Package: pcalg (via r-universe)

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Title Methods for Graphical Models and Causal Inference

Description 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 variables), and GIES (for a mix of data from observational studies (i.e. observational data) and data from experiments involving interventions (i.e. interventional data) without hidden variables). For causal inference the IDA algorithm, the Generalized Backdoor Criterion (GBC), the Generalized Adjustment Criterion (GAC) and some related functions are implemented. Functions for incorporating background knowledge are provided.

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`addBgKnowledge` *Add background knowledge to a CPDAG or PDAG*

Description

Add background knowledge x -> y to an adjacency matrix and complete the orientation rules from Meek (1995).

Usage

```
addBgKnowledge(gInput, x = c(), y = c(), verbose = FALSE, checkInput = TRUE)
```

Arguments

`gInput`	`graphNEL` object or adjacency matrix of type `amat.cpdag` (see `amatType`)
`x, y`	node labels of `x` or `y` in the adjacency matrix. `x` and `y` can be vectors representing several nodes (see details below).
`verbose`	If TRUE, detailed output is provided.
`checkInput`	If TRUE, the input adjacency matrix is carefully checked to see if it is a valid graph using function `isValidGraph`

Details

If the input is a `graphNEL` object, it will be converted into an adjacency matrix of type `amat.cpdag`. If `x` and `y` are given and if `amat[y,x] != 0`, this function adds orientation `x -> y` to the adjacency matrix `amat` and completes the orientation rules from Meek (1995). If `x` and `y` are not specified (or empty vectors) this function simply completes the orientation rules from Meek (1995). If `x` and `y` are vectors of length k, k>1, this function tries to add `x[i] -> y[i]` to the adjacency matrix amat and complete the orientation rules from Meek (1995) for every $i \in \{1, \ldots, k\}$ (see Algorithm 1 in Perkovic et. al, 2017).

Value

An adjacency matrix of type `amat.cpdag` of the maximally oriented pdag with added background knowledge `x -> y` or `NULL`, if the backgound knowledge is not consistent with any DAG represented by the PDAG with the adjacency matrix `amat`.

Author(s)

Emilija Perkovic and Markus Kalisch

References

C. Meek (1995). Causal inference and causal explanation with background knowledge, In Proceedings of UAI 1995, 403-410.

E. Perkovic, M. Kalisch and M.H. Maathuis (2017). Interpreting and using CPDAGs with background knowledge. In Proceedings of UAI 2017.

Examples

```
## a -- b -- c
amat <- matrix(c(0,1,0, 1,0,1, 0,1,0), 3,3)
colnames(amat) <- rownames(amat) <- letters[1:3]
## plot(as(t(amat), "graphNEL"))
addBgKnowledge(gInput = amat) ## amat is a valid CPDAG
## b -> c is directed; a -- b is not directed by applying
## Meek's orientation rules
bg1 <- addBgKnowledge(gInput = amat, x = "b", y = "c")
## plot(as(t(bg1), "graphNEL"))
## b -> c and b -> a are directed
bg2 <- addBgKnowledge(gInput = amat, x = c("b","b"), y = c("c","a"))
## plot(as(t(bg2), "graphNEL"))

## c -> b is directed; as a consequence of Meek's orientation rules,
## b -> a is directed as well
bg3 <- addBgKnowledge(gInput = amat, x = "c", y = "b")
## plot(as(t(bg3), "graphNEL"))

amat2 <- matrix(c(0,1,0, 1,0,1, 0,1,0), 3,3)
colnames(amat2) <- rownames(amat2) <- letters[1:3]
## new collider is inconsistent with original CPDAG; thus, NULL is returned
addBgKnowledge(gInput = amat2, x = c("c", "a"), y = c("b", "b"))
```

---

adjustment *Compute adjustment sets for covariate adjustment.*

Description

This function is a wrapper for convenience to the function `adjustmentSet` from package **dagitty**.

Usage

```
adjustment(amat, amat.type, x, y, set.type)
```

Arguments

amat	adjacency matrix of type amat.cpdag or amat.pag.
amat.type	string specifying the type of graph of the adjacency matrix amat. It can be a DAG (type="dag"), a CPDAG (type="cpdag") or a maximally oriented PDAG (type="pdag") from Meek (1995); then the type of adjacency matrix is assumed to be amat.cpdag. It can also be a MAG (type = "mag") or a PAG (type="pag"); then the type of the adjacency matrix is assumed to be amat.pag.
x	(integer) position of variable x in the adjacency matrix.
y	(integer) position of variable y in the adjacency matrix.
set.type	string specifying the type of adjustment set that should be computed. It can be "minimal" ,"all" and "canonical". See Details explanations.

Details

If set.type is "minimal", then only minimal sufficient adjustment sets are returned. If set.type is "all", all valid adjustment sets are returned. If set.type is "canonical", a single adjustment set is returned that consists of all (possible) ancestors of x and y, minus (possible) descendants of nodes on proper causal paths. This canonical adjustment set is always valid if any valid set exists at all.

Value

If adjustment sets exist, list of length at least one (list elements might be empty vectors, if the empty set is an adjustment set). If no adjustment set exists, an empty list is returned.

