence test for binary variables.
dseptest, gaussCItest and binCItest for similar functions for a d-separation oracle, a conditional independence test for gaussian variables and a conditional independence test for binary variables, respectively.

Examples

```r
## Simulate data
n <- 100
set.seed(123)
x <- sample(0:2, n, TRUE)
y <- sample(0:3, n, TRUE)
z <- sample(0:1, n, TRUE)
dat <- cbind(x, y, z)

## Analyze data
gSquareDis(1, 3, 2, dat, nlev = c(3, 4, 2))
gSquareDis(1, 3, 2, dat, nlev = c(3, 4, 2), verbose = TRUE, adaptDF = TRUE)

suffStat <- list(dm = dat, nlev = c(3, 4, 2), adaptDF = FALSE)
discItest(1, 3, 2, suffStat)
```
**dreach**

Compute $D$-SEP($x, y, G$)

**Description**

Let $x$ and $y$ be two distinct vertices in a mixed graph $G$. This function computes $D$-SEP($x, y, G$), which is defined as follows:

A node $v$ is in $D$-SEP($x, y, G$) iff $v$ is not equal to $x$ and there is a collider path between $x$ and $v$ in $G$ such that every vertex on this path is an ancestor of $x$ or $y$ in $G$.


**Usage**

```
dreach(x, y, amat, verbose = FALSE)
```

**Arguments**

- **x**: First argument of $D$-SEP, given as the column number of the node in the adjacency matrix.
- **y**: Second argument of $D$-SEP, given as the column number of the node in the adjacency matrix ($y$ must be different from $x$).
- **amat**: Adjacency matrix (coding 0,1,2,3 for no edge, circle, arrowhead, tail; e.g., amat[a,b] = 2 and amat[b,a] = 3 implies $a \rightarrow b$)
- **verbose**: Logical specifying details should be on output

**Value**

Vector of column positions indicating the nodes in $D$-SEP($x, y, G$).

**Author(s)**

Diego Colombo and Markus Kalisch (<kalisch@stat.math.ethz.ch>)

**References**


**See Also**

- backdoor uses this function; pag2magAM.
dsep

Test for d-separation in a DAG

Description
This function tests for d-separation of nodes in a DAG.

Usage

dsep(a, b, S=NULL, g, john.pairs = NULL)

Arguments

a Label (sic!) of node A
b Label (sic!) of node B
S Labels (sic!) of set of nodes on which it is conditioned, maybe empty
g The Directed Acyclic Graph (object of class "graph", see graph-class from the package graph)
john.pairs The shortest path distance matrix for all pairs of nodes as computed (also by default) in johnson.all.pairs.sp from package RBGL.

Details
This function checks separation in the moralized graph as explained in Lauritzen (2004).

Value
TRUE if a and b are d-separated by S in G, otherwise FALSE.

Author(s)
Markus Kalisch (<kalisch@stat.math.ethz.ch>)

References
S.L. Lauritzen (2004), Graphical Models, Oxford University Press, Chapter 3.2.2

See Also
dsepTest for a wrapper of this function that can easily be included into skeleton, pc or fci
Examples

```r
## generate random DAG
p <- 8
set.seed(45)
myDAG <- randomDAG(p, prob = 0.3)
if (require(Rgraphviz)) {
  plot(myDAG)
}

## Examples for d-separation
dsep("1","7",NULL,myDAG)
dsep("4","5",NULL,myDAG)
dsep("4","5","2",myDAG)
dsep("4","5",c("2","3"),myDAG)

## Examples for d-connection
dsep("1","3",NULL,myDAG)
dsep("1","6","3",myDAG)
dsep("4","5","8",myDAG)
```

---

dsepTest

Test for d-separation in a DAG

Description

Tests for d-separation of nodes in a DAG. `dsepTest()` is written to be easily used in `skeleton`, `pc`, `fci`.

Usage

```r
dsepTest(x, y, S=NULL, suffStat)
```

Arguments

- **x, y**: integer position of variable x and y in the adjacency matrix.
- **S**: integer positions of conditioning variables in the adjacency matrix, possibly empty.
- **suffStat**: a list with two elements,
  - "g" Containing the Directed Acyclic Graph (object of `class` "graph", see `graph-class` from the package `graph`), and
  - "jp" Containing the shortest path distance matrix for all pairs of nodes as computed by `johnson.all.pairs.sp` from package `RBGL`.

Details

The function is based on `dsep`. For details on d-separation see the reference Lauritzen (2004).
Value

If x and y are d-separated by S in DAG G the result is 1, otherwise it is 0. This is analogous to the p-value of an ideal (without sampling error) conditional independence test on any distribution that is faithful to the DAG G.

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>)

References

S.L. Lauritzen (2004), Graphical Models, Oxford University Press.

See Also

gaussCITest, discCITest and binCITest for similar functions for a conditional independence test for gaussian, discrete and binary variables, respectively.

Examples

```r
p <- 8
set.seed(45)
myDAG <- randomDAG(p, prob = 0.3)

if (require(Rgraphviz)) {
  ## plot the DAG
  plot(myDAG, main = "randomDAG(10, prob = 0.2)")
}

## define sufficient statistics (d-separation oracle)
suffStat <- list(g = myDAG, jp = RBGL::johnson.all.pairs.sp(myDAG))
dsepTest(1,6, S = NULL, suffStat) ## not d-separated
dsepTest(1,6, S = 3, suffStat) ## not d-separated by node 3
dsepTest(1,6, S = c(3,4), suffStat) ## d-separated by node 3 and 4
```

---

**EssGraph-class**  
**Class "EssGraph"**

Description

This class represents an (observational or interventional) essential graph.
Details

An observational or interventional Markov equivalence class of DAGs can be uniquely represented by a partially directed graph, the essential graph. Its edges have the following interpretation:

1. a directed edge $a \rightarrow b$ stands for an arrow that has the same orientation in all representatives of the Markov equivalence class;
2. an undirected edge $a - b$ stands for an arrow that is oriented in one way in some representatives of the equivalence class and in the other way in other representatives of the equivalence class.

Extends

All reference classes extend and inherit methods from "envRefClass".

Constructor

```
new("EssGraph", nodes, in.edges, ...)
```

- `nodes`: Vector of node names; cf. also field `nodes`.
- `in.edges`: A list of length $p$ consisting of index vectors indicating the edges pointing into the nodes of the DAG.

Fields

- `.nodes`: Vector of node names; defaults to `as.character(1:p)`, where $p$ denotes the number of nodes (variables) of the model.
- `.in.edges`: A list of length $p$ consisting of index vectors indicating the edges pointing into the nodes of the DAG.
- `targets`: List of mutually exclusive intervention targets with respect to which Markov equivalence is defined.
- `score`: Object of class `Score`; used internally for score-based causal inference.

Class-Based Methods

Most class-based methods are only for internal use. Methods of interest for the user are:

- `repr()`: Yields a representative causal model of the equivalence class, an object of a class derived from `Score`. Since the representative is not only characterized by the DAG, but also by appropriate parameters, the field `score` must be assigned for this method to work. The DAG is drawn at random; note that all representatives are statistically indistinguishable under a given set of intervention targets.
- `node.count()`: Yields the number of nodes of the essential graph.
- `edge.count()`: Yields the number of edges of the essential graph. Note that unoriented edges count as 2, whereas oriented edges count as 1 due to the internal representation.

Methods

```
plot signature(x = "EssGraph", y = "ANY")`: plots the essential graph. In the plot, undirected and bidirected edges are equivalent.
**fci**

Estimate a PAG, using the FCI-algorithm

---

**Description**

Estimate a Partial Ancestral Graph (PAG) from observational data, using the FCI Algorithm.

**Usage**

```r
fci(suffStat, indepTest, alpha, labels, p,
    skel.method = c("stable", "original", "stable.fast"),
    type = c("normal", "anytime", "adaptive"),
    fixedGaps = NULL, fixedEdges = NULL,
    NAdelete = TRUE, m.max = Inf, pdsep.max = Inf,
    rules = rep(TRUE, 10), dopdsep = TRUE, bicC = FALSE,
    conservative = FALSE, maj.rule = FALSE,
    verbose = FALSE)
```

**Arguments**

- `suffStat`: Sufficient statistics: List containing all necessary elements for the conditional independence decisions in the function `indepTest`.
- `indepTest`: Predefined function for testing conditional independence. The function is internally called as `indepTest(x, y, S, suffStat)`, and tests conditional independence of \( x \) and \( y \) given \( S \). Here, \( x \) and \( y \) are variables, and \( S \) is a (possibly empty) vector of variables (all variables are denoted by their column numbers in the adjacency matrix). `suffStat` is a list containing all relevant elements for the conditional independence decisions. The return value of `indepTest` is the p-value of the test for conditional independence.
- `alpha`: Significance level for the individual conditional independence tests.
- `labels`: (optional) character vector of variable (or “node”) names. Typically preferred to specifying `p`.
- `p`: (optional) number of variables (or nodes). May be specified if `labels` are not, in which case `labels` is set to `1:p`.

See Also

- ParDAG

Examples

```r
showClass("EssGraph")
```
skel.method  Character string specifying method; the default, "stable" provides an order-independent skeleton, see skeleton.

type  Character string specifying the version of the FCI algorithm to be used. By default, it is "normal", and so the normal FCI algorithm is called. If set to "anytime", the 'Anytime FCI' is called and m.max needs to be specified. If set to "adaptive", the 'Adaptive Anytime FCI' is called and m.max is not used. For more information, see Details.

fixedGaps  A logical matrix of dimension p*p. If entry [i, j] or [j, i] (or both) are TRUE, the edge i-j is removed before starting the algorithm. Therefore, this edge is guaranteed to be absent in the resulting graph.

fixedEdges  A logical matrix of dimension p*p. If entry [i, j] or [j, i] (or both) are TRUE, the edge i-j is never considered for removal. Therefore, this edge is guaranteed to be present in the resulting graph.

NAdelete  If indepTest returns NA and this option is TRUE, the corresponding edge is deleted. If this option is FALSE, the edge is not deleted.

m.max  Maximum size of the conditioning sets that are considered in the conditional independence tests.

pdsep.max  Maximum size of Possible-D-SEP for which subsets are considered as conditioning sets in the conditional independence tests. If the nodes x and y are adjacent in the graph and the size of Possible-D-SEP(x) \ x, y is bigger than pdsep.max, the edge is simply left in the graph. Note that if pdsep.max is less than Inf, the final PAG may be a supergraph of the one computed with pdsep.max = Inf, because fewer tests may have been performed in the former.

rules  Logical vector of length 10 indicating which rules should be used when directing edges. The order of the rules is taken from Zhang (2009).

doPdsep  If TRUE, Possible-D-SEP is computed for all nodes, and all subsets of Possible-D-SEP are considered as conditioning sets in the conditional independence tests, if not defined otherwise in pdsep.max. If FALSE, Possible-D-SEP is not computed, so that the algorithm simplifies to the Modified PC algorithm of Spirtes, Glymour and Scheines (2000, p.84).

biCC  If TRUE, only nodes on paths between nodes x and y are considered to be in Possible-D-SEP(x) when testing independence between x and y. Uses biconnected components, biConnComp from RBGL.

conservative  Logical indicating if the unshielded triples should be checked for ambiguity the second time when v-structures are determined. For more information, see details.

maj.rule  Logical indicating if the unshielded triples should be checked for ambiguity the second time when v-structures are determined using a majority rule idea, which is less strict than the standard conservative. For more information, see details.

verbose  If true, more detailed output is provided.

Details

This function is a generalization of the PC algorithm (see pc), in the sense that it allows arbitrarily many latent and selection variables. Under the assumption that the data are faithful to a DAG
that includes all latent and selection variables, the FCI algorithm (Fast Causal Inference algorithm) (Spirtes, Glymour and Scheines, 2000) estimates the Markov equivalence class of MAGs that describe the conditional independence relationships between the observed variables.

We estimate an equivalence class of **maximal ancestral graphs** (MAGs) instead of DAGs, since DAGs are not closed under marginalization and conditioning (Richardson and Spirtes, 2002).

An equivalence class of a MAG can be uniquely represented by a **partial ancestral graph** (PAG). A PAG contains the following types of edges: o-o, o-, o->, ->, <->, -. The bidirected edges come from hidden variables, and the undirected edges come from selection variables. The edges have the following interpretation: (i) there is an edge between x and y if and only if variables x and y are conditionally dependent given S for all sets S consisting of all selection variables and a subset of the observed variables; (ii) a tail on an edge means that this tail is present in all MAGs in the Markov equivalence class; (iii) an arrowhead on an edge means that this arrowhead is present in all MAGs in the Markov equivalence class; (iv) a o-edgemark means that there is at least one MAG in the Markov equivalence class where the edgemark is a tail, and at least one where the edgemark is an arrowhead. Information on the interpretation of edges in a MAG can be found in the references given below.

The first part of the FCI algorithm is analogous to the PC algorithm. It starts with a complete undirected graph and estimates an initial skeleton using **skeletonH*L method** which produces an initial order-independent skeleton, see **skeleton** for more details. All edges of this skeleton are of the form o-o. Due to the presence of hidden variables, it is no longer sufficient to consider only subsets of the neighborhoods of nodes x and y to decide whether the edge x oMo y should be removed. Therefore, the initial skeleton may contain some superfluous edges. These edges are removed in the next step of the algorithm which requires some orientations. Therefore, the v-structures are determined using the conservative method (see discussion on conservative below).

After the v-structures have been oriented, Possible-D-SEP sets for each node in the graph are computed at once. To decide whether edge x oMo y should be removed, one performs conditional independence tests of x and y given all possible subsets of Possible-D-SEP(x) and of Possible-D-SEP(y). The edge is removed if a conditional independence is found. This produces a fully order-independent final skeleton as explained in Colombo and Maathuis (2013). Subsequently, the v-structures are newly determined on the final skeleton (using information in sepset). Finally, as many as possible undetermined edge marks (o) are determined using (a subset of) the 10 orientation rules given by Zhang (2009).

The "Anytime FCI" algorithm was introduced by Spirtes (2001). It can be viewed as a modification of the FCI algorithm that only performs conditional independence tests up to and including order m.max when finding the initial skeleton, see **skeleton** for more details. All edges of this skeleton are of the form o-o. Due to the presence of hidden variables, it is no longer sufficient to consider only subsets of the neighborhoods of nodes x and y to decide whether the edge x oMo y should be removed. Therefore, the initial skeleton may contain some superfluous edges. These edges are removed in the next step of the algorithm which requires some orientations. Therefore, the v-structures are determined using the conservative method (see discussion on conservative below).

The "Adaptive Anytime FCI" algorithm was introduced by Colombo et. al (2012). The first part of the algorithm is identical to the normal FCI described above. But in the second part when the final skeleton is estimated using the function **pdsep**, the Adaptive Anytime FCI algorithm only performs conditional independence tests up to and including order m.max, where m.max is the maximum size of the conditioning sets that were considered to determine the initial skeleton using the function **skeleton**. Thus, m.max is chosen adaptively and does not have to be specified by the user.

Conservative versions of FCI, Anytime FCI, and Adaptive Anytime FCI are computed if **conservative = TRUE** is specified. After the final skeleton is computed, all potential v-structures a-b-c are checked in the
following way. We test whether \(a\) and \(c\) are independent conditioning on any subset of the neighbors of \(a\) or any subset of the neighbors of \(c\). When a subset makes \(a\) and \(c\) conditionally independent, we call it a separating set. If \(b\) is in no such separating set or in all such separating sets, no further action is taken and the normal version of the FCI, Anytime FCI, or Adaptive Anytime FCI algorithm is continued. If, however, \(b\) is in only some separating sets, the triple \(a-b-c\) is marked ‘ambiguous’. If \(a\) is independent of \(c\) given some \(S\) in the skeleton (i.e., the edge \(a-c\) dropped out), but \(a\) and \(c\) remain dependent given all subsets of neighbors of either \(a\) or \(c\), we will call all triples \(a-b-c\) ‘unambiguous’. This is because in the FCI algorithm, the true separating set might be outside the neighborhood of either \(a\) or \(c\). An ambiguous triple is not oriented as a v-structure. Furthermore, no further orientation rule that needs to know whether \(a-b-c\) is a v-structure or not is applied. Instead of using the conservative version, which is quite strict towards the v-structures, Colombo and Maathuis (2013) introduced a less strict version for the v-structures called majority rule. This adaptation can be called using \(\text{maj.rule} = \text{TRUE}\). In this case, the triple \(a-b-c\) is marked as ‘ambiguous’ if and only if \(b\) is in exactly 50 percent of such separating sets or no separating set was found. If \(b\) is in less than 50 percent of the separating sets it is set as a v-structure, and if in more than 50 percent it is set as a non v-structure (for more details see Colombo and Maathuis, 2013). Colombo and Maathuis (2013) showed that with both these modifications, the final skeleton and the decisions about the v-structures of the FCI algorithm are fully order-independent.

Note that the order-dependence issues on the 10 orientation rules are still present, see Colombo and Maathuis (2013) for more details.

Value

An object of class \texttt{fciAlg} (see \texttt{fciAlgo}) containing the estimated graph (in the form of an adjacency matrix with various possible edge marks), the conditioning sets that lead to edge removals (sepset) and several other parameters.

Author(s)

Diego Colombo and Markus Kalisch (<kalisch@stat.math.ethz.ch>).

References


**See Also**

- `skeleton` for estimating a skeleton using the PC algorithm; `pc` for estimating a CPDAG using the PC algorithm; `pdsep` for computing Possible-D-SEP for each node and testing and adapting the graph accordingly; `qreach` for a fast way of finding Possible-D-SEP for a given node.
- `gaussCItest`, `disCItest`, `binCItest` and `dsepTest` as examples for `indepTest`.

**Examples**

```r
#### Example without latent variables

```set.seed(42)
p <- 7
## generate and draw random DAG :
myDAG <- randomDAG(p, prob = 0.4)

## find skeleton and PAG using the FCI algorithm
suffStat <- list(C = cov2cor(trueCov(myDAG)), n = 10^9)
res <- fci(suffStat, indepTest = gaussCItest, 
   alpha = 0.9999, p = p, doDsep = FALSE)

#### Example with hidden variables

## Zhang (2008), Fig. 6, p.1882

```p <- 4
L <- 1 # 'l' is latent
V <- c("Ghost", "Max","Urs","Anna","Eva")
edL <- setNames(vector("list", length=length(V)), V)
edL[[1]] <- list(edges=c(2,4),weights=c(1,1))
edL[[2]] <- list(edges=c(2,4),weights=c(1,1))
edL[[3]] <- list(edges=c(2,4),weights=c(1,1))
edL[[4]] <- list(edges=c(2,4),weights=c(1,1))
g <- new("graphNEL", nodes=V, edgeL=edL, edgemode="directed")

## compute the true covariance matrix of g
cov.mat <- trueCov(g)

## delete rows and columns belonging to latent variable L
true.cov <- cov.mat[-L,-L]
## transform covariance matrix into a correlation matrix
```
true.corr <- cov2cor(true.cov)

## The same, for the following three examples
indepTest <- gaussCItest
suffStat <- list(C = true.corr, n = 10^9)

## find PAG with FCI algorithm.
## As dependence "oracle", we use the true correlation matrix in
## gaussCItest() with a large "virtual sample size" and a large alpha:
normal.pag <- fci(suffStat, indepTest, alpha = 0.9999, labels = V[-L],
                    verbose=TRUE)

## find PAG with Anytime FCI algorithm with m.max = 1
## This means that only conditioning sets of size 0 and 1 are considered.
## As dependence "oracle", we use the true correlation matrix in the
## function gaussCItest with a large "virtual sample size" and a large
## alpha
anytime.pag <- fci(suffStat, indepTest, alpha = 0.9999, labels = V[-L],
                   type = "anytime", m.max = 1,
                   verbose=TRUE)

## find PAG with Adaptive Anytime FCI algorithm.
## This means that only conditioning sets up to size K are considered
## in estimating the final skeleton, where K is the maximal size of a
## conditioning set found while estimating the initial skeleton.
## As dependence "oracle", we use the true correlation matrix in the
## function gaussCItest with a large "virtual sample size" and a large
## alpha
adaptive.pag <- fci(suffStat, indepTest, alpha = 0.9999, labels = V[-L],
                    type = "adaptive",
                    verbose=TRUE)

## define PAG given in Zhang (2008), Fig. 6, p.1882
corr.pag <- rbind(c(0,1,1,0),
                   c(1,0,0,2),
                   c(1,0,0,2),
                   c(0,3,3,0))

## check if estimated and correct PAG are in agreement
all(corr.pag == normal.pag @ amat) # TRUE
all(corr.pag == anytime.pag @ amat) # FALSE
all(corr.pag == adaptive.pag @ amat) # TRUE
ij <- rbind(cbind(1:4,1:4), c(2,3), c(3,2))
all(corr.pag[ij] == anytime.pag @ amat[ij]) # TRUE
Description

This class of objects is returned by the function `fci` to represent the estimated PAG. Objects of this class have methods for the functions `plot`, `show` and `summary`.

Creation of objects

Objects can be created by calls of the form `new("fcialgo", ...)`, but are typically the result of `fci(...)`.

Slots

The slots `call`, `n`, `max.ord`, `n.edgetests`, `sepset`, and `pMax` are inherited from class "gAlgo", see there.

In addition, "fcialgo" has slots

- `amat`: a matrix: The the estimated graph, represented by its adjacency matrix. The edge marks are encoded by numbers: 0 = no edge, 1 = circle, 2 = arrowhead, 3 = tail. If `amat[i,j] = 1` and `amat[j,i] = 2`, this represents the edge `i < Mo j`.
- `allPdsep`: a list: the ith entry of this list contains Possible D-SEP of node number i.
- `n.edgetestsPDSEP` the number of new conditional independence tests (i.e., tests that were not done in the first part of the algorithm) that were performed while checking subsets of Possible D-SEP.
- `max.ordPDSEP` an integer: the maximum size of the conditioning sets used in the new conditional independence that were performed when checking subsets of Possible D-SEP.

Extends

Class "gAlgo".

Methods

- `plot` signature(x = "fcialgo"): Plot the resulting graph
- `show` signature(object = "fcialgo"): Show basic properties of the fitted object
- `summary` signature(object = "fcialgo"): Show details of the fitted object

Author(s)

Markus Kalisch and Martin Maechler

See Also

`fci`, `pcAlgo`
find.unsh.triple

Find all Unshielded Triples in an Undirected Graph

Description

Find all unshielded triples in an undirected graph, \( q \), i.e., the ordered \((x, y, z)\) with \( x < z \) list of all the triples in the graph.

Usage

find.unsh.triple(g, check=TRUE)

Arguments

g            adjacency matrix \((p \times p)\) of (the skeleton of) the graph. \( g \) must be symmetric, with 0/1 entries for presence of edges.

check        logical indicating that the symmetry of \( g \) should be checked.

Details

A triple of nodes \( x, y \) and \( z \) is “unshielded”, if (all of these are true):

(i) \( x \) and \( y \) are connected;
(ii) \( y \) and \( z \) are connected;
(iii) \( x \) and \( z \) are not connected.

Value

unshTripl    Matrix with 3 rows containing in each column an unshielded triple
unshVect     Vector containing the unique number for each column in unshTripl (for internal use only)
Author(s)

Diego Colombo, Markus Kalisch (<kalisch@stat.math.ethz.ch>), and Martin Maechler

Examples

data(gmG)
if (require(Rgraphviz)) {
  ## show graph
  plot(gmG$g, main = "True DAG")
}

## prepare skeleton use in example
g <- wgtMatrix(gmG$g)  # compute weight matrix
q <- t(g)  # still lower triangular
print.table(q, zero.print="")
skel <- g + t(g)  # adjacency matrix of skeleton

## estimate unshielded triples -- there are 13:
(uTr <- find.unsh.triple(skel))

---

**gAlgo-class**  Class "gAlgo"

Description

"gAlgo" is a "VIRTUAL" class, the common basis of classes "pcAlgo" and "fciAlgo". We describe the common slots here; for more see the help pages of the specific classes.

Slots

call: a call object: the original function call.

n: an "integer", the sample size used to estimate the graph.

max.ord: an integer, the maximum size of the conditioning set used in the conditional independence tests of the (first part of the algorithm), in function skeleton.

n.edgetests: the number of conditional independence tests performed by the (first part of the) algorithm.

sepset: a list, the conditioning sets that led to edge deletions. The set that led to the removal of the edge i-j is saved in either sepset[[i]][[j]] or in sepset[[j]][[i]].

pMax: a numeric square matrix, where the (i,j)th entry contains the maximum p-value of all conditional independence tests for edge i-j.

Author(s)

Martin Maechler
**GaussL0penIntScore-class**

**See Also**

"pcAlgo" and "fciAlgo".

**Examples**

```
showClass("gAlgo")
```

---

**Description**

This class represents a score for causal inference from jointly interventional and observational Gaussian data; it is used in the causal inference functions `gies` and `simy`.

**Details**

The class implements an $\ell_0$-penalized Gaussian maximum likelihood estimator. The penalization is a constant (specified by the argument `lambda` in the constructor) times the number of parameters of the DAG model. By default, the constant $\lambda$ is chosen as $\log(n)/2$, which corresponds to the BIC score.

**Extends**

Class "Score", directly.

All reference classes extend and inherit methods from "envRefClass".

**Fields**

The class `GaussL0penIntScore` has the same fields as `Score`. They need not be accessed by the user.

**Constructor**

```r
new("GaussL0penIntScore",
    data = matrix(1, 1, 1),
    targets = list(integer(0)),
    target.index = rep(as.integer(1), nrow(data)),
    lambda = 0.5*log(nrow(data)),
    intercept = FALSE,
    use.cpp = TRUE,
    ...
)
```

- **data** Data matrix with $n$ rows and $p$ columns. Each row corresponds to one realization, either interventional or observational.
- **targets** List of mutually exclusive intervention targets that have been used for data generation.
target.index Vector of length \( n \); the \( i \)-th entry specifies the index of the intervention target in targets under which the \( i \)-th row of data was measured.

\( \lambda \) Penalization constant (cf. details)

intercept Indicates whether an intercept is allowed in the linear structural equations, or, equivalently, if a mean different from zero is allowed for the observational distribution.

use.cpp Indicates whether the calculation of the score should be done by the C++ library of the package, which speeds up calculation. This parameter should only be set to FALSE in the case of problems.

Methods

local.score(vertex, parents, ...) Calculates the local score of a vertex and its parents. Since this score has no obvious interpretation, it is rather for internal use.

global.score.int(edges, ...) Calculates the global score of a DAG, represented as a list of in-edges: for each vertex in the DAG, this list contains a vector of parents.

global.score(dag, ...) Calculates the global score of a DAG, represented as an object of a class derived from ParDAG.

local.mle(vertex, parents, ...) Calculates the local MLE of a vertex and its parents. The result is a vector of parameters encoded as follows:

- First element: variance of the Gaussian error term
- Second element: intercept
- Following elements: regression coefficients; one per parent vertex

global.mle(dag, ...) Calculates the global MLE of a DAG, represented by an object of a class derived from ParDAG. The result is a list of vectors, one per vertex, each in the same format as the result vector of local.mle.

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

See Also
gies, simy, GaussLOpenObsScore, Score

Examples

```
# Using Gaussian Data
data(gmInt)

# Define the score object
score <- new("GaussLOpenIntScore", gmInt$x, gmInt$targets, gmInt$target.index)

# Score of the true underlying DAG
score$global.score(as(gmInt$g, "GaussParDAG"))
```
GaussL0penObsScore-class

## Description

This class represents a score for causal inference from observational Gaussian data; it is used in the causal inference function `ges`.

## Details

The class implements an $\ell_0$-penalized Gaussian maximum likelihood estimator. The penalization is a constant (specified by the argument `lambda` in the constructor) times the number of parameters of the DAG model. By default, the constant $\lambda$ is chosen as $\log(n)/2$, which corresponds to the BIC score.

## Extends

Class "Score", directly.

All reference classes extend and inherit methods from "envRefClass".

## Fields

The class GaussL0penObsScore has the same fields as Score. They need not be accessed by the user.

## Constructor

```r
new("GaussL0penObsScore",
    data = matrix(1, 1, 1),
    lambda = 0.5*log(nrow(data)),
    intercept = FALSE,
    use.cpp = TRUE,
    ...
)
```

data  Data matrix with $n$ rows and $p$ columns. Each row corresponds to one observational realization.

lambda  Penalization constant (cf. details)

intercept  Indicates whether an intercept is allowed in the linear structural equations, or, equivalently, if a mean different from zero is allowed for the observational distribution.

use.cpp  Indicates whether the calculation of the score should be done by the C++ library of the package, which speeds up calculation. This parameter should only be set to `FALSE` in the case of problems.
Methods

local.score(vertex, parents, ...) Calculates the local score of a vertex and its parents. Since this score has no obvious interpretation, it is rather for internal use.

global.score.int(edges, ...) Calculates the global score of a DAG, represented as a list of in-edges: for each vertex in the DAG, this list contains a vector of parents.

global.score(dag, ...) Calculates the global score of a DAG, represented as an object of a class derived from ParDAG.

local.mle(vertex, parents, ...) Calculates the local MLE of a vertex and its parents. The result is a vector of parameters encoded as follows:
  • First element: variance of the Gaussian error term
  • Second element: intercept
  • Following elements: regression coefficients; one per parent vertex

global.mle(dag, ...) Calculates the global MLE of a DAG, represented by an object of a class derived from ParDAG. The result is a list of vectors, one per vertex, each in the same format as the result vector of local.mle.

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

See Also

ges, GaussL0penIntScore, Score

Examples

#############################################################
## Using Gaussian Data
#############################################################
## Load predefined data
data(gmG)

## Define the score object
score <- new("GaussL0penObsScore", gmG$x)

## Score of the true underlying DAG
score$global.score(as(gmG$g, "GaussParDAG"))

## Score of the DAG that has only one edge from 1 to 2
A <- matrix(0, ncol(gmG$x), ncol(gmG$x))
A[1, 2] <- 1
score$global.score(as(A, "GaussParDAG"))
## (Note: this is lower than the score of the true DAG.)
The "GaussParDAG" class represents a Gaussian causal model.

The class "GaussParDAG" is used to simulate observational and/or interventional data from Gaussian causal models as well as for parameter estimation (maximum-likelihood estimation) for a given DAG structure in the presence of a data set with jointly observational and interventional data.

A Gaussian causal model can be represented as a set of $p$ linear structural equations with Gaussian noise variables. Those equations are fully specified by indicating the regression parameters, the intercept and the variance of the noise or error terms. More details can be found e.g. in Kalisch and Bühlmann (2007) or Hauser and Bühlmann (2012).

Extends

Class "ParDAG", directly.

All reference classes extend and inherit methods from "envRefClass".

Constructor

```
new("GaussParDAG", nodes, in.edges, params)
```

- `nodes` Vector of node names; cf. also field `.nodes`.
- `in.edges` A list of length $p$ consisting of index vectors indicating the edges pointing into the nodes of the DAG.
- `params` A list of length $p$ consisting of parameter vectors modeling the conditional distribution of a node given its parents; cf. also field `.params` for the meaning of the parameters.

Fields

- `.nodes`: Vector of node names; defaults to `as.character(1:p)`, where $p$ denotes the number of nodes (variables) of the model.
- `.in.edges`: A list of length $p$ consisting of index vectors indicating the edges pointing into the nodes of the DAG. The $i$-th entry lists the indices of the parents of the $i$-th node.
- `.params`: A list of length $p$ consisting of parameter vectors modeling the conditional distribution of a node given its parents. The $i$-th entry models the conditional (normal) distribution of the $i$-th variable in the model given its parents. It is a vector of length $k + 2$, where $k$ is the number of parents of node $i$; the first entry encodes the error variance of node $i$, the second entry the intercept, and the remaining entries the regression coefficients (see above). In most cases, it is easier to access the parameters via the wrapper functions `err.var`, `intercept` and `weight.mat`. 
Class-Based Methods

set.err.var(value): Sets the error variances. The argument must be a vector of length \( p \), where \( p \) denotes the number of nodes in the model.

err.var(): Yields the vector of error variances.

intercept(): Yields the vector of intercepts.

set.intercept(value): Sets the intercepts. The argument must be a vector of length \( p \), where \( p \) denotes the number of nodes in the model.

weight.mat(target): Yields the (observational or interventional) weight matrix of the model. The weight matrix is an \( p \times p \) matrix whose \( i \)-th columns contains the regression coefficients of the \( i \)-th structural equation, if node \( i \) is not intervened (i.e., if \( i \) is not contained in the vector target), and is empty otherwise.

cov.mat(target, ivent.var): Yields the covariance matrix of the observational or an interventional distribution of the causal model. If target has length 0, the covariance matrix of the observational distribution is returned; otherwise target is a vector of the intervened nodes, and ivent.var is a vector of the same length indicating the variances of the intervention levels. Deterministic interventions with fix intervention levels would correspond to vanishing intervention variances; with non-zero intervention variances, stochastic interventions are considered in which intervention values are realizations of Gaussian variables (Korb et al., 2004).

The following methods are inherited (from the corresponding class): node.count ("ParDAG"), edge.count ("ParDAG"), simulate ("ParDAG")

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

References


See Also

*ParDAG*

Examples

```r
set.seed(307)
myDAG <- r.gauss.pardag(p = 5, prob = 0.4)
myDAG$weight.mat()
myDAG$err.var()
```
Description

Estimate the observational or interventional essential graph representing the Markov equivalence class of a DAG by greedily optimizing a score function in the space of DAGs. In practice, greedy search should always be done in the space of equivalence classes instead of DAGs, giving the functions `gies` or `ges` the preference over `gds`.

Usage

gds(p, targets, score, verbose = FALSE, ...)

Arguments

- `p` number of variables.
- `targets` a list of intervention targets (cf. details). A list of vectors, each vector listing the vertices of one intervention target.
- `score` an instance of a class derived from `Score`.
- `verbose` if TRUE, detailed output is provided.
- `...` additional arguments for debugging purposes and fine tuning.

Details

This function estimates the observational or interventional Markov equivalence class of a DAG based on a data sample with interventional data originating from various interventions and possibly observational data. The intervention targets used for data generation must be specified by the argument `targets` as a list of (integer) vectors listing the intervened vertices; observational data is specified by an empty set, i.e. a vector of the form `integer(0)`. As an example, if data contains observational samples as well as samples originating from an intervention at vertices 1 and 4, the intervention targets must be specified as `list(integer(0), as.integer(1), as.integer(c(1, 4)))`.

An interventional Markov equivalence class of DAGs can be uniquely represented by a partially directed graph called interventional essential graph. Its edges have the following interpretation:

1. a directed edge \(a \rightarrow b\) stands for an arrow that has the same orientation in all representatives of the interventional Markov equivalence class;
2. an undirected edge \(a - b\) stands for an arrow that is oriented in one way in some representatives of the equivalence class and in the other way in other representatives of the equivalence class.
Note that when plotting the object, undirected and bidirected edges are equivalent.

Greedy DAG search (GDS) maximizes a score function (typically the BIC, passed to the function via the argument `score`) of a DAG in three phases, starting from the empty DAG:

**Forward phase** In the forward phase, GDS adds single arrows to the DAG as long as this augments the score.

**Backward phase** In the backward phase, the algorithm removes arrows from the DAG as long as this augments the score.

**Turning phase** In the turning phase, the algorithm reverts arrows of the DAG as long as this augments the score.

GIES cycles through these three phases until no augmentation of the score is possible any more. In the end, `gds` returns the (interventional or observational) essential graph of the last visited DAG.

It is well-known that a greedy search in the space of DAGs instead of essential graphs is more prone to be stuck in local optima of the score function and hence expected to yield worse estimation results than GIES (function `gies`) or GES (function `ges`) (Chickering, 2002; Hauser and Bühlmann, 2012). The function `gds` is therefore not of practical use, but can be used to compare causal inference algorithms to an elementary and straightforward approach.

**Value**

`gds` returns a list with the following two components:

- `essgraph` An object of class `EssGraph` containing an estimate of the equivalence class of the underlying DAG.
- `repr` An object of a class derived from `ParDAG` containing a (random) representative of the estimated equivalence class.

**Author(s)**

Alain Hauser (<alain.hauser@biology.unibe.ch>)

**References**


**See Also**

`gies, ges, Score, EssGraph`
Examples

```r
## Load predefined data
data(gmInt)

## Define the score (BIC)
score <- new("GaussL0penIntScore", gmInt$x, gmInt$targets, gmInt$target.index)

## Estimate the essential graph
gds.fit <- gds(ncol(gmInt$x), gmInt$targets, score)

## Plot the estimated essential graph and the true DAG
if (require(Rgraphviz)) {
  par(mfrow=c(1,2))
  plot(gds.fit$essgraph, main = "Estimated ess. graph")
  plot(gmInt$g, main = "True DAG")
}
```

---

Estimate the Markov equivalence class of a DAG using GES

Description

Estimate the observational essential graph representing the Markov equivalence class of a DAG using the greedy equivalence search (GES) algorithm of Chickering (2002).

Usage

```r
ges(p, score, fixedGaps = NULL,
   turning = TRUE, maxDegree = integer(0), verbose = FALSE, ...)
```

Arguments

- **p**: Number of variables.
- **score**: An instance of a class derived from `Score` which only accounts for observational data.
- **fixedGaps**: logical symmetric matrix of dimension p*p. If entry [i, j] is TRUE, the result is guaranteed to have no edge between nodes i and j.
- **turning**: Logical indicating whether the function should try to augment the score by turning edges (cf. details).
- **maxDegree**: Parameter used to limit the vertex degree of the estimated graph. Valid arguments:
  1. Vector of length 0 (default): vertex degree is not limited.
  2. Real number r, 0 < r < 1: degree of vertex v is limited to r \cdot n_v, where n_v denotes the number of data points where v was not intervened.
  3. Single integer: uniform bound of vertex degree for all vertices of the graph.
4. Integer vector of length p: vector of individual bounds for the vertex degrees.

verbose if TRUE, detailed output is provided.

Additional arguments for debugging purposes and fine tuning.

Details

Under the assumption that the distribution of the observed variables is faithful to a DAG, this function estimates the Markov equivalence class of the DAG. It does not estimate the DAG itself, because this is typically impossible (even with an infinite amount of data): different DAGs (forming a Markov equivalence class) can describe the same conditional independence relationships and be statistically indistinguishable from observational data alone.

All DAGs in an equivalence class have the same skeleton (i.e., the same adjacency information) and the same v-structures (i.e., the same induced subgraphs of the form \( a \rightarrow b \leftarrow c \)). However, the direction of some edges may be undetermined, in the sense that they point one way in one DAG in the equivalence class, while they point the other way in another DAG in the equivalence class.

An equivalence class can be uniquely represented by a partially directed graph called (observational) essential graph or CPDAG (completed partially directed acyclic graph). Its edges have the following interpretation:

1. a directed edge \( a \rightarrow b \) stands for an arrow that has the same orientation in all representatives of the Markov equivalence class;
2. an undirected edge \( a \sim b \) stands for an arrow that is oriented in one way in some representatives of the equivalence class and in the other way in other representatives of the equivalence class.

Note that when plotting the object, undirected and bidirected edges are equivalent.

GES (greedy equivalence search) is a score-based algorithm that greedily maximizes a score function (typically the BIC, passed to the function via the argument score) in the space of (observational) essential graphs in three phases, starting from the empty graph:

**Forward phase** In the forward phase, GES moves through the space of essential graphs in steps that correspond to the addition of a single edge in the space of DAGs; the phase is aborted as soon as the score cannot be augmented any more.

**Backward phase** In the backward phase, the algorithm performs moves that correspond to the removal of a single edge in the space of DAGs until the score cannot be augmented any more.

**Turning phase** In the turning phase, the algorithm performs moves that correspond to the reversal of a single arrow in the space of DAGs until the score cannot be augmented any more.

GES cycles through these three phases until no augmentation of the score is possible any more. Note that the turning phase (activated with turning = TRUE, the default behaviour) was not part of the original implementation of Chickering (2002), but was introduced by Hauser and Bühlmann (2012) and shown to improve the overall estimation performance.

GES has the same purpose as the PC algorithm (see pc). While the PC algorithm is based on conditional independence tests (requiring the choice of an independence test and a significance level, see pc), the GES algorithm is a score-based method (requiring the choice of a score function) and does not depend on conditional independence tests. Since GES always operates in the space of essential graphs, it returns a valid essential graph (or CPDAG) in any case.
Value

ges returns a list with the following two components:

- essgraph: An object of class EssGraph containing an estimate of the equivalence class of the underlying DAG.
- repr: An object of a class derived from ParDAG containing a (random) representative of the estimated equivalence class.

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

References


See Also

- pc, Score, EssGraph

Examples

```r
## Load predefined data
data(gmG)

## Define the score (BIC)
score <- new("GaussL0penObsScore", gmG$x)

## Estimate the essential graph
ges.fit <- ges(ncol(gmG$x), score)

## Plot the estimated essential graph and the true DAG
if (require(Rgraphviz)) {
  par(mfrow=c(1,2))
  plot(ges.fit$essgraph, main = "Estimated CPDAG")
  plot(gmG$g, main = "True DAG")
} else { # alternative:
  str(ges.fit, max=2)
  as(as(ges.fit$essgraph,"graphNEL"),"Matrix")
}
```
getGraph

Get the "graph" Part or Aspect of R Object

Description
Get the graph part or “aspect” of an R object, notably from our pc(), skeleton(), fci(), etc, results.

Usage
getGraph(x)

Arguments
x potentially any R object which can be interpreted as a graph (with nodes and edges).

Value
a graph object, i.e., one inheriting from (the virtual) class "graph", package graph.

Methods
signature(x = "ANY") the default method just tries as(x, "graph"), so works when a coerce (S4) method is defined for x.
signature(x = "pcAlgo") and
signature(x = "fciAlgo") extract the graph part explicitly.
signature(x = "matrix") interpret x as adjacency matrix and return the corresponding "graphAM" object.

For sparseMatrix methods, see the ‘Note’.

Note
For large graphs, it may be attractive to work with sparse matrices from the Matrix package. If desired, you can activate this by

require(Matrix)
setMethod("getGraph", "SparseMatrix", function(x) as(x, "graphNEL"))
setMethod("getGraph", "Matrix", function(x) as(x, "graphAM"))

Author(s)
Martin Maechler
getNextSet

See Also

fci, etc. The graph class description in package graph.

Examples

```r
A <- rbind(c(0,1,0,0,1),
            c(0,0,0,0,1),
            c(1,0,0,1,0),
            c(1,0,0,0,1),
            c(0,0,0,0,1))
sum(A) # 9
getGraph(A) ## a graph with 5 nodes and 'sum(A)' edges
```

<table>
<thead>
<tr>
<th>getNextSet</th>
<th>Iteration through a list of all combinations of choose(n,k)</th>
</tr>
</thead>
</table>

Description

Given a combination of \( k \) elements out of the elements \( 1, \ldots, n \), the next set of size \( k \) in a specified sequence is computed.

Usage

g getNextSet(n,k,set)

Arguments

- **n**: Number of elements to choose from (integer)
- **k**: Size of chosen set (integer)
- **set**: Previous set in list (numeric vector)

Details

The initial set is \( 1:k \). Last index varies quickest. Using the dynamic creation of sets reduces the memory demands dramatically for large sets. If complete lists of combination sets have to be produced and memory is no problem, the function `combn` from package combinat is an alternative.

Value

List with two elements:

- **nextInt**: Next set in list (numeric vector)
- **wasLast**: Logical indicating whether the end of the specified sequence is reached.

Author(s)

Markus Kalisch <kalisch@stat.math.ethz.ch> and Martin Maechler
See Also

This function is used in skeleton.

Examples

```r
## start from first set (1,2) and get the next set of size 2 out of 1:5
## notice that res$wasLast is FALSE:
str(r <- getNextSet(5,2,c(1,2)))

## input is the last set; notice that res$wasLast now is TRUE:
str(r2 <- getNextSet(5,2,c(4,5)))

## Show all sets of size k out of 1:n:
## (if you really want this in practice, use something like combn() !)
n <- 5
k <- 3
currentSet <- 1:k
(res <- rbind(currentSet, deparse.level = 0))
repeat {
  newEl <- getNextSet(n,k,currentSet)
  if (newEl$wasLast)
    break
## otherwise continue:
  currentSet <- newEl$nextSet
  res <- rbind(res, currentSet, deparse.level = 0)
}
res
stopifnot(choose(n,k) == nrow(res)) ## must be identical
```

---

gies

Estimate Interventional Markov Equivalence Class of a DAG by GIES

Description

Estimate the interventional essential graph representing the Markov equivalence class of a DAG using the greedy interventional equivalence search (GIES) algorithm of Hauser and Bühlmann (2012).

Usage

gies(p, targets, score, fixedGaps = NULL, turning = TRUE, maxDegree = integer(0), verbose = FALSE, ...)

Arguments

p Number of variables.

targets A list of intervention targets (cf. details). A list of vectors, each vector listing the vertices of one intervention target.

score An instance of a class derived from Score.
fixedGaps logical symmetric matrix of dimension p*p. If entry [i, j] is TRUE, the result is guaranteed to have no edge between nodes i and j.

turning Logical indicating whether the function should try to augment the score by turning edges (cf. details).

maxDegree Parameter used to limit the vertex degree of the estimated graph. Possible values:
1. Vector of length 0 (default): vertex degree is not limited.
2. Real number r, 0 < r < 1: degree of vertex v is limited to r * n_v, where n_v denotes the number of data points where v was not intervened.
3. Single integer: uniform bound of vertex degree for all vertices of the graph.
4. Integer vector of length p: vector of individual bounds for the vertex degrees.

verbose if TRUE, detailed output is provided.

... Additional arguments for debugging purposes and fine tuning.

Details

This function estimates the interventional Markov equivalence class of a DAG based on a data sample with interventional data originating from various interventions and possibly observational data. The intervention targets used for data generation must be specified by the argument targets as a list of (integer) vectors listing the intervened vertices; observational data is specified by an empty set, i.e. a vector of the form integer(0). As an example, if data contains observational samples as well as samples originating from an intervention at vertices 1 and 4, the intervention targets must be specified as list(integer(0), as.integer(1), as.integer(c(1, 4))).

An interventional Markov equivalence class of DAGs can be uniquely represented by a partially directed graph called interventional essential graph. Its edges have the following interpretation:

1. a directed edge a → b stands for an arrow that has the same orientation in all representatives of the interventional Markov equivalence class;
2. an undirected edge a–b stands for an arrow that is oriented in one way in some representatives of the equivalence class and in the other way in other representatives of the equivalence class.

Note that when plotting the object, undirected and bidirected edges are equivalent.

GIES (greedy interventional equivalence search) is a score-based algorithm that greedily maximizes a score function (typically the BIC, passed to the function via the argument score) in the space of interventional essential graphs in three phases, starting from the empty graph:

Forward phase In the forward phase, GIES moves through the space of interventional essential graphs in steps that correspond to the addition of a single edge in the space of DAGs; the phase is aborted as soon as the score cannot be augmented any more.

Backward phase In the backward phase, the algorithm performs moves that correspond to the removal of a single edge in the space of DAGs until the score cannot be augmented any more.

Turning phase In the turning phase, the algorithm performs moves that correspond to the reversal of a single arrow in the space of DAGs until the score cannot be augmented any more.
GIES cycles through these three phases until no augmentation of the score is possible any more. GIES is an interventional extension of the GES (greedy equivalence search) algorithm of Chickering (2002) which is limited to observational data and hence operates on the space of observational instead of interventional Markov equivalence classes.

Value

gies returns a list with the following two components:

- `essgraph`: An object of class `EssGraph` containing an estimate of the equivalence class of the underlying DAG.
- `repr`: An object of a class derived from `ParDAG` containing a (random) representative of the estimated equivalence class.

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

References


See Also

`ges`, `Score`, `EssGraph`

Examples

```r
## Load predefined data
data(gmInt)

## Define the score (BIC)
score <- new("GaussianOpenIntScore", gmInt$x, gmInt$targets, gmInt$target.index)

## Estimate the essential graph
gies.fit <- gies(ncol(gmInt$x), gmInt$targets, score)

## Plot the estimated essential graph and the true DAG
if (require(Rgraphviz)) {
  par(mfrow=c(1,2))
  plot(gies.fit$essgraph, main = "Estimated ess. graph")
  plot(gmInt$g, main = "True DAG")
}
```
**Description**

This data set contains a matrix containing information on five binary variables (coded as 0/1) and the corresponding DAG model.

**Usage**

data(gmB)

**Format**

The format is a list of two components

x: Int [1:5000, 1:5] 0 1 1 0 0 1 1 0 1 1 ...

g: Formal class 'graphNEL' [package "graph"] with 6 slots
   .. ..@ nodes : chr [1:5] "1" "2" "3" "4" ...
   .. ..@ edgeL :List of 5
   .......

**Details**

The data was generated using Tetrad in the following way. A random DAG on five nodes was generated; binary variables were assigned to each node; then conditional probability tables corresponding to the structure of the generated DAG were constructed. Finally, 5000 samples were drawn using the conditional probability tables.

**Examples**

data(gmB)

## maybe str(gmB); plot(gmB) ...

---

**Description**

This data set contains a matrix containing information on five discrete variables (levels are coded as numbers) and the corresponding DAG model.

**Usage**

data(gmD)
Format

The format is a list of two components

\[ \textbf{x}: \text{Int [1:10000, 1:5]} 2 2 1 1 2 0 2 0 \ldots \]

\[ \textbf{g}: \text{formal class 'graphNEL' [package "graph"] with 6 slots} \]

\[ \ldots @ \text{nodes}: \text{chr [1:5]} "1" "2" "3" "4" \ldots \]

\[ \ldots @ \text{edgeL}: \text{List of 5} \]

Details

The data was generated using Tetrad in the following way. A random DAG on five nodes was generated; discrete variables were assigned to each node (with 3, 2, 3, 4 and 2 levels); then conditional probability tables corresponding to the structure of the generated DAG were constructed. Finally, 10000 samples were drawn using the conditional probability tables.

Examples

```r
data(gmG)
## maybe str(gmG) ; plot(gmG) ...
```

---

**gmG**

*Graphical Model 8-Dimensional Gaussian Example Data*

Description

These two data sets contain a matrix containing information on eight gaussian variables and the corresponding DAG model.

Usage

```r
data(gmG)
```

Format

\textit{gmG} and \textit{gmG8} are each a \textbf{list} of two components

\[ \textbf{x}: \text{a numeric matrix 5000 } \times 8. \]

\[ \textbf{g}: \text{a graph, i.e., of formal class "graphNEL" from package graph with 6 slots} \]

\[ \ldots @ \text{nodes}: \text{chr [1:8]} "1" "2" "3" "4" \ldots \]

\[ \ldots @ \text{edgeL}: \text{List of 8} \]

Details

The data was generated as indicated below. First, a random DAG model was generated, then 5000 samples were drawn from “almost” this model, for \textit{gmG}: In the previous version, the data generation \textit{wgtMatrix} had the non-zero weights in reversed order for each node. On the other hand, for \textit{gmG8}, the correct weights were used in all cases
Source

The data set is identical to the one generated by

```r
## Used to generate "gmG"
set.seed(40)
p <- 8
n <- 5000
## true DAG:
vars <- c("Author", "Bar", "Ctrl", "Goal", paste0("V",5:8))
gGtrue <- randomDAG(p, prob = 0.3, V = vars)
gmG <- list(x = rmvDAG(n, gGtrue, back.compat=TRUE), g = gGtrue)
gmG8 <- list(x = rmvDAG(n, gGtrue), g = gGtrue)
```

Examples

```r
data(gmG)
str(gmG, max=3)
stopifnot(identical(gmG $ g, gmG8 $ g))
if(dev.interactive()) { ## to save time in tests
  round(as(gmG $ g, "Matrix"), 2) # weight ("adjacency") matrix
  plot(gmG $ g)
  pairs(gmG$x, gap = 0,
        panel=function(...) smoothScatter(..., add=TRUE))
}
```

Description

This data set contains a matrix containing information on seven gaussian variables and the corresponding DAG model.

Usage

```r
data(gmI)
```

Format

The two gmI* objects are each a list of two components x, an \( n \times 7 \) numeric matrix, and g, a DAG, a graph generated by `randomDAG`.

See `gmG` for more

Details

The data was generated as indicated below. First, a random DAG was generated, then samples were drawn from this model, strictly speaking for gmI7 only.
Source

The data sets are identical to those generated by

```r
## Used to generate "gmi"
set.seed(123)
p <- 7
myDAG <- randomDAG(p, prob = 0.2) ## true DAG
gmI <- list(x = rmvDAG(10000, myDAG, back.compatible=TRUE), g = myDAG)
gmI7 <- list(x = rmvDAG( 8000, myDAG),
g = myDAG)
```

Examples

```r
data(gmI)
str(gmI, max=3)
stopifnot(identical(gmI $ g, gmi7 $ g))
if(dev.interactive()) { ## to save time in tests
  round(as(gmI $ g, "Matrix"), 2) # weight ("adjacency") matrix
  plot(gmI $ g)
  pairs(gmIx, gap = 0,
    panel=function(...) smoothScatter(..., add=TRUE))
}
```

---

**gmInt**  
*Graphical Model 8-Dimensional Interventional Gaussian Example*  
*Data*

**Description**

This data set contains a matrix with an ensemble of observational and interventional data from eight Gaussian variables. The corresponding (data generating) DAG model is also stored.

**Usage**

`data(gmInt)`

**Format**

The format is a list of four components

- **x**: Matrix with 5000 rows (one row a measurement) and 8 columns (corresponding to the 8 variables)
- **targets**: List of (mutually exclusive) intervention targets. In this example, the three entries `integer(0), 3` and `5` indicate that the data set consists of observational data, interventional data originating from an intervention at vertex `3`, and interventional data originating from an intervention at vertex `5`.
- **target.index**: Vector with 5000 elements. Each entry maps a row of `x` to the corresponding intervention target. Example: `gmInt$target.index[3322] == 2` means that `x[3322]` was simulated from an intervention at `gmInt$targets[[2]]`, i.e. at vertex `3`.  

---

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---

**gmInt**
Formal class 'graphNEL' [package "graph"] with 6 slots, representing the true DAG from which observational and interventional data was sampled.

Details

The data was generated as indicated below. First, a random DAG model was generated, then 5000 samples were drawn from this model: 3000 observational ones, and 1000 each from an intervention at vertex 3 and 5, respectively (see gmInt$target.index).

Source

The data set is identical to the one generated by

```r
set.seed(40)
p <- 8
n <- 5000
gGtrue <- randomDAG(p, prob = 0.3)
pardag <- as(gGtrue, "GaussParDAG")
pardag$set.err.var(rep(1, p))
targets <- list(integer(0), 3, 5)
target.index <- c(rep(1, 0.6*n), rep(2, n/5), rep(3, n/5))
x1 <- rmvnorm.ivent(0.6*n, pardag)
x2 <- rmvnorm.ivent(n/5, pardag, targets[[2]],
                        matrix(rnorm(n/5, mean = 4, sd = 0.02), ncol = 1))
x3 <- rmvnorm.ivent(n/5, pardag, targets[[3]],
                        matrix(rnorm(n/5, mean = 4, sd = 0.02), ncol = 1))
gmInt <- list(x = rbind(x1, x2, x3),
               targets = targets,
               target.index = target.index,
               g = gGtrue)
```

Examples

```r
data(gmInt)
str(gmInt, max = 3)
pairs(gmInt$x, gap = 0, pch = ".")
```

Latent Variable 4-Dim Graphical Model Data Example

Description

This data set contains a matrix containing information on four gaussian variables and the corresponding DAG model containing four observed and one latent variable.
Usage

data(gmL)

Format

The format is a list of 2 components

\[ x: \text{num [1:10000, 1:4] 0.924 -0.189 1.016 0.363 0.497 ... ..- attr(*, "dimnames")=List of 2 .. ..$ : NULL .. ..$ : chr [1:4] "2" "3" "4" "5" \]

\[ g: \text{Formal class 'graphNEL' [package "graph"] with 6 slots .. @ nodes : chr [1:5] "1" "2" "3" "4" ... .. @ edgeL :List of 5 .......} \]

Details

The data was generated as indicated below. First, a random DAG model was generated with five nodes; then 10000 samples were drawn from this model; finally, variable one was declared to be latent and the corresponding column was deleted from the simulated data set.

Source

```r
## Used to generate "gmL"
set.seed(47)
p <- 5
n <- 10000
gGtrue <- randomDAG(p, prob = 0.3) ## true DAG
myX <- rmvDAG(n, gGtrue)
colnames(myX) <- as.character(1:5)
gmL <- list(x = myX[, -1], g = gGtrue)
```

Examples

```r
data(gmL)
str(gmL, max=3)

## the graph:
gML$g
graph::nodes(gML$g) ; str(graph::edges(gML$g))
if(require("igraphviz"))
  plot(gML$g, main = "gmL $ g -- latent variable example data")

pairs(gML $x) # the data
```
Estimate Multiset of Possible Total Causal Effects

Description

ida() estimates the multiset of possible total causal effects of one variable (x) onto another variable (y) from observational data.

causalEffect(g, y, x) computes the true causal effect ($\beta_{\text{true}}$) of x on y in g.

Usage

ida(x.pos, y.pos, mcov, graphEst, method = c("local", "global"),
     y.notparent = FALSE, verbose = FALSE, all.dags = NA)

causalEffect(g, y, x)

Arguments

x.pos, x (integer) position of variable x in the covariance matrix.
y.pos, y (integer) position of variable y in the covariance matrix.
mcov Covariance matrix that was used to estimate graphEst.
graphEst Estimated CPDAG, typically from pc(): If the result of pc is pc.fit, the estimated CPDAG can be obtained by pc.fit@graph.
method Character string specifying the method with default "local".
   "global": The algorithm considers all DAGs in the equivalence class of the CPDAG, hence is slow.
   "local": The algorithm only considers the local neighborhood of x in the CPDAG, hence is faster.
See details below.
y.notparent Logical; if true, any edge between x and y is assumed to be of the form x$\rightarrow$y.
verbose If TRUE, details on the regressions are printed.
all.dags All DAGs in the equivalence class of the CPDAG can be precomputed by allDags() and passed via this argument. In that case, allDags(...) is not called internally.
This option is only relevant when using method="global".
g Graph in which the causal effect is sought.

Details

It is assumed that we have observational data that are multivariate Gaussian and faithful to the true (but unknown) underlying causal DAG (without hidden variables). Under these assumptions, this function estimates the multiset of possible total causal effects of x on y, where the total causal effect is defined via Pearl’s do-calculus as $E(Y|do(X = z + 1)) - E(Y|do(X = z))$ (this value does not depend on z, since Gaussianity implies that conditional expectations are linear).
We estimate a set of possible total causal effects instead of the unique total causal effect, since it is typically impossible to identify the latter when the true underlying causal DAG is unknown (even with an infinite amount of data). Conceptually, the method works as follows. First, we estimate the equivalence class of DAGs that describe the conditional independence relationships in the data, using the function \texttt{pc} (see the help file of this function). For each DAG \( G \) in the equivalence class, we apply Pearl's do-calculus to estimate the total causal effect of \( x \) on \( y \). This can be done via a simple linear regression: if \( y \) is not a parent of \( x \), we take the regression coefficient of \( x \) in the regression \( \text{lm}(y \sim x + \text{pa}(x)) \), where \( \text{pa}(x) \) denotes the parents of \( x \) in the DAG \( G \); if \( y \) is a parent of \( x \) in \( G \), we set the estimated causal effect to zero.

If the equivalence class contains \( k \) DAGs, this will yield \( k \) estimated total causal effects. Since we do not know which DAG is the true causal DAG, we do not know which estimated total causal effect of \( x \) on \( y \) is the correct one. Therefore, we return the entire multiset of \( k \) estimated effects (it is a multiset rather than a set because it can contain duplicate values).

One can take summary measures of the multiset. For example, the minimum absolute value provides a lower bound on the size of the true causal effect: If the minimum absolute value of all values in the multiset is larger than one, then we know that the size of the true causal effect (up to sampling error) must be larger than one.

If \texttt{method="global"}, the method as described above is carried out, where all DAGs in the equivalence class of the estimated CPDAG are computed using the function \texttt{allDags}. This method is suitable for small graphs (say, up to 10 nodes).

If \texttt{method="local"}, we do not determine all DAGs in the equivalence class of the CPDAG. Instead, we only consider the local neighborhood of \( x \) in the CPDAG. In particular, we consider all possible directions of undirected edges that have \( x \) as endpoint, such that no new \( v \)-structure is created. For each such configuration, we estimate the total causal effect of \( x \) on \( y \) as above, using linear regression.

At first sight, it is not clear that such a local configuration corresponds to a DAG in the equivalence class of the CPDAG, since it may be impossible to direct the remaining undirected edges without creating a directed cycle or a \( v \)-structure. However, Maathuis, Kalisch and Buehlmann (2009) showed that there is at least one DAG in the equivalence class for each such local configuration.

As a result, it follows that the multisets of total causal effects of the "global" and the "local" method have the same unique values. They may, however, have different multiplicities.

For example, a CPDAG may represent eight DAGs, and the global method may produce the multiset \{1.3, -0.5, 0.7, 1.3, 1.3, -0.5, 0.7, 0.7\}. The unique values in this set are -0.5, 0.7 and 1.3, and the multiplicities are 2, 3 and 3. The local method, on the other hand, may yield \{1.3, -0.5, -0.5, 0.7\}. The unique values are again -0.5, 0.7 and 1.3, but the multiplicities are now 2, 1 and 1. The fact that the unique values of the multisets of the "global" and "local" method are identical implies that summary measures of the multiset that only depend on the unique values (such as the minimum absolute value) can be estimate by the local method.

\textbf{Value}

A vector that represents the multiset containing the estimated possible total causal effects of \( x \) on \( y \).

\textbf{Author(s)}

Markus Kalisch (<kalisch@stat.math.ethz.ch>)
References


See Also

`idaFast` for estimating the multiset of possible total causal effects for several target variables simultaneously.

`pc` for estimating a CPDAG.

Examples

```r
## Simulate the true DAG
set.seed(123)
p <- 7
myDAG <- randomDAG(p, prob = 0.2) ## true DAG
myCPDAG <- dag2cpdag(myDAG) ## true CPDAG
covTrue <- trueCov(myDAG) ## true covariance matrix

## simulate Gaussian data from the true DAG
n <- 10000
dat <- rmvDAG(n, myDAG)

## estimate CPDAG -- see help(pc)
suffStat <- list(C = cor(dat), n = n)
pc.fit <- pc(suffStat, indepTest = gaussCItest, p=p, alpha = 0.01)

if (require(Rgraphviz)) {
  ## plot the true and estimated graphs
  par(mfrow = c(1,2))
  plot(myDAG, main = "True DAG")
  plot(pc.fit, main = "Estimated CPDAG")
}

## Suppose we know the true CPDAG and covariance matrix
(l.ida <- ida(2.5, covTrue, myCPDAG, method = "local"))
(g.ida <- ida(2.5, covTrue, myCPDAG, method = "global"))
## The global and local method produce the same unique values.
stopifnot(all.equal(sort(unique(g.ida)),
                   sort(unique(l.ida))))

## From the true DAG, we can compute the true causal effect of Z on 5
(ce.2.5 <- causalEffect(myDAG, 5, 2))
## Indeed, this value is contained in the values found by both the
```
### idaFast

#### Description

This function estimates the multiset of possible total causal effects of one variable \( x \) on a *several* (i.e., a vector of) target variables \( y \) from observational data. idaFast() is more efficient than looping over ida. Only method="local" (see ida) is available.

#### Usage

```r
idaFast(x.pos, y.pos.set, mcov, graphEst)
```

#### Arguments

- `x.pos`  
  integer position of variable \( x \) in the covariance matrix.
- `y.pos.set`  
  integer vector of positions of the target variables \( y \) in the covariance matrix.
- `mcov`  
  covariance matrix that was used to estimate graphEst
- `graphEst`  
  estimated CPDAG from the function pc. If the output of pc is pc.fit, then the estimated CPDAG can be obtained by pc.fit@graph.

#### Details

This function performs ida(x.pos, y.pos, mcov, graphEst, method="local", y.notparent=FALSE, verbose=FALSE) for all values of y.pos in y.pos.set simultaneously, in an efficient way. See (the help about) ida for more details. Note that the option y.notparent = TRUE is not implemented, since it is not clear how to do that efficiently without orienting all edges away from y.pos.set at the same time, which seems not to be desirable. Suggestions are welcome.

#### Value

Matrix with length(y.pos.set) rows. Row \( i \) contains the multiset of estimated possible total causal effects of \( x \) on \( y.pos.set[i] \). Note that all multisets in the matrix have the same length, since the parents of \( x \) are the same for all elements of \( y.pos.set \).
**Author(s)**

Markus Kalisch (<kalisch@stat.math.ethz.ch>)

**References**

see the list in **ida**.

**See Also**

**pc** for estimating a CPDAG, and **ida** for estimating the multiset of possible total causal effects from observational data on only one target variable but with many more options (than here in **idaFast**).

**Examples**

```r
## Simulate the true DAG
set.seed(123)
p <- 7
myDAG <- randomDAG(p, prob = 0.2) ## true DAG
myCPDAG <- dag2cpdag(myDAG) ## true CPDAG
covTrue <- trueCov(myDAG) ## true covariance matrix

## simulate data from the true DAG
n <- 10000
dat <- rmvDAG(n, myDAG)
cov.d <- cov(dat)

cov.d <- cov(dat)

## estimate CPDAG (see help on the function "pc")
suffStat <- list(C = cor(dat), n = n)
pc.fit <- pc(suffStat, indepTest = gaussCttest, alpha = 0.01, p=p)

if(require(Rgraphviz)) {
op <- par(mfrow=c(1,3))
plot(myDAG, main="true DAG")
plot(myCPDAG, main="true CPDAG")
plot(pc.fit@graph, main="pc()-estimated CPDAG")
par(op)
}

(eff.est1 <- ida(2,5, cov.d, pc.fit@graph))## method = "local" is default
(eff.est2 <- ida(2,6, cov.d, pc.fit@graph))
(eff.est3 <- ida(2,7, cov.d, pc.fit@graph))
## These three computations can be combined in an efficient way
## by using idaFast :
(eff.estF <- idaFast(2, c(5,6,7), cov.d, pc.fit@graph))
```
iplotPC

Plotting a pcAlgo object using the package igraph

Description

Notably, when the Rgraphviz package is not easily available, iplotPC() is an alternative for plotting a "pcAlgo" object, making use of package igraph. It extracts the adjacency matrix and converts it into an object from package igraph which is then plotted.

Usage

iplotPC(pc.fit, labels = NULL)

Arguments

pc.fit an R object of class pcAlgo, as returned from skeleton() or pc().
labels optional labels for nodes; by default, the labels from the pc.fit object are used.

Value

Nothing. As side effect, the plot of pcAlgo object pc.fit.

Note

Note that this function does not work on fcilgo objects, as those need different edge marks.

Author(s)

Markus Kalisch <kalisch@stat.math.ethz.ch>

See Also

showEdgeList for printing the edge list of a pcAlgo object; showAtamat for printing the adjacency matrix of a pcAlgo object.

Examples

## Load predefined data
data(gmG)
n <- nrow(gmG$x)
V <- colnames(gmG$x)

## define sufficient statistics
suffStat <- list(C = cor(gmG$x), n = n)
## estimate CPDAG
pc.fit <- pc(suffStat, indepTest = gaussCitest,
alpha = 0.01, labels = V, verbose = TRUE)
legal.path (Check if a 3-node-path is Legal)

Description
Check if the path \(a \rightarrow b \leftarrow c\) is legal.
A 3-node path \(a \rightarrow b \leftarrow c\) is “legal” iff either \(b\) is a collider or \(a \rightarrow b \rightarrow c\) is a triangle.

Usage
legal.path(a, b, c, amat)

Arguments
- \(a, b, c\): Integer positions in adjacency matrix of nodes \(a, b,\) and \(c,\) respectively.
- \(amat\): Adjacency matrix (coding 0,1,2,3 for no edge, circle, arrowhead, tail; e.g., amat\([a, b]\) = 2 and amat\([b, a]\) = 3 implies \(a \rightarrow b\))

Value
TRUE if path is legal, otherwise FALSE.

Note
Prerequisite: \(a \rightarrow b \leftarrow c\) must be in a path (and this is not checked by \texttt{legal.path()}).

Author(s)
Markus Kalisch (<kalisch@stat.math.ethz.ch>)

Examples
amat <- matrix(c(0,1,1,0,0, 2,0,1,0,0, 2,2,0,2,1, 0,0,1,0,0, 0,0,2,0,0, 5,5)
legal.path(1,3,5, amat)
legal.path(1,2,3, amat)
legal.path(2,3,4, amat)
Construct a list of intervention targets and a target index vector

Description

This function constructs a list of intervention targets and a corresponding vector of target indices from a matrix specifying intervened vertices. The input matrix has the same dimensions as the usual data matrix; the output can be used to create scoring objects (see Score) and to run causal inference methods based on interventional data such as gies or simy.

Usage

mat2targets(A)

Arguments

A Logical matrix with \( n \) rows and \( p \) columns, where \( n \) is the sample size of a data set with jointly interventional and observational data, and \( p \) is the number of variables. \( A[i, j] \) is TRUE iff variable \( j \) is intervened in data point \( i \).

Value

mat2targets returns a list with two components:

- targets A list of unique intervention targets.
- target.index A vector of intervention target indices. The intervention target of data point \( i \) is encoded as \( \text{targets}[\text{target.index[i]}] \).

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

See Also

Score, gies, simy

Examples

```r
## Specify interventions using a matrix
p <- 5
n <- 10
A <- matrix(FALSE, nrow = n, ncol = p)
for (i in 1:n) A[i, (i-1) %% p + 1] <- TRUE

## Generate list of intervention targets and corresponding indices
target.list <- mat2targets(A)

for (i in 1:length(target.list$target.index))
  sprintf("Intervention target of %d-th data point: %d",
    i, target.list$targets[[target.list$target.index[i]]])
```
**mcor**

*Compute (Large) Correlation Matrix*

**Description**

Compute a correlation matrix, possibly by robust methods, applicable also for the case of a large number of variables.

**Usage**

```r
cmp(dm, method = c("standard", "Qn", "QnStable", "ogkScaleTau2", "ogkQn", "shrink"))
```

**Arguments**

- `dm`: Numeric matrix of data; rows are samples, columns are variables.
- `method`: "standard" (default), "Qn", "QnStable", "ogkQn" and "shrink" envokes standard, elementwise robust (based on $Q_n$ scale estimator, see `Qn`), robust (Qn using OGK, see `covOGK`) or shrinked () correlation estimate respectively.

**Details**

The "standard" method envokes a standard correlation estimator. "Qn" envokes a robust, elementwise correlation estimator based on the Qn scale estimator. "QnStable" also uses the Qn scale estimator, but uses an improved way of transforming that into the correlation estimator. "ogkQn" envokes a correlation estimator based on Qn using OGK. "shrink" is only useful when used with pcSelect. An optimal shrinkage parameter is used. Only correlation between response and covariates is shrinked.

**Value**

A correlation matrix estimated by the specified method.

**Author(s)**

Markus Kalisch <kalisch@stat.math.ethz.ch> and Martin Maechler

**References**

See those in the help pages for Qn and covOGK from package **robustbase**.

**See Also**

Qn and covOGK from package **robustbase**, pcorOrder for computing partial correlations.
Examples

```r
## produce uncorrelated normal random variables
set.seed(42)
x <- rnorm(100)
y <- 2*x + rnorm(100)
## compute correlation of var1 and var2
mcor(cbind(x,y), method="standard")

## repeat but this time with heavy-tailed noise
yNoise <- 2*x + rcauchy(100)
mcor(cbind(x,yNoise), method="standard") ## shows almost no correlation
mcor(cbind(x,yNoise), method="Qn") ## shows a lot correlation
mcor(cbind(x,yNoise), method="QnStable") ## shows still much correlation
mcor(cbind(x,yNoise), method="ogkQn") ## ditto
```

pag2mag

Transform a PAG into a MAG in the Corresponding Markov Equivalence Class

Description

Transform a Partial Ancestral Graph (PAG) into a valid Maximal Ancestral Graph (MAG) that belongs to the Markov equivalence class represented by the given PAG, with no additional edges into node x.

Usage

```r
pag2mag(amat.pag, x, max.chordal = 10, verbose = FALSE)
```

Arguments

- `amat.pag`: Adjacency matrix (coding 0,1,2,3 for no edge, circle, arrowhead, tail; e.g., amat[a,b] = 2 and amat[b,a] = 3 implies a -> b)
- `x`: Node in the PAG into which no additional edges are oriented.
- `max.chordal`: Positive integer: graph paths larger than `max.chordal` are considered to be too large to be checked for chordality.
- `verbose`: Logical; if true, some output is produced during computation.

Details

This function converts a PAG (adjacency matrix) to a valid MAG (adjacency matrix) that belongs to the Markov equivalence class represented by the given PAG. Note that we assume that there are no selection variables, meaning that the edges in the PAG can be of the following types: ->, <-, o->, and o-o. In a first step, it uses the Arrowhead Augmentation of Zhang (2006), i.e., any o-> edge is oriented into ->. Afterwards, it orients each chordal component into a valid DAG without orienting any additional edges into x.

This function is used in the Generalized Backdoor Criterion `backdoor` with type="pag", see Maathuis and Colombo (2013) for details.
**Value**

The output is an adjacency matrix $M$ of a valid MAG with edge marks. The edge marks are coded in the following way: $M[i,j]=M[j,i]=0$: no edge; $M[i,j]=2, M[j,i]=3$: $i \rightarrow j$; $M[i,j]=2, M[j,i]=2$: $i \leftarrow j$.

**Author(s)**

Diego Colombo, Markus Kalisch and Martin Maechler.

**References**


**See Also**

fci, dag2pag, backdoor

**Examples**

```r
## create the graph
set.seed(78)
p <- 12
g <- randomDAG(p, prob = 0.4)
## Compute the true covariance and then correlation matrix of g:
true.corr <- cov2cor(trueCov(g))

## define nodes 2 and 6 to be latent variables
L <- c(2, 6)

## Find PAG
## As dependence "oracle", we use the true correlation matrix in
## gaussCITest() with a large "virtual sample size" and a large alpha:
true.pag <- dag2pag(suffStat = list(C= true.corr, n= 10^9),
                   indepTest = gaussCITest, graph=g, L=L, alpha= 0.9999)

## find a valid MAG such that no additional edges are directed into
(amat.mag <- pag2magAM(true.pag@amat, 4)) # -> the adj.matrix of the MAG
```

---

**Description**

This virtual base class represents a parametric causal model.
Details
The class "ParDAG" serves as a basis for simulating observational and/or interventional data from causal models as well as for parameter estimation (maximum-likelihood estimation) for a given causal model in the presence of a data set with jointly observational and interventional data.

The virtual base class "ParDAG" provides a "skeleton" for all functions relied to the aforementioned task. In practical cases, a user may always choose an appropriate class derived from ParDAG which represents a specific parametric model class. The base class itself does not represent such a model class.

Extends
All reference classes extend and inherit methods from "envRefClass".

Constructor

new("ParDAG", nodes, in.edges, params)

nodes Vector of node names; cf. also field .nodes.
in.edges A list of length p consisting of index vectors indicating the edges pointing into the nodes of the DAG.
params A list of length p consisting of parameter vectors modeling the conditional distribution of a node given its parents; cf. also field .params.

Fields

.nodes: Vector of node names; defaults to as.character(1:p), where p denotes the number of nodes (variables) of the model.
in.edges: A list of length p consisting of index vectors indicating the edges pointing into the nodes of the DAG.
params: A list of length p consisting of parameter vectors modeling the conditional distribution of a node given its parents. The entries of the parameter vectors only get a concrete meaning in derived classes belonging to specific parametric model classes.

Class-Based Methods

node.count(): Yields the number of nodes (variables) of the model.
simulate(n, target, int.level): Generates n (observational or interventional) samples from the parametric causal model. The intervention target to be used is specified by the parameter target; if the target is empty (target = integer(0)), observational samples are generated. int.level indicates the values of the intervened variables; if it is a vector of the same length as target, all samples are drawn from the same intervention levels; if it is a matrix with n rows and as many columns as target has entries, its rows are interpreted as individual intervention levels for each sample.

edge.count(): Yields the number of edges (arrows) in the DAG.
mle.fit(score): Fits the parameters using an appropriate Score object.
Methods

plot signature(x = "ParDAG", y = "ANY"): plots the underlying DAG of the causal model. Parameters are not visualized.

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

See Also

GaussParDAG

---

pc

Estimate the Equivalence Class of a DAG using the PC Algorithm

Description

Estimate the equivalence class of a directed acyclic graph (DAG) from observational data, using the PC-algorithm.

Usage

pc(suffstat, indeptest, alpha, labels, p,
fixedgaps = NULL, fixedEdges = NULL, NAdelete = TRUE, m.max = Inf,
ucnp = c("relaxed", "rand", "retry"),
skel.method = c("stable", "original", "stable.fast"),
conservative = FALSE, maj.rule = FALSE, solve.conf1 = FALSE, verbose = FALSE)

Arguments

suffStat A list of sufficient statistics, containing all necessary elements for the conditional independence decisions in the function indepTest.

indepTest A function for testing conditional independence. It is internally called as indepTest(x,y,S,suffStat), and tests conditional independence of x and y given S. Here, x and y are variables, and S is a (possibly empty) vector of variables (all variables are denoted by their column numbers in the adjacency matrix). suffStat is a list, see the argument above. The return value of indepTest is the p-value of the test for conditional independence.

alpha significance level (number in (0, 1) for the individual conditional independence tests.

labels (optional) character vector of variable (or “node”) names. Typically preferred to specifying p.

p (optional) number of variables (or nodes). May be specified if labels are not, in which case labels is set to 1:p.

verbose If TRUE, detailed output is provided.
fixedGaps

A logical matrix of dimension p*p. If entry $[i,j]$ or $[j,i]$ (or both) are TRUE, the edge i-j is removed before starting the algorithm. Therefore, this edge is guaranteed to be absent in the resulting graph.

fixedEdges

A logical matrix of dimension p*p. If entry $[i,j]$ or $[j,i]$ (or both) are TRUE, the edge i-j is never considered for removal. Therefore, this edge is guaranteed to be present in the resulting graph.

NA.delete

If indepTest returns NA and this option is TRUE, the corresponding edge is deleted. If this option is FALSE, the edge is not deleted.

m.max

Maximal size of the conditioning sets that are considered in the conditional independence tests.

u2pd

String specifying the method for dealing with conflicting information when trying to orient edges (see details below).

skel.method

Character string specifying method; the default, "stable" provides an order-independent skeleton, see skeleton.

conservative

Logical indicating if the conservative PC is used. In this case, only option u2pd = "relaxed" is supported. Note that therefore the resulting object might not be extendable to a DAG. See details for more information.

maj.rule

Logical indicating that the triples shall be checked for ambiguity using a majority rule idea, which is less strict than the conservative PC algorithm. For more information, see details.

solve.confl

If TRUE, the orientation of the v-structures and the orientation rules work with lists for candidate sets and allow bi-directed edges to resolve conflicting edge orientations. In this case, only option u2pd = relaxed is supported. Note, that therefore the resulting object might not be a CPDAG because bi-directed edges might be present. See details for more information.

Details

Under the assumption that the distribution of the observed variables is faithful to a DAG, this function estimates the Markov equivalence class of the DAG. We do not estimate the DAG itself, because this is typically impossible (even with an infinite amount of data), since different DAGs can describe the same conditional independence relationships. Since all DAGs in an equivalence class describe the same conditional independence relationships, they are equally valid ways to describe the conditional dependence structure that was given as input.

All DAGs in a Markov equivalence class have the same skeleton (i.e., the same adjacency information) and the same v-structures (see definition below). However, the direction of some edges may be undetermined, in the sense that they point one way in one DAG in the equivalence class, while they point the other way in another DAG in the equivalence class.

A Markov equivalence class can be uniquely represented by a completed partially directed acyclic graph (CPDAG). A CPDAG contains undirected and directed edges. The edges have the following interpretation: (i) there is a (directed or undirected) edge between i and j if and only if variables i and j are conditionally dependent given S for all possible subsets S of the remaining nodes; (ii) a directed edge i->j means that this directed edge is present in all DAGs in the Markov equivalence class; (iii) an undirected edge i-j means that there is at least one DAG in the Markov equivalence class with edge i->j and there is at least one DAG in the Markov equivalence class with edge i<j.
The CPDAG is estimated using the PC algorithm (named after its inventors Peter Spirtes and Clark Glymour). The skeleton is estimated by the function skeleton which uses a modified version of the original PC algorithm (see Colombo and Maathuis (2013) for details). The original PC algorithm is known to be order-dependent, in the sense that the output depends on the order in which the variables are given. Therefore, Colombo and Maathuis (2013) proposed a simple modification, called PC-stable, that yields order-independent adjacencies in the skeleton (see the help file of this function for details). Subsequently, as many edges as possible are oriented. This is done in two steps. It is important to note that if no further actions are taken (see below) these two steps still remain order-dependent.

The edges are oriented as follows. First, the algorithm considers all triples \((a, b, c)\), where \(a\) and \(b\) are adjacent, \(b\) and \(c\) are adjacent, but \(a\) and \(c\) are not adjacent. For all such triples, we direct both edges towards \(b\) \((a \rightarrow b \leftarrow c)\) if and only if \(b\) was not part of the conditioning set that made the edge between \(a\) and \(c\) drop out. These conditioning sets were saved in sepset. The structure \(a \rightarrow b < c\) is called a v-structure.

After determining all v-structures, there may still be undirected edges. It may be possible to direct some of these edges, since one can deduce that one of the two possible directions of the edge is invalid because it introduces a new v-structure or a directed cycle. Such edges are found by repeatedly applying rules R1-R3 of the PC algorithm as given in Algorithm 2 of Kalisch and Bühlmann (2007). The algorithm stops if none of the rules is applicable to the graph.

The conservative PC algorithm \((\text{conservative} = \text{TRUE})\) is a slight variation of the PC algorithm (see Ramsey et al. 2006). After the skeleton is computed, all potential v-structures \(a-b-c\) are checked in the following way. We test whether \(a\) and \(c\) are independent conditioning on all subsets of the neighbors of \(a\) and all subsets of the neighbors of \(c\). When a subset makes \(a\) and \(c\) conditionally independent, we call it a separating set. If \(b\) is in no such separating set or in all such separating sets, no further action is taken and the usual PC is continued. If, however, \(b\) is in only some separating sets, the triple \(a-b-c\) is marked as ‘ambiguous’. Moreover, if no separating set is found among the neighbors, the triple is also marked as ‘ambiguous’. An ambiguous triple is not oriented as a v-structure. Furthermore, no further orientation rule that needs to know whether \(a-b-c\) is a v-structure or not is applied. Instead of using the conservative version, which is quite strict towards the v-structures, Colombo and Maathuis (2013) introduced a less strict version for the v-structures called majority rule. This adaptation can be called using \(\text{maj.rule} = \text{TRUE}\). In this case, the triple \(a-b-c\) is marked as ‘ambiguous’ if and only if \(b\) is in exactly 50 percent of such separating sets or no separating set was found. If \(b\) is in less than 50 percent of the separating sets it is set as a v-structure, and if in more than 50 percent it is set as a non-v-structure (for more details see Colombo and Maathuis, 2013). The usage of both the conservative and the majority rule versions resolve the order-dependence issues of the determination of the v-structures.

Sampling errors (or hidden variables) can lead to conflicting information about edge directions. For example, one may find that \(a-b-c\) and \(b-c-d\) should both be directed as v-structures. This gives conflicting information about the edge \(b-c\), since it should be directed as \(b<c\) in v-structure \(a->b<c\), while it should be directed as \(b>c\) in v-structure \(b->c<d\). With the option \(\text{solve.conf1} = \text{FALSE}\), in such cases, we simply overwrite the directions of the conflicting edge. In the example above this means that we obtain \(a->b>c<d\) if \(a-b-c\) was visited first, and \(a->b<c<d\) if \(b-c-d\) was visited first, meaning that the final orientation on the edge depends on the ordering in which the v-structures were considered. With the option \(\text{solve.conf1} = \text{TRUE}\) (which is only supported with option \(\text{u2pd} = "\text{relaxed}"\)), we first generate a list of all (unambiguous) v-structures (in the example above \(a-b-c\) and \(b-c-d\)), and then we simply orient them allowing both directions on the edge \(b-c\), namely we allow the bi-directed edge \(b <-> c\) resolving the order-dependence issues on the edge.
orientations. We denote bi-directed edges in the adjacency matrix $M$ of the graph as $M[b,c]=2$ and $M[c,b]=2$. In a similar way, using lists for the candidate edges for each orientation rule and allowing bi-directed edges, the order-dependence issues in the orientation rules can be resolved. Note that bi-directed edges merely represent a conflicting orientation and they should not be interpreted causally. The usage of these lists for the candidate edges and allowing bi-directed edges resolves the order-dependence issues on the orientation of the v-structures and on the orientation rules, see Colombo and Maathuis (2013) for more details.

Note that calling `conservative = TRUE`, `maj.rule = TRUE`, together with `solve.conf1 = TRUE` produces a fully order-independent output, see Colombo and Maathuis (2013).

Sampling errors, non faithfulness, or hidden variables can also lead to non-extendable CPDAGs, meaning that there does not exist a DAG that has the same skeleton and v-structures as the graph found by the algorithm. An example of this is an undirected cycle consisting of the edges a-b-c-d and d-a. In this case it is impossible to direct the edges without creating a cycle or a new v-structure. The option `u2pd` specifies what should be done in such a situation. If the option is set to "relaxed", the algorithm simply outputs the invalid CPDAG. If the option is set to "rand", all direction information is discarded and a random DAG is generated on the skeleton, which is then converted into its CPDAG. If the option is set to "retry", up to 100 combinations of possible directions of the ambiguous edges are tried, and the first combination that results in an extendable CPDAG is chosen. If no valid combination is found, an arbitrary DAG is generated on the skeleton as in the option "rand", and then converted into its CPDAG. Note that the output can also be an invalid CPDAG, in the sense that it cannot arise from the oracle PC algorithm, but be extendible to a DAG, for example a->b<-c<-d. In this case, u2pd is not used.

Notes: (1) Throughout, the algorithm works with the column positions of the variables in the adjacency matrix, and not with the names of the variables. (2) When plotting the object, undirected and bidirected edges are equivalent.

**Value**

An object of class "pcAlgo" (see `pcAlgo`) containing an estimate of the equivalence class of the underlying DAG.

**Author(s)**

Markus Kalisch (<kalisch@stat.math.ethz.ch>), Martin Maechler, and Diego Colombo.

**References**


See Also

`skeleton` for estimating a skeleton of a DAG; `udag2pdag` for converting the skeleton to a CPDAG; `gaussCItest`, `disCItest`, `binCItest` and `dsepTest` as examples for `indepTest`.

Examples

```r
### Using Gaussian Data
### Load predefined data
data(gmG)
n <- nrow(gmG$x)
V <- colnames(gmG$x)  # labels aka node names

### estimate CPDAG
pc.fit <- pc(suffStat = list(C = cor(gmG$x), n = n),
             indepTest = gaussCItest,  # indep.test: partial correlations
             alpha=0.01, labels = V, verbose = TRUE)
if (require(Rgraphviz)) {
  ### show estimated CPDAG
  par(mfrow=c(1,2))
  plot(pc.fit, main = "Estimated CPDAG")
  plot(gmG$x, main = "True DAG")
}

### Using d-separation oracle
### define sufficient statistics (d-separation oracle)
suffStat <- list(g = gmG$x, jp = RBGL::johnson.all.pairs.sp(gmG$x))
### estimate CPDAG
fit <- pc(suffStat, indepTest = dsepTest, labels = V,
          alpha=0.01)  # value is irrelevant as dsepTest returns either 0 or 1
if (require(Rgraphviz)) {
  ### show estimated CPDAG
  plot(fit, main = "Estimated CPDAG")
  plot(gmG$x, main = "True DAG")
}

### Using discrete data
### Load data
data(gmD)
V <- colnames(gmD$x)
### define sufficient statistics
suffStat <- list(dm = gmD$x, nlev = c(3,2,3,4,2), adaptDF = FALSE)
### estimate CPDAG
pc.D <- pc(suffStat,
```

pc.cons.intern

Utility for conservative and majority rule in PC and FCI

Description

The `pc.cons.intern()` function is used in `pc` and `fci`, notably when `conservative = TRUE` (conservative orientation of v-structures) or `maj.rule = TRUE` (majority rule orientation of v-structures).

Usage

```r
pc.cons.intern(sk, suffStat, indepTest, alpha, version.unf = c(NA, NA),
                 maj.rule = FALSE, verbose = FALSE)
```

Arguments

- **sk**: A skeleton object as returned from `skeleton()`.
- **suffStat**: Sufficient statistic: List containing all necessary elements for the conditional independence decisions in the function `indepTest`.
- **indepTest**: Pre-defined function for testing conditional independence. The function is internally called as `indepTest(x, y, S, suffStat)`, and tests conditional independence of `x` and `y` given `S`. Here, `x` and `y` are variables, and `S` is a (possibly
empty) vector of variables (all variables are denoted by their column numbers in the adjacency matrix). `suffstat` is a list containing all relevant elements for the conditional independence decisions. The return value of `indepTest` is the p-value of the test for conditional independence.

**alpha** Significance level for the individual conditional independence tests.

**version.unf** Vector of length two. If `version.unf[2]==1`, the initial separating set found by the PC/FCI algorithm is added to the set of separating sets; if `version.unf[2]==2`, it is not added. In the latter case, if the set of separating sets is empty, the triple is marked as unambiguous if `version.unf[1]==1`, and as ambiguous if `version.unf[1]==2`.

**maj.rule** Logical indicating if the triples are checked for ambiguity using the majority rule idea, which is less strict than the standard conservative method.

**verbose** Logical asking for detailed output.

**Details**

For any unshielded triple A-B-C, consider all subsets of the neighbors of A and of the neighbors of C, and record all such sets D for which A and C are conditionally independent given D. We call such sets “separating sets”.

If `version.unf[2]==1`, the initial separating set found in the PC/FCI algorithm is added to this set of separating sets. If `version.unf[2]==2`, the initial separating set is not added (as in Tetrad).

In the latter case, if the set of separating sets is empty, then the triple is marked as ‘ambiguous’ if `version.unf[1]==2`, for example in `pc`, or as ‘unambiguous’ if `version.unf[1]==1`, for example in `fci`. Otherwise, there is at least one separating set. If `maj.rule=FALSE`, the conservative PC algorithm is used (Ramsey et al., 2006): If B is in some but not all separating sets, the triple is marked as ambiguous. Otherwise it is treated as in the standard PC algorithm. If `maj.rule=TRUE`, the majority rule is applied (Colombo and Maathuis, 2013): The triple is marked as ‘ambiguous’ if B is in exactly 50 percent of the separating sets. If it is in less than 50 percent it is marked as a v-structure, and if it is in more than 50 percent it is marked as a non v-structure.

Note: This function modifies the separating sets for unambiguous triples in the skeleton object (adding or removing B) to ensure that the usual orientations rules later on lead to the correct v-structures/non v-structures.

**Value**

- **unfTripl** numeric vector of triples coded as numbers (via `triple2numb()`) that were marked as ambiguous.
- **vers** Vector containing the version (1 or 2) of the corresponding triple saved in `unfTripl` (1=normal ambiguous triple, i.e., B is in some sepsets but not all or none; 2=triple coming from `version.unf[1]==2`, i.e., a and c are indep given the initial sepset but there does not exist a subset of the neighbours of a or of c that d-separates them.)
- **sk** The updated skeleton-object (separating sets might have been updated).

**Author(s)**

Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Diego Colombo.
References


See Also

skeleton, pc, fci

---

**pcAlgo**

*PC-Algorithm [OLD]: Estimate Skeleton or Equivalence Class of a DAG*

**Description**

This function is DEPRECATED! Use skeleton, pc or fci instead.

Use the PC-algorithm to estimate the underlying graph ("skeleton") or the equivalence class (CPDAG) of a DAG.

**Usage**

```r
pcAlgo(dm = NA, C = NA, n = NA, alpha, corMethod = "standard",
       verbose = FALSE, directed = FALSE, G = NULL, datatype = "continuous",
       NAdetete = TRUE, m.max = Inf, u2pd = "rand", psepset = FALSE)
```

**Arguments**

- `dm` Data matrix; rows correspond to samples, cols correspond to nodes.
- `C` Correlation matrix; this is an alternative for specifying the data matrix.
- `n` Sample size; this is only needed if the data matrix is not provided.
- `alpha` Significance level for the individual partial correlation tests.
- `corMethod` A character string specifying the method for (partial) correlation estimation. "standard", "QnStable", "Qn" or "ogkQn" for standard and robust (based on the Qn scale estimator without and with OGK) correlation estimation. For robust estimation, we recommend "QnStable".
- `verbose` 0-no output, 1-small output, 2-details; using 1 and 2 makes the function very much slower
- `directed` If FALSE, the underlying skeleton is computed; if TRUE, the underlying CPDAG is computed
- `G` The adjacency matrix of the graph from which the algorithm should start (logical)
pcAlgo-class

datatype
Delete edge if pval=NA (for discrete data)
m.max
Maximal size of conditioning set
u2pd
Function used for converting skeleton to cpdag. "rand" (use udag2pdag); "relaxed" (use udag2pdagRelaxed); "retry" (use udag2pdagSpecial)
psepset
If true, also possible separation sets are tested.

Value

An object of class "pcAlgo" (see pcAlgo) containing an undirected graph (object of class "graph", see graph-class from the package graph) (without weighths) as estimate of the skeleton or the CPDAG of the underlying DAG.

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Martin Maechler.

References


Description

This class of objects is returned by the functions skeleton and pc to represent the (skeleton) of an estimated CPDAG. Objects of this class have methods for the functions plot, show and summary.

Creation of objects

Objects are typically created as result from skeleton() or pc(), but could be be created by calls of the form new("pcAlgo", ...).

Slots

The slots call, n, max.ord, n.edgetests, sepset, and pMax are inherited from class "gAlgo", see there.
In addition, "pcAlgo" has slots

graph: Object of class "graph": the undirected or partially directed graph that was estimated.
zMin: Deprecated.
**pcorOrder**

**Description**

This function computes partial correlations given a correlation matrix using a recursive algorithm.

**Extends**

Class "gAlgo".

**Methods**

- **plot** signature(x = "pcAlgo"): Plot the resulting graph. If argument "zvalue.lwd" is true, the linewidth an edge reflects zMin, so that thicker lines indicate more reliable dependencies. The argument "lwd.max" controls the maximum linewidth.
- **show** signature(object = "pcAlgo"): Show basic properties of the fitted object
- **summary** signature(object = "pcAlgo"): Show details of the fitted object

**Author(s)**

Markus Kalisch and Martin Maechler

**See Also**

`pc`, `skeleton`, `fciaalgo`

**Examples**

```r
showClass("pcAlgo")

## generate a pcAlgo object
p <- 8
set.seed(45)
myDAG <- randomDAG(p, prob = 0.3)
n <- 10000
d.mat <- rmvDAG(n, myDAG, errDist = "normal")
suffStat <- list(C = cor(d.mat), n = n)
pc.fit <- pc(suffStat, indepTest = gaussCIttest, alpha = 0.01, p = p)

## use methods of class pcAlgo
show(pc.fit)
if(require(Rgraphviz))
  plot(pc.fit)
summary(pc.fit)

## access slots of this object
(g <- pc.fit@graph)
str(ss <- pc.fit@sepset, max=1)
```
Usage

pcorOrder(i, j, k, C, cut.at = 0.9999999)

Arguments

i, j  Integer variable numbers to compute partial correlations of.
k  Conditioning set for partial correlations (vector of integers).
C  Correlation matrix (matrix)
cut.at  Number slightly smaller than one; if \( c \) is cut.at, values outside of \([-c, c]\) are set to \(-c\) or \(c\) respectively.

Details

The partial correlations are computed using a recursive formula if the size of the conditioning set is one. For larger conditioning sets, the pseudoinverse of parts of the correlation matrix is computed (by \texttt{pseudoinverse()} from package \texttt{corpcor}). The pseudoinverse instead of the inverse is used in order to avoid numerical problems.

Value

The partial correlation of \(i\) and \(j\) given the set \(k\).

Author(s)

Markus Kalisch <kalisch@stat.math.ethz.ch> and Martin Maechler

See Also

c\texttt{condIndFisherZ} for testing zero partial correlation.

Examples

```r
## produce uncorrelated normal random variables
mat <- matrix(rnorm(3*20),20,3)
## compute partial correlation of var1 and var2 given var3
pcorOrder(1, 2, 3, cor(mat))

## define graphical model, simulate data and compute
## partial correlation with bigger conditional set
genDAG <- randomDAG(20, prob = 0.2)
dat <- rmvDAG(1000, genDAG)
C <- cor(dat)
pcorOrder(2, 5, k = c(3,7,8,14,19), C)
```
pcSelect  

**PC-Select: Estimate subgraph around a response variable**

**Description**

The goal is feature selection: If you have a response variable $y$ and a data matrix $dm$, we want to know which variables are "strongly influential" on $y$. The type of influence is the same as in the PC-Algorithm, i.e., $y$ and $x$ (a column of $dm$) are associated if they are correlated even when conditioning on any subset of the remaining columns in $dm$. Therefore, only very strong relations will be found and the result is typically a subset of other feature selection techniques. Note that there are also robust correlation methods available which render this method robust.

**Usage**

```r
pcSelect(y, dm, alpha, corMethod = "standard", 
    verbose = FALSE, directed = FALSE)
```

**Arguments**

- **y**: Response vector.
- **dm**: Data matrix (rows: samples/observations, columns: variables); `nrow(dm) == length(y)`.
- **alpha**: Significance level of individual partial correlation tests.
- **corMethod**: "standard" or "Qn" for standard or robust correlation estimation
- **verbose**: Logical or in `{0, 1, 2}`; 
  - `FALSE, 0`: No output,
  - `TRUE, 1`: Little output,
  - `2`: Detailed output.

Note that such output makes the function very much slower.
- **directed**: Logical; should the output graph be directed?

**Details**

This function basically applies `pc` on the data matrix obtained by joining $y$ and $dm$. Since the output is not concerned with the edges found within the columns of $dm$, the algorithm is adapted accordingly. Therefore, the runtime and the ability to deal with large datasets is typically increased substantially.

**Value**

- **G**: A logical vector indicating which column of $dm$ is associated with $y$.
- **zMin**: The minimal $z$-values when testing partial correlations between $y$ and each column of $dm$. The larger the number, the more consistent is the edge with the data.
Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Martin Maechler.

References


See Also

*pc* which is the more general version of this function; *pcSelect.preSel* which applies *pcSelect()* twice.

Examples

```r
p <- 10
## generate and draw random DAG :
set.seed(101)
myDAG <- randomDAG(p, prob = 0.2)
if (require(Rgraphviz)) {
  plot(myDAG, main = "randomDAG(10, prob = 0.2")
}
## generate 1000 samples of DAG using standard normal error distribution
n <- 1000
d.mat <- rmvDAG(n, myDAG, errDist = "normal")

## let's pretend that the 10th column is the response and the first 9
## columns are explanatory variable. Which of the first 9 variables
## "cause" the tenth variable?
y <- d.mat[,10]
dm <- d.mat[,1:9]
(pcS <- pcSelect(dm[,10], dm[,1:9], alpha=0.05))
## You see, that variable 4,5,6 are considered as important
## By inspecting zMin,
with(pcS, zMin[GI])
## you can also see that the influence of variable 6
## is very evident from the data (zMin is 21.32, so quite large - as
## a rule of thumb for judging what is large, you could use quantiles
## of the Standard Normal Distribution)

## The result should be the same when using pcAlgo
resU <- pcAlgo(d.mat, alpha = 0.05, corMethod = "standard", directed=TRUE)
resU
if (require(Rgraphviz))
  plot(resU,zvalue.lwd=TRUE)
## as can be seen, the pcAlgo function also finds 4,5,6 as the important
## variables
## Again, variable 6 seems to be very evident from the data
```
pcSelect.presel  Estimate Subgraph around a Response Variable using Preselection

Description
This function uses `pcSelect` to preselect some covariates and then runs `pcSelect` again on the reduced data set.

Usage
```r
pcSelect.presel(y, dm, alpha, alphapre, corMethod = "standard", verbose = 0, directed=FALSE)
```

Arguments
- **y**: Response vector.
- **dm**: Data matrix (rows: samples, cols: nodes; i.e., `length(y) == nrow(dm)`).
- **alpha**: Significance level of individual partial correlation tests.
- **alphapre**: Significance level for `pcSelect` in preselection.
- **corMethod**: "standard" or "Qn" for standard or robust correlation estimation.
- **verbose**: 0-no output, 1-small output, 2-details (using 1 and 2 makes the function very much slower).
- **directed**: Logical; should the output graph be directed?

Details
First, `pcSelect` is run using `alphapre`. Then, only the important variables are kept and `pcSelect` is run on them again.

Value
- **pcs**: Logical vector indicating which column of `dm` is associated with `y`.
- **zMin**: The minimal z-values when testing partial correlations between `y` and each column of `dm`. The larger the number, the more consistent is the edge with the data.
- **Xnew**: Preselected Variables.

Author(s)
Philipp Ruetimann

See Also
- `pcSelect`
Examples

```r
p <- 10
## generate and draw random DAG:
set.seed(101)
myDAG <- randomDAG(p, prob = 0.2)
if(require(Rgraphviz))
  plot(myDAG, main = "randomDAG(10, prob = 0.2)"

## generate 1000 samples of DAG using standard normal error distribution
n <- 1000
d.mat <- rmvDAG(n, myDAG, errDist = "normal")

## let's pretend that the 10th column is the response and the first 9 
## columns are explanatory variable. Which of the first 9 variables  
## "cause" the tenth variable?
y <- d.mat[,10]
dm <- d.mat[,-10]
res <- pcSelect.presel(d.mat[,10], d.mat[,-10], alpha=0.05, alphapre=0.6)
```

---

**pdag2dag**

Extend a Partially Directed Acyclic Graph (PDAG) to a DAG

**Description**

This function extends a PDAG (Partially Directed Acyclic Graph) to a DAG, if this is possible.

**Usage**

```r
pdag2dag(g, keepVstruct=TRUE)
```

**Arguments**

- `g` Input PDAG (graph object)
- `keepVstruct` Logical indicating if the v-structures in `g` are kept. Otherwise they are ignored and an arbitrary extension is generated.

**Details**

Direct undirected edges without creating directed cycles or additional v-structures. The PDAG is consistently extended to a DAG using the algorithm by Dor and Tarsi (1992). If no extension is possible, a DAG corresponding to the skeleton of the PDAG is generated and a warning message is produced.

**Value**

List with entries

- `graph` Contains a consistent DAG extension (graph object).
- `success` Is TRUE iff the extension was possible.
**pdsep**

*Estimate Final Skeleton in the FCI algorithm*

**Description**

Estimate the final skeleton in the FCI algorithm (Spirtes et al, 2000), as described in Steps 2 and 3 of Algorithm 3.1 in Colombo et al. (2012). The input of this function consists of an initial skeleton that was estimated by the PC algorithm (Step 1 of Algorithm 3.1 in Colombo et al. (2012)).

Given the initial skeleton, all unshielded triples are considered and oriented as colliders when appropriate. Then, for all nodes x in the resulting partially directed graph G, Possible-D-SEP(x,G) is computed, using the function qreach. Finally, for any edge y-z that is present in G, conditional independence between Y and Z is tested given all subsets of Possible-D-SEP(y,G) and all subsets of Possible-D-SEP(z,G). These tests are done at level alpha, using indeptest. If the pair of nodes is judged to be independent given some set S, then S is recorded in sepset(y,z) and sepset(z,y) and the edge y-z is deleted. Otherwise, the edge remains and there is no change to sepset.

**Usage**

```r
pdsep(skel, suffStat, indepTest, p, sepset, alpha, pMax, m.max = Inf, 
      pdsep.max = Inf, NAdelete = TRUE, unfVect = NULL, 
      bicCC = FALSE, verbose = FALSE)
```

**Author(s)**

Markus Kalisch <kalisch@stat.math.ethz.ch>

**References**


**Examples**

```r
p <- 10 # number of random variables
n <- 10000 # number of samples
s <- 0.4 # sparseness of the graph

## generate random data
set.seed(42)
g <- randomDAG(p, prob = s) # generate a random DAG
d <- rmvDAG(n,g) # generate random samples

gSkel <- pcAlgo(d, alpha=0.05) # estimate of the skeleton
(gPDAG <- udag2pdag(gSkel))
(gDAG <- pdag2dag(gPDAG@graph))
```
Arguments

**skel**
Graph object returned by `skeleton`.

**suffStat**
Sufficient statistic: A list containing all necessary elements for making conditional independence decisions using function `indepTest`.

**indepTest**
Predefined function for testing conditional independence. The function is internally called as `indepTest(x, y, S, suffStat)` for testing conditional independence of $x$ and $y$ given $S$. Here, $x$ and $y$ are node numbers of the adjacency matrix, $S$ is a (possibly empty) vector of node numbers of the adjacency matrix and `suffStat` is a list containing all relevant elements for making conditional independence decisions. The return value of `indepTest` is the p-value of the test for conditional independence.

**p**
Number of variables.

**sepset**
List of length $p$; each element of the list contains another list of length $p$. The element `sepset[[x]][[y]]` contains the separation set that made the edge between $x$ and $y$ drop out. This object is thought to be obtained from a `pcAlgo`-object or `fciAlgo`-object.

**alpha**
Significance level for the individual conditional independence tests.

**pMax**
Matrix with the maximal p-values of conditional independence tests in a previous call of `skeleton`, `pc` or `fci` which produced $G$. This object is thought to be obtained from a `pcAlgo`-object or `fciAlgo`-object.

**m.max**
Maximum size of the conditioning sets that are considered in the conditional independence tests.

**pdsep.max**
Maximum size of Possible-D-SEP for which subsets are considered as conditioning sets in the conditional independence tests. If the nodes $x$ and $y$ are adjacent in the graph and the size of Possible-D-SEP($x,G \backslash x,y$) is bigger than `pdsep.max`, the edge is simply left in the graph. Note that if `pdsep.max` is less than Inf, the final PAG is typically a supergraph of the one computed with `pdsep.max = Inf`, because fewer tests may have been performed in the former.

**NAdelete**
If `indepTest` returns `NA` and this option is `TRUE`, the corresponding edge is deleted. If this option is `FALSE`, the edge is not deleted.

**unfVect**
Vector containing numbers that encode the unfaithful triple (as returned by `pc.cons.intern`). This is needed in the conservative FCI.

**biCC**
Logical; if `TRUE`, only nodes on paths between nodes $a$ and $c$ are considered to be in `sepset(a,c)`. This uses biconnected components, see `biConnComp` from `RBGL`.

**verbose**
Logical indicating that detailed output is to be provided.

Details

To make the code more efficient, we only perform tests that were not performed in the estimation of the initial skeleton.

Note that the Possible-D-SEP sets are computed once in the beginning. They are not updated after edge deletions, in order to make sure that the output of the algorithm does not depend on the ordering of the variables (see also Colombo and Maathuis (2013)).
Value
A list with the following elements:

- **G**: Updated adjacency matrix representing the final skeleton
- **sepset**: Updated sepsets
- **pMax**: Updated matrix containing maximal p-values
- **allPdsep**: Possible-D-Sep for each node
- **max.ord**: Maximal order of conditioning sets during independence tests
- **n.edgetests**: Number of conditional edgetests performed, grouped by the size of the conditioning set.

Author(s)
Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Diego Colombo.

References

See Also
- `qreach` to find Possible-D-SEP(x,G); `fci`.

Examples
```r
p <- 10
## generate and draw random DAG:
set.seed(44)
myDAG <- randomDAG(p, prob = 0.2)

## generate 10000 samples of DAG using gaussian distribution
library(RBGL)
n <- 10000
d.mat <- rmvDAG(n, myDAG, errDist = "normal")

## estimate skeleton
indepTest <- gaussCItest
suffStat <- list(C = cor(d.mat), n = n)
alpha <- 0.01
skel <- skeleton(suffStat, indepTest, alpha = alpha, p = p)

## prepare input for pdsep
sepset <- skel@sepset
```
plotAG

pMax <- skel@pMax

## call pdsep to find Possible-D-Sep and enhance the skeleton
pdsepRes <- pdsep(skel@graph, suffStat, indepTest, p, sepset, alpha,
pMax, verbose = TRUE)

## call pdsep with biconnected components to find Possible-D-Sep and enhance the skeleton
pdsepResBicc <- pdsep(skel@graph, suffStat, indepTest, p, sepset, alpha,
pMax, biCC= TRUE, verbose = TRUE)

plotAG

Plot partial ancestral graphs (PAG)

Description

This function is DEPRECATED! Use the plot method of the fciAlgo class instead.

Usage

plotAG(amat)

Arguments

amat  Adjacency matrix (coding 0,1,2,3 for no edge, circle, arrowhead, tail; e.g., amat[a,b] = 2 and amat[b,a] = 3 implies a -> b)

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>)

See Also

ci

plotSG

Plot the subgraph around a Specific Node in a Graph Object

Description

Plots a subgraph for a specified starting node and a given graph. The subgraph consists of those
nodes that can be reached from the starting node by passing no more than a specified number of
edges.

Usage

plotSG(graphObj, y, dist, amat = NA, directed = TRUE, main = )
Arguments

- **graphObj**: An R object of class `graph`.
- **y**: Starting node.
- **dist**: Distance of nodes included in subgraph from starting node `y`.
- **amat**: Adjacency matrix of skeleton graph (optional).
- **directed**: Logical indicating if the subgraph should be directed.
- **main**: Title to be used, with a sensible default; see `title`.

Details

Commencing at the starting point `y` the function looks for the neighbouring nodes. Beginning with direct parents and children it will continue hierarchically through the distances to `y`. If `directed` is true (as per default), the orientation of the edges is taken from the initial graph.

The package `Rgraphviz` must be installed, and is used for the plotting.

Value

the desired subgraph is plotted and returned via `invisible`.

Author(s)

Daniel Stekhoven (<hoven@stat.math.ethz.ch>)

Examples

```r
if (require(Rgraphviz)) {
  ## generate a random DAG:
  p <- 10
  set.seed(45)
  myDAG <- randomDAG(p, prob = 0.3)

  ## plot whole the DAG
  plot(myDAG, main = "randomDAG(10, prob = 0.3)"

  op <- par(mfrow = c(3,2))
  ## plot the neighbours of node number 8 up to distance 1
  plotSG(myDAG, 8, 1, directed = TRUE)
  plotSG(myDAG, 8, 1, directed = FALSE)

  ## plot the neighbours of node number 8 up to distance 2
  plotSG(myDAG, 8, 2, directed = TRUE)
  plotSG(myDAG, 8, 2, directed = FALSE)

  ## plot the neighbours of node number 8 up to distance 3
  plotSG(myDAG, 8, 3, directed = TRUE)
  plotSG(myDAG, 8, 3, directed = FALSE)

  ## Note that the layout of the subgraph might be different than in the
  ## original graph, but the graph structure is identical
```
possibleDe

```r
par(op) }
```

---

possibleDe  

*Find possible descendants on definite status paths.*

**Description**

In a DAG, CPDAG, MAG or PAG determine which nodes are possible descendants of x on definite status paths.

**Usage**

```r
possibleDe(amat, x)
```

**Arguments**

- `amat`: Adjacency matrix of the DAG, CPDAG, MAG or PAG.
- `x`: Node of interest.

**Details**

A non-endpoint vertex $X$ on a path $p$ in a partial mixed graph is said to be of a definite status if it is either a collider or a definite non-collider on $p$. The path $p$ is said to be of a definite status if all non-endpoint vertices on the path are of a definite status (see e.g. Maathuis and Colombo (2013), Def. 3.4).

A possible descendent of $x$ can be reached moving to adjacent nodes of $x$ but never going against an arrowhead.

**Value**

Vector with possible descendents.

**Author(s)**

Diego Colombo

**References**


**See Also**

`backdoor`
Examples

amat <- matrix( c(0,3,0,0,0,0, 2,0,2,0,0,0, 0,3,0,0,0,0,0,0,0,1,0, 0,0,0,1,0,1, 0,0,0,0,1,0), 6,6)
colnames(amat) <- rownames(amat) <- letters[1:6]
if(require(Rgraphviz)) {
  plotAG(amat)
}
possibleDe(amat, 1)  ## a, b are poss. desc. of a
possibleDe(amat, 4)  ## d, e, f are poss. desc. of d

qreach(x, amat, verbose = FALSE)

Description

Let G be a graph with the following edge types: o-o, o-> or <->, and let x be a vertex in the graph. Then this function computes Possible-D-SEP(x,G), which is defined as follows:

v is in Possible-D-SEP(x,G) iff there is a path p between x and v in G such that for every subpath <s,t,u> of p, t is a collider on this subpath or <s,t,u> is a triangle in G.


Usage

qreach(x, amat, verbose = FALSE)

Arguments

x Integer: column position of node in adjacency matrix, of which Possible-D-SEP set is to be computed.
amat Adjacency matrix (coding 0,1,2,3 for no edge, circle, arrowhead, tail; e.g., amat[a,b] = 2 and amat[b,a] = 3 implies a -> b)
verbose Logical, asking for details on output

Value

Vector of column positions indicating the nodes in Possible-D-SEP of x.

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>)

References


Generate a Gaussian Causal Model Randomly

Description
Generate a random Gaussian causal model. Parameters specifying the connectivity as well as coefficients and error terms of the corresponding linear structural equation model can be specified. The observational expectation value of the generated model is always 0, meaning that no interception terms are drawn.

Usage
r.gauss.pardag(p, prob, top.sort = FALSE, normalize = FALSE, lbe = 0.1, ube = 1, neg.coef = TRUE, lbv = 0.5, ubv = 1)

Arguments
- p: Number of nodes
- prob: Probability of connecting a node to another node.
- top.sort: Logical indicating whether the output graph should be topologically sorted, meaning that arrows always point from lower to higher node indices.
- normalize: Logical indicating whether weights and error variances should be normalized such that the diagonal of the corresponding observational covariance matrix is 1.
- lbe, ube: Lower and upper bounds of the absolute values of edge weights.
- neg.coef: Logical indicating whether negative edge weights are also admissible.
- lbv, ubv: Lower and upper bound on error variances of the noise terms in the structural equations.

Details
The underlying directed acyclic graph (DAG) is generated by drawing an undirected graph from an Erdős-Rényi model orienting the edges according to a random topological ordering drawn uniformly from the set of permutations of p variables. This means that any two nodes are connected with the same probability prob, and that the connectivity of different pairs of nodes is independent.

A Gaussian causal model can be represented as a set of linear structural equations. The regression coefficients of the model can be represented as "edge weights" of the DAG. Edge weights are drawn uniformly and independently from the interval between lbe and ube; if neg.coef = TRUE, their sign is flipped with probability 0.5. Error variances are drawn uniformly and independently from the interval between lbv and ubv.

If normalize = TRUE, the edge weights and error variances are normalized in the end to ensure that the diagonal elements of the observational covariance matrix are all 1; the procedure used is described in Hauser and Bühlmann (2012). Note that in this case the error variances and edge weights are no longer guaranteed to lie in the specified intervals after normalization.
Value

An object of class "GaussParDAG".

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

References


See Also

GaussParDAG, randomDAG

Examples

```r
set.seed(307)

## Plot some random DAGs
if (require(Rgraphviz)) {
  ## Topologically sorted random DAG
  myDAG <- r.gauss.pardag(p = 10, prob = 0.2, top.sort = TRUE)
  plot(myDAG)

  ## Unsorted DAG
  myDAG <- r.gauss.pardag(p = 10, prob = 0.2, top.sort = FALSE)
  plot(myDAG)
}

## Without normalization, edge weights and error variances lie within the
## specified borders
set.seed(307)
myDAG <- r.gauss.pardag(p = 10, prob = 0.4,
  lbe = 0.1, ube = 1, lbv = 0.5, ubv = 1.5, neg.coef = FALSE)
B <- myDAG$weight.mat()
V <- myDAG$err.var()
any((B > 0 & B < 0.1) | B > 1)
any(V < 0.5 | V > 1.5)

## After normalization, edge weights and error variances are not necessarily
## within the specified range, but the diagonal of the observational covariance
## matrix consists of ones only
set.seed(308)
myDAG <- r.gauss.pardag(p = 10, prob = 0.4, normalize = TRUE,
  lbe = 0.1, ube = 1, lbv = 0.5, ubv = 1.5, neg.coef = FALSE)
B <- myDAG$weight.mat()
```
Generate a Directed Acyclic Graph (DAG) randomly

Description
Generate a random Directed Acyclic Graph (DAG). The resulting graph is topologically ordered from low to high node numbers.

Usage
randomDAG(n, prob = 0.1, lb = 1, ub = 1, V = as.character(1:n))

Arguments
- **n**: Number of nodes, \( n \geq 2 \).
- **prob**: Probability of connecting a node to another node with higher topological ordering.
- **lb, ub**: Lower and upper limit of edge weights, chosen uniformly at random, i.e., by \( \text{runif}(., \min=lb, \max=ub) \).
- **V**: character vector length \( n \) of node names.

Details
The \( n \) nodes are ordered. Start with first node. Let the number of nodes with higher order be \( k \). Then, the number of neighbouring nodes is drawn as Bin(\( k \), \( prob \)). The neighbours are then drawn without replacement from the nodes with higher order. For each node, a weight is uniformly sampled from \( lb \) to \( ub \). This procedure is repeated for the next node in the original ordering and so on.

Value
An object of class "graphNEL", see \texttt{graph-class} from package \texttt{graph}, with \( n \) named ("1" to "n") nodes and directed edges. The graph is topologically ordered. Each edge has a weight between \( lb \) and \( ub \).

Author(s)
Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Martin Maechler

See Also
\texttt{rmvdag} for generating Data according to a DAG; \texttt{compareGraphs} for comparing the skeleton of a DAG with some other undirected graph (in terms of TPR, FPR and TDR).
Examples

```r
if (require(Rgraphviz)) {
  set.seed(101)
  myDAG <- randomDAG(n = 20, prob = 0.2, lB = 0.1, uB = 1)
  plot(myDAG)
}
```

---

**rfci**  
*Estimate an RFCI-PAG using the RFCI Algorithm*

**Description**

Estimate an RFCI-PAG from observational data, using the RFCI-algorithm.

**Usage**

```r
rfci(suffStat, indepTest, alpha, labels, p,
     skel.method = c("stable", "original", "stable.fast"),
     fixedGaps = NULL, fixedEdges = NULL, NAdelete = TRUE,
     m.max = Inf, rules = rep(TRUE, 10),
     conservative = FALSE, maj.rule = FALSE, verbose = FALSE)
```

**Arguments**

- `suffStat`: Sufficient statistics: List containing all necessary elements for the conditional independence decisions in the function `indepTest`.
- `indepTest`: Predefined function for testing conditional independence. The function is internally called as `indepTest(x,y,S,suffStat)`, and tests conditional independence of `x` and `y` given `S`. Here, `x` and `y` are variables, and `S` is a (possibly empty) vector of variables (all variables are denoted by their column numbers in the adjacency matrix). `suffStat` is a list containing all relevant elements for the conditional independence decisions. The return value of `indepTest` is the p-value of the test for conditional independence.
- `alpha`: significance level (number in (0, 1) for the individual conditional independence tests.
- `labels`: (optional) character vector of variable (or “node”) names. Typically preferred to specifying `p`.
- `p`: (optional) number of variables (or nodes). May be specified if `labels` are not, in which case `labels` is set to `1:p`.
- `skel.method`: Character string specifying method; the default, "stable" provides an order-independent skeleton, see `skeleton`.
- `fixedGaps`: A logical matrix of dimension `p*p`. If entry `[i,j]` or `[j,i]` (or both) are TRUE, the edge `i-j` is removed before starting the algorithm. Therefore, this edge is guaranteed to be absent in the resulting graph.
fixedEdges A logical matrix of dimension p*p. If entry [i, j] or [j, i] (or both) are TRUE, the edge i-j is never considered for removal. Therefore, this edge is guaranteed to be present in the resulting graph.

NAdelete If indepTest returns NA and this option is TRUE, the corresponding edge is deleted. If this option is FALSE, the edge is not deleted.

m.max Maximum size of the conditioning sets that are considered in the conditional independence tests.

rules Logical vector of length 10 indicating which rules should be used when directing edges. The order of the rules is taken from Zhang (2009).

conservative Logical indicating if the unshielded triples should be checked for ambiguity after the skeleton has been found, similar to the conservative PC algorithm.

maj.rule Logical indicating if the unshielded triples should be checked for ambiguity after the skeleton has been found using a majority rule idea, which is less strict than the conservative.

verbose If true, more detailed output is provided.

Details

This function is rather similar to fci. However, it does not compute any Possible-D-SEP sets and thus does not make tests conditioning on subsets of Possible-D-SEP. This makes RFCI much faster than FCI. The orientation rules for v-structures and rule 4 were modified in order to produce an RFCI-PAG which, in the oracle version, is guaranteed to have the correct ancestral relationships.

The first part of the RFCI algorithm is analogous to the PC and FCI algorithm. It starts with a complete undirected graph and estimates an initial skeleton using the function skeleton, which produces an initial order-independent skeleton, see skeleton for more details. All edges of this skeleton are of the form o-o. Due to the presence of hidden variables, it is no longer sufficient to consider only subsets of the neighborhoods of nodes x and y to decide whether the edge x oMo y should be removed. The FCI algorithm performs independence tests conditioning on subsets of Possible-D-SEP to remove those edges. Since this procedure is computationally infeasible, the RFCI algorithm uses a different approach to remove some of those superfluous edges before orienting the v-structures and the discriminating paths in orientation rule 4.

Before orienting the v-structures, we perform the following additional conditional independence tests. For each unshielded triple a-b-c in the initial skeleton, we check if both a and b and b and c are conditionally dependent given the separating of a and c (sepset(a,c)). These conditional dependencies may not have been checked while estimating the initial skeleton, since sepset(a,c) does not need to be a subset of the neighbors of a nor of the neighbors of c. If both conditional dependencies hold and b is not in the sepset(a,c), the triple is oriented as a v-structure a->b<-c. On the other hand, if an additional conditional independence relationship may be detected, say a is independent from b given the sepset(a,c), the edge between a and c is removed from the graph and the set responsible for that is saved in sepset(a,b). The removal of an edge can destroy or create new unshielded triples in the graph. To solve this problem we work with lists (for details see Colombo et al., 2012).

Before orienting discriminating paths, we perform the following additional conditional independence tests. For each triple a <-* b o- *c with a -> c, the algorithm searches for a discriminating path p = <d, . . . , a,b,c> for b of minimal length, and checks that the vertices in every consecutive pair (f1,f2) on p are conditionally dependent given all subsets of sepset(d,c) \ f1,f2 . If we do not find any conditional independence relationship, the path is oriented as in rule (R4). If one or
more conditional independence relationships are found, the corresponding edges are removed, their minimal separating sets are stored.

Conservative RFCI can be computed if the argument of conservative is `TRUE`. After the final skeleton is computed and the additional local tests on all unshielded triples, as described above, have been done, all potential v-structures a-b-c are checked in the following way. We test whether a and c are independent conditioning on any subset of the neighbors of a or any subset of the neighbors of c. When a subset makes a and c conditionally independent, we call it a separating set. If b is in no such separating set or in all such separating sets, no further action is taken and the normal version of the RFCI algorithm is continued. If, however, b is in only some separating sets, the triple a-b-c is marked ‘ambiguous’. If a is independent of c given some S in the skeleton (i.e., the edge a-c dropped out), but a and c remain dependent given all subsets of neighbors of either a or c, we will call all triples a-b-c ‘unambiguous’. This is because in the RFCI algorithm, the true separating set might be outside the neighborhood of either a or c. An ambiguous triple is not oriented as a v-structure. Furthermore, no further orientation rule that needs to know whether a-b-c is a v-structure or not is applied. Instead of using the conservative version, which is quite strict towards the v-structures, Colombo and Maathuis (2013) introduced a less strict version for the v-structures called majority rule. This adaptation can be called using `maj.rule = TRUE`. In this case, the triple a-b-c is marked as ‘ambiguous’ if and only if b is in exactly 50 percent of such separating sets or no separating set was found. If b is in less than 50 percent of the separating sets it is set as a v-structure, and if in more than 50 percent it is set as a non v-structure (for more details see Colombo and Maathuis, 2013).

The implementation uses the stabilized skeleton `skeleton`, which produces an initial order-independent skeleton. The final skeleton and edge orientations can still be order-dependent, see Colombo and Maathuis (2013).

Value

An object of class `fcialgo` (see `fcialgo`) containing the estimated graph (in the form of an adjacency matrix with various possible edge marks), the conditioning sets that lead to edge removals (sepset) and several other parameters.

Author(s)

Diego Colombo and Markus Kalisch (<kalisch@stat.math.ethz.ch>).

References


See Also

`fci` for estimating a PAG using the FCI algorithm; `skeleton` for estimating an initial skeleton using the RFCI algorithm; `pc` for estimating a CPDAG using the PC algorithm; `gaussCitest`, `discCitest`, `binCitest` and `dsepTest` as examples for `indepTest`. 
Examples

```r
# Example without latent variables
set.seed(42)
p <- 7
# generate and draw random DAG:
myDAG <- randomDAG(p, prob = 0.4)

# find skeleton and PAG using the RFCl algorithm
suffStat <- list(C = cov2cor(trueCov(myDAG)), n = 10^9)
indeptest <- gaussCItest
res <- rfci(suffStat, indeptest, alpha = 0.9999, p=p, verbose=TRUE)
```

```r
# Example with hidden variables
# Zhang (2008), Fig. 6, p.1882

# create the DAG:
V <- LETTERS[1:5]
edl <- setNames(vector("list", length = 5), V)
edL[[1]] <- list(edges=c(2,4), weights=c(1,1))
edL[[2]] <- list(edges=c(3,1), weights=c(1))
edL[[3]] <- list(edges=c(5,1), weights=c(1))
edL[[4]] <- list(edges=c(5,1), weights=c(1))
# and leave edL[[5]] empty
g <- new("graphNEL", nodes=V, edgeL=edL, edgemode="directed")
if (require(Rgraphviz))
  plot(g)

# define the latent variable
L <- 1

# compute the true covariance matrix of g
cov.mat <- trueCov(g)
# delete rows and columns belonging to latent variable L
true.cov <- cov.mat[-L,-L]
# transform covariance matrix into a correlation matrix
true.corr <- cov2cor(true.cov)

# find PAG with RFCl algorithm
# as dependence "oracle", we use the true correlation matrix in
gaussCItest() with a large "virtual sample size" and a large alpha:
rfci.pag <- rfci(suffStat = list(C = true.corr, n = 10^9),
  indepTest = gaussCItest, alpha = 0.9999, labels = V[-L],
  verbose=TRUE)

# define PAG given in Zhang (2008), Fig. 6, p.1882
corr.pag <- rbind(c(0,1,1,0),
  c(1,0,0,2),
  c(0,0,0,0),
  c(0,1,1,0),
  c(0,0,0,0),
  c(0,0,0,0))
```

```r
```
Generate Multivariate Data according to a DAG

Description

Generate multivariate data with dependency structure specified by a (given) DAG (Directed Acyclic Graph) with nodes corresponding to random variables. The DAG has to be topologically ordered.

Usage

```r
rmvdag(n, dag, 
  errDist = c("normal", "cauchy", "t4", "mix", "mix3", "mixN100"), 
  mix = 0.1, errMat = NULL, back.compatible = FALSE, 
  use.node.names = !back.compatible)
```

Arguments

- `n` number of samples that should be drawn. (integer)
- `dag` a graph object describing the DAG; must contain weights for all the edges. The nodes must be topologically sorted. (For topological sorting use `tsort` from the RBGL package.)
- `errDist` string specifying the distribution of each node. Currently, the options "normal", "t4", "cauchy", "mix", "mix3" and "mixN100" are supported. The first three generate standard normal-, t(df=4)- and cauchy-random numbers. The options containing the word "mix" create standard normal random variables with a mix of outliers. The outliers for the options "mix", "mix3", "mixN100" are drawn from a standard cauchy, t(df=3) and N(0,100) distribution, respectively. The fraction of outliers is determined by the `mix` argument.
- `mix` for the "mix*" error distribution, `mix` specifies the fraction of "outlier" samples (i.e., Cauchy, t3 or N(0,100)).
- `errMat` numeric `n * p` matrix specifying the error vectors `e_i` (see Details), instead of specifying `errDist` (and maybe `mix`).
- `back.compatible` logical indicating if the data generated should be the same as with `pcalg` version 1.0-6 and earlier (where `wgtMatrix()` differed).
- `use.node.names` logical indicating if the column names of the result matrix should equal `nodes(dag)`, very sensibly, but new, hence the default.
Details

Each node is visited in the topological order. For each node \( i \) we generate a \( p \)-dimensional value \( X_i \) in the following way: Let \( X_1, \ldots, X_k \) denote the values of all neighbours of \( i \) with lower order. Let \( w_1, \ldots, w_k \) be the weights of the corresponding edges. Furthermore, generate a random vector \( E_i \) according to the specified error distribution. Then, the value of \( X_i \) is computed as

\[
X_i = w_1 \cdot X_1 + \ldots + w_k \cdot X_k + E_i.
\]

If node \( i \) has no neighbors with lower order, \( X_i = E_i \) is set.

Value

A \( n \times p \) matrix with the generated data. The \( p \) columns correspond to the nodes (i.e., random variables) and each of the \( n \) rows correspond to a sample.

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Martin Maechler.

See Also

randomDAG for generating a random DAG; skeleton and pc for estimating the skeleton and the CPDAG of a DAG that corresponds to the data.

Examples

```r
## generate random DAG
p <- 20
rdag <- randomDAG(p, prob = 0.2, lb=0.1, uB=1)

if (require(Rgraphviz)) {
  ## plot the DAG
  plot(rdag, main = "randomDAG(20, prob = 0.2, ..")
}

## generate 1000 samples of DAG using standard normal error distribution
n <- 1000
d.normMat <- rmvdag(n, rdag, errDist="normal")

## generate 1000 samples of DAG using standard t(df=4) error distribution
d.t4Mat <- rmvdag(n, rdag, errDist="t4")

## generate 1000 samples of DAG using standard normal with a cauchy
## mixture of 30 percent

d.mixMat <- rmvdag(n, rdag, errDist="mix",mix=0.3)

require(MASS) ## for mvrnorm()
Sigma <- toeplitz(ARMAacf(0.2, lag.max = p - 1))
dim(Sigma)# p x p

## *correlated* normal error matrix "e_i" (against model assumption)
eMat <- mvrnorm(n, mu = rep(0, p), Sigma = Sigma)
d.CnormMat <- rmvdag(n, rdag, errMat = eMat)
```
rmvnorm.ivent

Simulate from a Gaussian Causal Model

Description

Produces one or more samples from the observational or an interventional distribution associated to a Gaussian causal model.

Usage

```
rmvnorm.ivent(n, object, target = integer(0), target.value = numeric(0))
```

Arguments

- `n`: Number of samples required.
- `object`: An instance of `GaussParDAG`.
- `target`: Intervention target: vector of intervened nodes. If the vector is empty, samples from the observational distribution are generated. Otherwise, samples from an interventional distribution are simulated.
- `target.value`: Values of the intervened variables. If `target.value` is a vector of the same length as `target`, the indicated intervention levels are used for all `n` samples. If `target.value` is a matrix of dimension `n` by `length(target)`, the `i`-th sample is simulated using the `i`-th row of the matrix as intervention levels.

Value

If `n = 1` a vector of length `p` is returned, where `p` denotes the number of nodes of `object`. Otherwise an `n` by `p` matrix is returned with one sample per row.

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

Examples

```
set.seed(307)
myDAG <- r.gauss.pardag(5, 0.5)
var(rmvnorm.ivent(n = 1000, myDAG))
myDAG$cov.mat()
var(rmvnorm.ivent(n = 1000, myDAG, target = 1, target.value = 1))
myDAG$cov.mat(target = 1, ivent.var = 0)
```
Score-class

Virtual Class "Score"

Description

This virtual base class represents a score for causal inference; it is used in the causal inference functions `ges`, `gies` and `simy`.

Details

Score-based structure learning algorithms for causal inference such as Greedy Equivalence Search (GES, implemented in the function `ges`), Greedy Interventional Equivalence Search (GIES, implemented in the function `gies`) and the dynamic programming approach of Silander and Myllymäki (2006) (implemented in the function `simy`) try to find the DAG model which maximizes a scoring criterion for a given data set. A widely-used scoring criterion is the Bayesian Information Criterion (BIC).

The virtual class `score` is the base class for providing a scoring criterion to the mentioned causal inference algorithms. It does not implement a concrete scoring criterion, but it defines the functions that must be provided by its descendants (cf. methods).

Knowledge of this class is only required if you aim to implement an own scoring criterion. At the moment, it is recommended to use the predefined scoring criteria for multivariate Gaussian data derived from `score`, `GaussLPenIntScore` and `GaussLPenObsScore`.

Fields

The fields of `score` are mainly of interest for users who aim at deriving an own class from this virtual base class, i.e., implementing an own score function.

- `decomp`: Indicates whether the represented score is decomposable (cf. details). At the moment, only decomposable scores are supported by the implementation of the causal inference algorithms; support for non-decomposable scores is planned.
- `pp.dat`: List representing the preprocessed input data; this is typically a statistic which is sufficient for the calculation of the score.
- `.par.dag.class`: Name of the class of the parametric DAG model corresponding to the score. This must name a class derived from `ParDAG`.
- `c.fcn`: Only used internally; must remain empty for (user specified) classes derived from `score`.

Constructor

```r
new("Score",
data = matrix(1, 1, 1),
targets = list(integer(0)),
target.index = rep(as.integer(1), nrow(data)),
...)
```

data Data matrix with n rows and p columns. Each row corresponds to one realization, either interventional or observational.
targets List of mutually exclusive intervention targets that have been used for data generation.
target.index Vector of length \( n \); the \( i \)-th entry specifies the index of the intervention target in targets under which the \( i \)-th row of data was measured.

\[ \text{... Additional parameters used by derived (and non-virtual) classes.} \]

Methods

Note that since Score is a virtual class, its methods cannot be called directly, but only on derived classes.

local.score(vertex, parents, ...) For decomposable scores, this function calculates the local score of a vertex and its parents. Must throw an error in derived classes that do not represent a decomposable score.

global.score.int(edges, ...) Calculates the global score of a DAG, represented as a list of in-edges: for each vertex in the DAG, this list contains a vector of parents.

global.score(dag, ...) Calculates the global score of a DAG, represented as object of a class derived from ParDAG.

local.mle(vertex, parents, ...) Calculates the local MLE of a vertex and its parents. The result is a vector of parameters whose meaning depends on the model class; it matches the convention used in the corresponding causal model (cf. .pardag.class).

global.mle(dag, ...) Calculates the global MLE of a DAG, represented by an object of the class specified by .pardag.class. The result is a list of vectors, one per vertex, each in the same format as the result vector of local.mle.

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

References


See Also

ges, gies, simy, GaussL0penIntScore, GaussL0penObsScore

shd Compute Structural Hamming Distance (SHD)

Description

Compute the Structural Hamming Distance (SHD) between two graphs. In simple terms, this is the number of edge insertions, deletions or flips in order to transform one graph to another graph.
Usage

\texttt{shd(g1, g2)}

Arguments

\begin{itemize}
  \item \texttt{g1} \hspace{1cm} Graph object
  \item \texttt{g2} \hspace{1cm} Graph object
\end{itemize}

Value

The value of the SHD (numeric).

Author(s)

Markus Kalisch \texttt{<kalisch@stat.math.ethz.ch>} and Martin Maechler

References


Examples

\begin{verbatim}
# generate two graphs
g1 <- randomDAG(10, prob = 0.2)
g2 <- randomDAG(10, prob = 0.2)
# compute SHD
(shd.val <- shd(g1, g2))
\end{verbatim}

---

\texttt{showAmat} \hspace{1cm} \textit{Show Adjacency Matrix of pcAlgo object}

Description

Show the adjacency matrix of a "pcAlgo" object; this is intended to be an alternative if the \texttt{Rgraphviz} package does not work.

Usage

\texttt{showAmat(object)}

Arguments

\begin{itemize}
  \item \texttt{object} \hspace{1cm} an \texttt{R} object of class \texttt{pcAlgo}, as returned from \texttt{skeleton()} or \texttt{pc()}.
\end{itemize}

Value

The adjacency matrix.
Note

For "fcialgo" objects, the show method produces a similar result.

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>)

See Also

showedgelist for showing the edge list of a pcAlgo object. iplotPC for plotting a "pcAlgo" object using the package igraph also for an example of showAmat().

Description

Show the list of edges (of the graph) of a pcAlgo object; this is intended to be an alternative if Rgraphviz does not work.

Usage

showEdgeList(object, labels = NULL)

Arguments

  object      an R object of class pcAlgo, as returned from skeleton() or pc().
  labels      optional labels for nodes; by default, the labels from the object are used.

Value

one; the purpose is in (the side effect of) printing the edge list.

Note

This is not quite ok for "fcialgo" objects, yet.

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>)

See Also

showAmat for the adjacency matrix of a pcAlgo object. iplotPC for plotting a pcAlgo object using the package igraph, also for an example of showEdgeList().
Estimate Interventional Markov Equivalence Class of a DAG

Description

Estimate the interventional essential graph representing the Markov equivalence class of a DAG using the dynamic programming (DP) approach of Silander and Myllymäki (2006). This algorithm maximizes a decomposable scoring criterion in exponential runtime.

Usage

\texttt{simy(p, targets, score, verbose = FALSE, ...)}

Arguments

- \texttt{p} \hspace{1cm} \text{Number of variables.}
- \texttt{targets} \hspace{1cm} \text{A list of intervention targets (cf. details). A list of vectors, each vector listing the vertices of one intervention target.}
- \texttt{score} \hspace{1cm} \text{An instance of a class derived from \texttt{Score}.}
- \texttt{verbose} \hspace{1cm} \text{if TRUE, detailed output is provided.}
- \texttt{...} \hspace{1cm} \text{Additional arguments for debugging purposes and fine tuning.}

Details

This function estimates the interventional Markov equivalence class of a DAG based on a data sample with interventional data originating from various interventions and possibly observational data. The intervention targets used for data generation must be specified by the argument \texttt{targets} as a list of (integer) vectors listing the intervened vertices; observational data is specified by an empty set, i.e. a vector of the form \texttt{integer(0)}. As an example, if data contains observational samples as well as samples originating from an intervention at vertices 1 and 4, the intervention targets must be specified as \texttt{list(integer(0), as.integer(1), as.integer(c(1, 4)))}.

An interventional Markov equivalence class of DAGs can be uniquely represented by a partially directed graph called interventional essential graph. Its edges have the following interpretation:

1. A directed edge \(a \rightarrow b\) stands for an arrow that has the same orientation in all representatives of the interventional Markov equivalence class;
2. An undirected edge \(a \sim b\) stands for an arrow that is oriented in one way in some representatives of the equivalence class and in the other way in other representatives of the equivalence class.

Note that when plotting the object, undirected and bidirected edges are equivalent.

The DP approach of Silander and Myllymäki (2006) is a score-based algorithm that guarantees to find the optimum of any decomposable scoring criterion. Its CPU and memory consumption grow exponentially with the number of variables in the system, irrespective of the sparseness of the true or estimated DAG. The implementation in the pcalg package is feasible up to approximately 20 variables, depending on the user’s computer.
Value

simy returns a list with the following two components:

- **essgraph**: An object of class `EssGraph` containing an estimate of the equivalence class of the underlying DAG.
- **repr**: An object of a class derived from `ParDAG` containing a (random) representative of the estimated equivalence class.

Author(s)

Alain Hauser (<alain.hauser@biology.unibe.ch>)

References


See Also

gies, Score, EssGraph

Examples

```
# Using Gaussian Data
## Load predefined data
data(gmInt)

## Define the score (BIC)
score <- new("GaussL0penIntScore", gmInt$x, gmInt$targets, gmInt$target.index)

## Estimate the essential graph
simy.fit <- simy(ncol(gmInt$x), gmInt$targets, score)

## Plot the estimated essential graph and the true DAG
if (require(Rgraphviz)) {
  par(mfrow=c(1,2))
  plot(simy.fit$essgraph, main = "Estimated ess. graph")
  plot(gmInt$g, main = "True DAG")
}
```
Estimate (Initial) Skeleton of a DAG using the PC / PC-Stable Algorithm

Description

Estimate the skeleton of a DAG without latent and selection variables using the PC Algorithm or estimate an initial skeleton of a DAG with arbitrarily many latent and selection variables using the FCI and the RFCI algorithms.

If used in the PC algorithm, it estimates the order-independent “PC-stable” ("stable") or original PC ("original") “skeleton” of a directed acyclic graph (DAG) from observational data.

When used in the FCI and RFCI algorithms, this function estimates only an initial order-independent (or PC original) “skeleton”. Because of the presence of latent and selection variables, to find the final skeleton those algorithms need to perform additional tests later on and consequently some edges can be further deleted.

Usage

skeleton(suffStat, indepTest, alpha, labels, p, method = c("stable", "original", "stable.fast"), m.max = Inf, fixedGaps = NULL, fixedEdges = NULL, NAdelete = TRUE, verbose = FALSE)

Arguments

- suffStat: Sufficient statistics: List containing all necessary elements for the conditional independence decisions in the function indepTest.
- indepTest: Predefined function for testing conditional independence. The function is internally called as indepTest(x, y, S, suffStat) and tests conditional independence of x and y given S. Here, x and y are variables, and S is a (possibly empty) vector of variables (all variables are denoted by their column numbers in the adjacency matrix). suffStat is a list containing all relevant elements for the conditional independence decisions. The return value of indepTest is the p-value of the test for conditional independence.
- alpha: significance level (number in (0, 1) for the individual conditional independence tests.
- labels: (optional) character vector of variable (or “node”) names. Typically preferred to specifying p.
- p: (optional) number of variables (or nodes). May be specified if labels are not, in which case labels is set to 1:p.
- method: Character string specifying method: the default, "stable" provides an order-independent skeleton, see ‘Details’ below.
- m.max: Maximal size of the conditioning sets that are considered in the conditional independence tests.
fixedGaps logical symmetric matrix of dimension p*p. If entry \([i,j]\) is true, the edge \(i-j\) is removed before starting the algorithm. Therefore, this edge is guaranteed to be absent in the resulting graph.

fixedEdges a logical symmetric matrix of dimension p*p. If entry \([i,j]\) is true, the edge \(i-j\) is never considered for removal. Therefore, this edge is guaranteed to be present in the resulting graph.

NAdelete logical needed for the case indepTest(*) returns NA. If it is true, the corresponding edge is deleted, otherwise not.

verbose if TRUE, detailed output is provided.

Details
Under the assumption that the distribution of the observed variables is faithful to a DAG and that there are no latent and selection variables, this function estimates the skeleton of the DAG. The skeleton of a DAG is the undirected graph resulting from removing all arrowheads from the DAG. Edges in the skeleton of a DAG have the following interpretation:

There is an edge between \(i\) and \(j\), \(i-j\), if and only if variables \(i\) and \(j\) are conditionally dependent given \(S\) for all possible subsets \(S\) of the remaining nodes.

On the other hand, the distribution of the observed variables is faithful to a DAG with arbitrarily many latent and selection variables, skeleton() estimates the initial skeleton of the DAG. Edges in this initial skeleton of a DAG have the following interpretation:

There is an edge \(i-j\) if and only if variables \(i\) and \(j\) are conditionally dependent given \(S\) for all possible subsets \(S\) of the neighbours of \(i\) and the neighbours of \(j\).

The data are not required to follow a specific distribution, but one should make sure that the conditional independence test used in indepTest is appropriate for the data. Pre-programmed versions of indepTest are available for Gaussian data (gausscitest), discrete data (disCItest), and binary data (see binCItest). Users may also specify their own indepTest function.

The PC algorithm (Spirtes, Glymour and Scheines, 2000) (method = "original") is known to be order-dependent, in the sense that the output may depend on the order in which the variables are given. Therefore, Colombo and Maathuis (2013) proposed a simple modification, called “PC-stable”, which yields order-independent adjacencies in the skeleton, provided by pc() with the new default method = "stable". This stable variant of the algorithm is also available with the method = "stable.fast": it runs the algorithm of Colombo and Maathuis (2013) faster than method = "stable" in general, but should be regarded as an experimental option at the moment.

The algorithm starts with a complete undirected graph. In each step, it visits all pairs \((i,j)\) of adjacent nodes in the current graph, and determines based on conditional independence tests whether the edge \(i-j\) should be removed. In particular, for each step \(m (m = 0, 1, \ldots)\) of the size of the conditioning sets, the algorithm at first determines the neighbours \(a(i)\) of each node \(i\) in the graph. Then, the algorithm visits all pairs \((i,j)\) of adjacent nodes in the current graph, and the edge \(i-j\) is kept if and only if the null hypothesis \(i\) and \(j\) are conditionally independent given \(S\) is rejected at significance level \(\alpha\) for all subsets \(S\) of size \(m\) of \(a(i)\) and of \(a(j)\) (as judged by the function indepTest). For the "stable" method, the neighborhoods \(a(i)\) are kept fixed within each value of \(m\), and this makes the algorithm order-independent. Method "original", the original PC algorithm would update the neighbour list after each edge change.

The algorithm stops when \(m\) is larger than the largest neighbourhood size of all nodes, or when \(m\) has reached the limit \(m_{\text{max}}\) which may be set by the user.
Since the FCI (Spirtes, Glymour and Scheines, 2000) and RFCI (Colombo et al., 2012) algorithms are built up from the PC algorithm, they are also order-dependent in the skeleton. To resolve their order-dependence issues in the skeleton is more involved, see Colombo and Maathuis (2013). However now, with method = "stable", this function estimates an initial order-independent skeleton in these algorithms (for additional details on how to make the final skeleton of FCI fully order-independent see fci and Colombo and Maathuis (2013)).

The information in fixedGaps and fixedEdges is used as follows. The gaps given in fixedGaps are introduced in the very beginning of the algorithm by removing the corresponding edges from the complete undirected graph. Pairs \((i, j)\) in fixedEdges are skipped in all steps of the algorithm, so that these edges remain in the graph.

Note: Throughout, the algorithm works with the column positions of the variables in the adjacency matrix, and not with the names of the variables.

Value

An object of class "pcAlgo" (see pcAlgo) containing an estimate of the skeleton of the underlying DAG, the conditioning sets (sepset) that led to edge removals and several other parameters.

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>), Martin Maechler, and Diego Colombo.

References


See Also

pc for generating a partially directed graph using the PC algorithm; fci for generating a partial ancestral graph using the FCI algorithm; rfci for generating a partial ancestral graph using the RFCI algorithm; udag2pdag for converting the skeleton to a CPDAG.

Further, gaussCItest, disCItest, binCItest and dsepTest as examples for indepTest.

Examples

```r
# Using Gaussian Data

## Load predefined data
data(gmG)
n <- nrow(gmG$x)
```
V <- colnames(gmG8$x) # labels aka node names

## estimate Skeleton
skel.fit <- skeleton(suffStat = list(C = cor(gmG8$x), n = n),
                     indepTest = gaussCItest, ## (partial correlations)
                     alpha = 0.01, labels = V, verbose = TRUE)
if (require(Rgraphviz)) {
  ## show estimated Skeleton
  par(mfrow=c(1,2))
  plot(skel.fit, main = "Estimated Skeleton")
  plot(gmG8$g, main = "True DAG")
}

#########################################################################
## Using d-separation oracle
#########################################################################

## define sufficient statistics (d-separation oracle)
Ora.stat <- list(g = gmG8$g, jp = RBGL::johnson.all.pairs.sp(gmG8$g))
## estimate Skeleton
fit.Ora <- skeleton(suffStat=Ora.stat, indepTest = dsepTest, labels = V,
                     alpha=0.01) # <- irrelevant as dsepTest returns either 0 or 1
if (require(Rgraphviz)) {
  ## show estimated Skeleton
  plot(fit.Ora, main = "Estimated Skeleton (d-sep oracle)")
  plot(gmG8$g, main = "True DAG")
}

#########################################################################
## Using discrete data
#########################################################################

## Load data
data(gmD)
V <- colnames(gmD$x) # labels aka node names

## define sufficient statistics
suffStat <- list(dm = gmD$x, nlev = c(3,2,3,4,2), adaptDF = FALSE)

## estimate Skeleton
skel.fit <- skeleton(suffStat,
                     indepTest = disCItest, ## (G^2 statistics independence test)
                     alpha = 0.01, labels = V, verbose = TRUE)
if (require(Rgraphviz)) {
  ## show estimated Skeleton
  par(mfrow = c(1,2))
  plot(skel.fit, main = "Estimated Skeleton")
  plot(gmD$g, main = "True DAG")
}

#########################################################################
## Using binary data
#########################################################################

## Load binary data
trueCov

Covariance matrix of a DAG.

Description
Compute the (true) covariance matrix of a generated DAG.

Usage
trueCov(dag, back.compatible = FALSE)

Arguments
- **dag**  
  Graph object containing the DAG.
- **back.compatible**  
  logical indicating if the data generated should be the same as with pcalg version 1.0-6 and earlier (where wgtMatrix() differed).

Value
Covariance matrix.

Note
This function can *not* be used to estimate the covariance matrix from an estimated DAG or corresponding data.

Author(s)
Markus Kalisch

See Also
- randomDAG for generating a random DAG
Examples

```r
set.seed(123)
g <- randomDAG(n = 5, prob = 0.3) ## generate random DAG
if(require(Rgraphviz)) {
  plot(g)
}

## Compute true covariance matrix
trueCov(g)

## For comparison:
## Estimate true covariance matrix after generating data from g
d <- rmvDAG(10000, g)
cov(d)
```

Description

This function performs the last step of the RFCI algorithm: It transforms a partially oriented graph in which the v-structures have been oriented into an RFCI Partial Ancestral Graph (PAG) (see Colombo et al (2012)).

While orienting the edges, this function performs some additional conditional independence tests in orientation rule 4 to ensure correctness of the ancestral relationships. As a result of these additional tests, some additional edges can be deleted. The result is the final adjacency matrix indicating also the edge marks and the updated sepsets.

Usage

```r
udag2apag(apag, suffStat, indepTest, alpha, sepset, rules = rep(TRUE, 10), unfVect = NULL, verbose = FALSE)
```

Arguments

- **apag**: Adjacency matrix of the pcAlgo-object of size p*p where the v-structures have already been oriented (coding 0,1,2,3 for no edge, circle, arrowhead, tail; e.g., amat[a,b] = 2 and amat[b,a] = 3 implies a -> b).
- **suffStat**: Sufficient statistics: A list containing all necessary elements for the conditional independence decisions in the function indepTest.
- **indepTest**: Pre-defined function for testing conditional independence. The function is internally called as indepTest(x, y, S, suffStat), and tests conditional independence of x and y given S. Here, x and y are variables, and S is a (possibly empty) set of variables (all variables are coded by their column numbers in the adjacency matrix). suffStat is a list containing all relevant elements for the conditional independence decisions. The return value of indepTest is the p-value of the test for conditional independence.
alpha  Significance level for the individual conditional independence tests.

sepset  List of length p; each element of the list contains another list of length p. The element sepset[[x]][[y]] contains the separation set that made the edge between x and y drop out. This object is thought to be obtained from a pcAlgo-object.

rules  Logical vector of length 10 with TRUE or FALSE for each rule, where TRUE in position i means that rule i (Ri) will be applied. By default, all rules are active.

unfVect  Vector containing numbers that encode the ambiguous triples (as returned by pc.cons.intern). This is needed in the conservative and in the majority rule versions of RFCI.

verbose  Logical indicating if detailed output is to be given.

Details

The partially oriented graph in which the v-structures have been oriented is transformed into an RFCI-PAG using adapted rules of Zhang (2008). This function is similar to udag2pag used to orient the skeleton into a PAG in the FCI algorithm. However, it is slightly more complicated because we perform additional conditional independence tests when applying rule 4, to ensure correctness of the ancestral relationships. As a result, some additional edges can be deleted, see Colombo et al. (2012). Because of these additional tests, we need to give suffStat, indepTest, and alpha as inputs. Since edges can be deleted, the input adjacency matrix apag and the input separating sets sepset can change in this algorithm.

If unfVect = NULL (no ambiguous triples), the orientation rules are applied to each eligible structure until no more edges can be oriented. On the other hand, hand, if one uses conservative or majority rule FCI and ambiguous triples have been found in pc.cons.intern, unfVect contains the numbers of all ambiguous triples in the graph. In this case, the orientation rules take this information into account. For example, if a *-> b o-* c and <a,b,c> is an unambiguous unshielded triple and not a v-structure, then we obtain b -* c (otherwise we would create an additional v-structure). On the other hand, if a *-> b o-* c but <a,b,c> is an ambiguous unshielded triple, then the circle mark at b is not oriented.

Note that the algorithm works with columns’ position of the adjacency matrix and not with the names of the variables.

Note that this function does not resolve possible order-dependence in the application of the orientation rules, see Colombo and Maathuis (2013).

Value

apag  Final adjacency matrix (coding 0,1,2,3 for no edge, circle, arrowhead, tail; e.g., amat[a,b] = 2 and amat[b,a] = 3 implies a -> b)

sepset  Updated list of separating sets

Author(s)

Diego Colombo and Markus Kalisch (<kalisch@stat.math.ethz.ch>)
References


See Also

rfci,.udag2pag, dag2pag, udag2pdag, udag2pdagSpecial, udag2pdagRelaxed

Examples

```r
---------------------------------------------------------------------------------------------%  -------
## Example with hidden variables
## Zhang (2008), Fig. 6, p.1882
---------------------------------------------------------------------------------------------

## create the DAG:
amat <- t(matrix(c(0,1,0,0,1, 0,0,1,0, 0,0,0,0, 0,0,0,0, 0,0,1,0),5,5))
V <- LETTERS[1:5]
colnames(amat) <- rownames(amat) <- V
edL[1][1] <- list(edges=c(2,4), weights=c(1,1))
edL[2][2] <- list(edges=3, weights=c(1))
edL[3][3] <- list(edges=5, weights=c(1))
edL[4][4] <- list(edges=5, weights=c(1))
## and leave edL[[5]] empty
if (require(Rgraphviz))
plot(g)

## define the latent variable
L <- 1

## compute the true covariance matrix of g
cov.mat <- trueCov(g)

## delete rows and columns belonging to latent variable L
true.cov <- cov.mat[-L,-L]

## transform covariance matrix into a correlation matrix
true.corr <- cov2cor(true.cov)

## generate 100000 samples of DAG using standard normal error distribution
require(mvtnorm)
n <- 100000
alpha <- 0.01
```
udag2pag

p <- ncol(true.corr)
d.mat <- rmvnorm(n, mean = rep(0, p), sigma = true.cov)

## estimate the skeleton of given data
suffStat <- list(C = cor(d.mat), n = n)
indepTest <- gaussCItest
resD <- skeleton(suffStat, indepTest, alpha = alpha, labels=colnames(true.corr))

## estimate all ordered unshielded triples
amat.resD <- as(resD@graph, "matrix")
(u.t <- find.unsh.triple(amat.resD)) # four of them

## check and orient v-structures
vstrucs <- rfcivStruc(suffStat, indepTest, alpha=alpha,
    sepset = resD@sepset, g.amat = amat.resD,
    unshTriple= u.t$unshTriple, unshVect = u.t$unshVect,
    verbose = TRUE)

## Estimate the final skeleton and extend it into a PAG
## (using all 10 rules, as per default):
resP <- udag2pag(vstrucs$amat, suffStat, indepTest=indepTest, alpha=alpha,
    sepset=vstrucs$sepset, verbose = TRUE)
(Amat <- resP$graph)

udag2pag

Last steps of FCI algorithm: Transform Final Skeleton into FCI-PAG

Description
This function perform the last steps of the FCI algorithm, as it transforms an un-oriented final skeleton into a Partial Ancestral Graph (PAG). The final skeleton must have been estimated with `pdsep()`. The result is an adjacency matrix indicating also the edge marks.

Usage

udag2pag(pag, sepset, rules = rep(TRUE, 10), unfVect = NULL, verbose = FALSE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pag</td>
<td>Adjacency matrix of the final skeleton of size p*p (coding 0,1,2,3 for no edge, circle, arrowhead, tail; e.g., amat[a,b] = 2 and amat[b,a] = 3 implies a -&gt; b).</td>
</tr>
<tr>
<td>sepset</td>
<td>List of length p; each element of the list contains another list of length p. The element sepset[[x]][[y]] contains the separation set that made the edge between x and y drop out. This object is thought to be obtained from a pcAlgo-object.</td>
</tr>
<tr>
<td>rules</td>
<td>Array of length 10 containing TRUE or FALSE for each rule. TRUE in position i means that rule i (Ri) will be applied. By default, all rules are used.</td>
</tr>
</tbody>
</table>
unfVect  Vector containing numbers that encode ambiguous unshielded triples (as returned by `pc.cons.intern`). This is needed in the conservative and majority rule versions of FCI.

verbose  If TRUE, detailed output is provided.

Details

The skeleton is transformed into an FCI-PAG using rules by Zhang (2008).

If `unfVect` = NULL (i.e., one uses standard FCI or one uses conservative/majority rule FCI but there are no ambiguous triples), then the orientation rules are applied to each eligible structure until no more edges can be oriented. On the other hand, if one uses conservative or majority rule FCI and ambiguous triples have been found in `pc.cons.intern`, `unfVect` contains the numbers of all ambiguous triples in the graph. In this case, the orientation rules take this information into account. For example, if a `*-> b o-* c` and `<a,b,c>` is an unambiguous unshielded triple and not a v-structure, then we obtain `b -* c` (otherwise we would create an additional v-structure). On the other hand, if a `*-> b o-* c` but `<a,b,c>` is an ambiguous unshielded triple, then the circle mark at b is not oriented.

Note that the algorithm works with columns’ position of the adjacency matrix and not with the names of the variables.

Note that this function does not resolve possible order-dependence in the application of the orientation rules, see Colombo and Maathuis (2013).

Value

Adjacency matrix M with edge marks. The edge marks are coded in the following way: M[i,j]=M[j,i]=0: no edge; M[i,j]=1, M[j,i] != 0: i *-o j; M[i,j]=2, M[j,i]!=0: i*->j; M[i,j]=3, M[j,i]! =0: i*-j.

Author(s)

Diego Colombo and Markus Kalisch (<kalisch@stat.math.ethz.ch>)

References


See Also

`fci.udag2pag, dag2pag`; further `udag2pdag` (incl. udag2pdagSpecial and udag2pdagRelaxed).
Examples

########################################################################
# Example with hidden variables
# Zhang (2008), Fig. 6, p.1882
########################################################################

# draw a DAG with latent variables
# this example is taken from Zhang (2008), Fig. 6, p.1882 (see references)
amat <- t(matrix(c(0,1,0,0,1, 0,0,1,0, 0,0,0,0, 0,0,0,0, 0,0,1,0),5,5))
colnames(amat) <- rownames(amat) <- as.character(1:5)
V <- as.character(1:5)
edl <- vector("list",length=5)
names(edl) <- V
edl[[1]] <- list(edges=c(2,4),weights=c(1,1))
edl[[2]] <- list(edges=c(3,4),weights=c(1))
edl[[3]] <- list(edges=c(5,4),weights=c(1))
edl[[4]] <- list(edges=c(5,4),weights=c(1))
g <- new("graphNEL", nodes=V, edgeL=edl, edgemode="directed")
if(require(Rgraphviz)) {
    plot(g)
} else print(g)

# define the latent variable
L <- 1

# compute the true covariance matrix of g
cov.mat <- trueCov(g)

# delete rows and columns which belong to L
ttrue.cov <- cov.mat[-L,-L]

# transform it in a correlation matrix
ttrue.corr <- cov2cor(ttrue.cov)

# generate 100000 samples of DAG using standard normal error distribution
require(mvtnorm)
n <- 100000
alpha <- 0.01
d.mat <- rmvnorm(n, mean = rep(0,dim(ttrue.corr)[1]), sigma = ttrue.cov)

# estimate the skeleton of given data
suffStat <- list(C = cor(d.mat), n = n)
indepTest <- gaussCItest
resD <- skeleton(suffStat, indepTest, p=dim(ttrue.corr)[2], alpha = alpha)

# estimate v-structures conservatively
tmp <- pc.cons.intern(resD, suffStat, indepTest, alpha, version.unf = c(1, 1))
# tripleList <- tmp$unfTripl
resD <- tmp$sk

# estimate the final skeleton of given data using Possible-D-Sep
pdsepRes <- pdsep(resD$graph, suffStat, indepTest, p=dim(ttrue.corr)[2],
## udag2pdag

### Last PC Algorithm Step: Extend Object with Skeleton to Completed PDAG

**Description**

These functions perform the last step in the PC algorithm: Transform an object of the class "pcAlgo" containing a skeleton and corresponding conditional independence information into a completed partially directed acyclic graph (CPDAG). The functions first determine the v-structures, and then apply the three orientation rules as described in Sprirtes et al (2000) and Meek (1995) to orient as many of the remaining edges as possible.

In the oracle version and when all assumptions hold, all three functions yield the same CPDAG. In the sample version, however, the resulting CPDAG may be invalid in the sense that one cannot extend it a DAG without additional unshielded colliders by orienting the undirecting edges. This can for example happen due to errors in the conditional independence tests or violations of the faithfulness assumption. The three functions deal with such conflicts in different ways, as described in Details.

**Usage**

```r
udag2pdag(ginput, verbose)
udag2pdagRelaxed(ginput, verbose, unfVect=NULL, solve.conf1=FALSE)
udag2pdagSpecial(ginput, verbose, n.max=100)
```

**Arguments**

- `ginput` "pcAlgo"-object containing skeleton and conditional independence information.
- `verbose` 0: No output; 1: Details
- `unfVect` vector containing numbers that encode ambiguous triples (as returned by `pc.cons.intern`). This is needed in the conservative and majority rule PC algorithms.
- `solve.conf1` if TRUE, the orientation of the v-structures and the orientation rules work with lists for candidate sets and allow bi-directed edges to resolve conflicting edge orientations. Note that therefore the resulting object is order-independent but might not be a PDAG because bi-directed edges can be present.
- `n.max` maximum number of tries for re-orienting doubly visited edges in `udag2pdagSpecial`. 
Details

for udagRpdag: If there are edges that are part of more than one v-structure (i.e., the edge b - c in the v-structures a -> b <- c and b -> c <- d), earlier edge orientations are simply overwritten by later ones. Thus, if a -> b <- c is considered first, the edge b - c is first oriented as b <- c and later overwritten by b -> c. The v-structures are considered in lexicographical ordering. If the resulting graph is extendable to a DAG without additional v-structures, then the rules of Meek (1995) and Spirtes et al (2000) are applied to obtain the corresponding CPDAG. Otherwise, the edges are oriented randomly to obtain a DAG that fits on the skeleton, discarding all information about the v-structures. The resulting DAG is then transformed into its CPDAG. Note that the output of udag2pdag is random whenever the initial graph was not extendable.

Although the output of udagRpdag is always extendable, it is not necessarily a valid CPDAG in the sense that it describes a Markov equivalence class of DAGs. For example, two v-structures a -> b <- c and b -> c <- d (considered in this order) would yield the output a -> b -> c <- d. This is extendable to a DAG (it already IS a DAG), but it does not describe a Markov equivalence class of DAGs, since the DAG a <- b -> c <- d describes the same conditional independencies.

for udagRpdagSpecial: If the graph after orienting the v-structures as in udagRpdag is extendable to a DAG without additional v-structures, then the rules of Meek (1995) and Spirtes et al (2000) are applied to obtain the corresponding CPDAG. Otherwise, the algorithm tries at most n.max different random orderings of the v-structures (hence overwriting orientations in different orders), until it finds one that yields an extendable CPDAG. If this fails, the edges are oriented randomly to obtain a DAG that fits on the skeleton, discarding all information about the v-structures. The resulting DAG is then transformed into its CPDAG. Note that the output of udag2pdagSpecial is random whenever the initial graph was not extendable.

Although the output of udagRpdag is always extendable, it is not necessarily a valid CPDAG in the sense that it describes a Markov equivalence class of DAGs. For example, two v-structures a -> b <- c and b -> c <- d (considered in this order) would yield the output a -> b -> c <- d. This is extendable to a DAG (it already IS a DAG), but it does not describe a Markov equivalence class of DAGs, since the DAG a <- b -> c <- d describes the same conditional independencies.

for udagRpdagRelaxed: This is the default version in the PC/RFCI/FCI algorithm. It does not test whether the output is extendable to a DAG without additional v-structures.

If unfVect = NULL (no ambiguous triples), the three orientation rules are applied to each eligible structure until no more edges can be oriented. Otherwise, unfVect contains the numbers of all ambiguous triples in the graph as determined by pc.cons.intern. Then the orientation rules take this information into account. For example, if a -> b - c and <a,b,c> is an unambiguous triple and a non-v-structure, then rule 1 implies b -> c. On the other hand, if a -> b - c but <a,b,c> is an ambiguous triple, then the edge b - c is not oriented.

If solve.conf1 = FALSE, earlier edge orientations are overwritten by later ones as in udag2pdag and udag2pdagSpecial.

If solve.conf1 = TRUE, both the v-structures and the orientation rules work with lists for the candidate edges and allow bi-directed edges if there are conflicting orientations. For example, two v-structures a -> b <- c and b -> c <- d then yield a -> b <-> c <-> d. This option can be used to get an order-independent version of the PC algorithm (see Colombo and Maathuis (2013)). We denote bi-directed edges, for example between two variables i and j, in the adjacency matrix M of the graph as M[i,j]=2 and M[j,i]=2. Such edges should be interpreted as indications of conflicts in the algorithm, for example due to errors in the conditional independence tests or violations of the faithfulness assumption.
Value

for udag2pdag() and udag2pdagRelaxed(): oriented "pcAlgo"-object.

for udag2pdagSpecial: a list with components

  pcObj An oriented "pcAlgo"-object.
  evisit Matrix counting the number of orientation attempts per edge
  xtbl.orig Logical indicating whether the original graph with v-structures is extendable.
  xtbl Logical indicating whether the final graph with v-structures is extendable
  amat0 Adjacency matrix of original graph with v-structures (coding 0/1 for no edge or tail / arrowhead; e.g. amat[a,b] = 0 and amat[b,a] = 1 implies a -> b).
  amat1 Adjacency matrix of final graph with v-structures after changing the ordering in which the v-structures are considered (coding 0/1 for no edge or tail/arrowhead; e.g. amat[a,b] = 0 and amat[b,a] = 1 implies a -> b).
  status Integer code with values
    0: Original try is extendable;
    1: Reorienting double edge visits helps;
    2: Original try is not extendable; reorienting double visits does not help; result is acyclic, has original v-structures, but perhaps additional v-structures.
  counter Number of orderings of the v-structures until success or n.max.

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>)

References


See Also

pc, pdag2dag, dag2cpdag, udag2pag, udag2apag, dag2pag.

Examples

## simulate data
set.seed(123)
p <- 10
myDAG <- randomDAG(p, prob = 0.2)
trueCPDAG <- dag2cpdag(myDAG)
n <- 1000
visibleEdge

Check visible edge.

Description

Check if the directed edge from x to z in a MAG or in a PAG is visible or not.

Usage

visibleEdge(amat, x, z)

Arguments

amat Adjacency matrix (coding 0,1,2,3 for no edge, circle, arrowhead, tail; e.g., amat[a,b] = 2 and amat[b,a] = 3 implies a -> b).
x Node x.
z Node z.

Details

All directed edges in DAGs and CPDAGs are said to be visible. Given a MAG M / PAG P, a directed edge A -> B in M / P is visible if there is a vertex C not adjacent to B, such that there is an edge between C and A that is into A, or there is a collider path between C and A that is into A and every non-endpoint vertex on the path is a parent of B. Otherwise A -> B is said to be invisible. (see Maathuis and Colombo (2013), Def. 3.1)

Value

TRUE if edge is visible, otherwise FALSE.

Author(s)

Diego Colombo
References


See Also

backdoor

Examples

amat <- matrix(c(0,3,0,0, 2,0,2,3, 0,2,0,3, 0,2,2,0), 4,4)
colnames(amat) <- rownames(amat) <- letters[1:4]
if(require(Rgraphviz)) {
  plotAG(amat)
}
visibleEdge(amat, 3, 4) ## visible
visibleEdge(amat, 2, 4) ## visible
visibleEdge(amat, 1, 2) ## invisible

wgtMatrix  Compute weight matrix of simulated DAG.

Description

Transform a DAG that was generated by randomdag to a weight matrix.

Usage

wgtMatrix(g, transpose = TRUE)

Arguments

g  Graph object containing the DAG.
transpose  Transpose weight matrix (see details).

Details

When generating a DAG (e.g. using randomdag), a graph object is usually generated and edge weights are usually specified. This function extracts the edge weights and arranges them in a matrix M.

If transpose is TRUE (default), M[i,j] is the weight of the edge from j to i. If transpose is FALSE (default), M[i,j] is the weight of the edge from i to j.

Value

Weight matrix.
Note

Not that this function can *not* be used to estimate the edge weights in an estimated DAG / CPDAG.

Author(s)

Markus Kalisch

See Also

`randomDAG` for generating a random DAG; `rmvDAG` for simulating data from a generated DAG.

Examples

```r
set.seed(123)
g <- randomDAG(n = 5, prob = 0.3) ## generate random DAG
if(require(Rgraphviz)) {
  plot(g)
}

## edge weights as matrix
wgtMatrix(g)

## for comparison: edge weights in graph object
g@edgeData@data
```
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