Author(s)

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

References

E. Perkovic, J. Textor, M. Kalisch and M.H. Maathuis (2015). A Complete Generalized Adjustment Criterion. In *Proceedings of UAI 2015.*

E. Perkovic, J. Textor, M. Kalisch and M.H. Maathuis (2017). Complete graphical characterization and construction of adjustment sets in Markov equivalence classes of ancestral graphs. To appear in *Journal of Machine Learning Research.*

B. van der Zander, M. Liskiewicz and J. Textor (2014). Constructing separators and adjustment sets in ancestral graphs. In *Proceedings of UAI 2014.*

See Also

gac for testing if a set satisfies the Generalized Adjustment Criterion.

Examples

```
## Example 4.1 in Perkovic et. al (2015), Example 2 in Perkovic et. al (2017)
mFig1 <- matrix(c(0,1,1,0,0,0, 1,0,1,1,1,0, 0,0,0,0,0,1,
                  0,1,1,0,1,1, 0,1,0,1,0,1, 0,0,0,0,0,0), 6,6)
type <- "cpdag"
```

```
x <- 3; y <- 6
## plot(as(t(mFig1), "graphNEL"))

## all
if(requireNamespace("dagitty", quietly = TRUE)) {
adjustment(amat = mFig1, amat.type = type, x = x, y = y, set.type =
"all")
}
## finds adjustment sets: (2,4), (1,2,4), (4,5), (1,4,5), (2,4,5), (1,2,4,5)

## minimal
if(requireNamespace("dagitty", quietly = TRUE)) {
adjustment(amat = mFig1, amat.type = type, x = x, y = y, set.type =
"minimal")
}
## finds adjustment sets: (2,4), (4,5), i.e., the valid sets with the fewest elements

## canonical
if(requireNamespace("dagitty", quietly = TRUE)) {
adjustment(amat = mFig1, amat.type = type, x = x, y = y, set.type =
"canonical")
}
## finds adjustment set: (1,2,4,5)
```

---

ages *Estimate an APDAG within the Markov equivalence class of a DAG using AGES*

Description

Estimate an APDAG (a particular PDAG) using the aggregative greedy equivalence search (AGES) algorithm, which uses the solution path of the greedy equivalence search (GES) algorithm of Chickering (2002).

Usage

```
ages(data, lambda_min = 0.5 * log(nrow(data)), labels = NULL,
     fixedGaps = NULL, adaptive = c("none", "vstructures", "triples"),
     maxDegree = integer(0), verbose = FALSE, ...)
```

Arguments

data	A $n * p$ matrix (or data frame) containing the observational data.
lambda_min	The smallest penalty parameter value used when computing the solution path of GES.
labels	Node labels; if NULL the names of the columns of the data matrix (or the names in the data frame) are used. If these are not specified the sequence 1 to p is used.

`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.

`adaptive` indicating whether constraints should be adapted to newly detected v-structures or unshielded triples (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

This function tries to add orientations to the essential graph (CPDAG) found by `ges` (ran with lambda=lambda_min). It does it aggregating several CPDAGs present in the solution path of GES. Conceptually, AGES starts with the essential graph found by GES ran with `lambda = lambda_min`. Then, it checks for further (compatible) orientation information in other essential graphs present in the solution path of GES, i.e., in essential graphs outputted by GES for larger penalty parameters. With compatible we mean that the aggregation process is done such that the final APDAG is still within the Markov equivalence graph represented by the essential graph found by GES in the following sense: an APDAG can always be extended to a DAG without creating new v-structures. This DAG lies in the Markov equivalence class represented by the essential graph found by GES. The algorithm is explained in detail in Eigenmann, Nandy, and Maathuis (2017).

The arguments `fixedgaps` and `adaptive` work also with AGES. However, they have not been studied in Eigenmann, Nandy, and Maathuis (2017). Using the argument `fixedGaps`, one can make sure that certain edges will *not* be present in the resulting essential graph: if the entry `[i, j]` of the matrix passed to `fixedGaps` is `TRUE`, there will be no edge between nodes i and j. The argument `adaptive` can be used to relax the constraints encoded by `fixedGaps` according to a modification of GES called ARGES (adaptively restricted greedy equivalence search) which has been presented in Nandy, Hauser and Maathuis (2018):

- When `adaptive = "vstructures"` and the algorithm introduces a new v-structure $a \longrightarrow b \longleftarrow c$ in the forward phase, then the edge $a - c$ is removed from the list of fixed gaps, meaning that the insertion of an edge between a and c becomes possible even if it was forbidden by the initial matrix passed to `fixedGaps`.
- When `adaptive = "triples"` and the algorithm introduces a new unshielded triple in the forward phase (i.e., a subgraph of three nodes a, b and c where a and b as well as b and c are adjacent, but a and c are not), then the edge $a - c$ is removed from the list of fixed gaps.

With one of the adaptive modifications, the successive application of a skeleton estimation method and GES restricted to an estimated skeleton still gives a *consistent* estimator of the DAG, which is not the case without the adaptive modification.

For a detailed explanation of the GES function as well as its related object like essential graphs, we refer to the ges function.

Differences in the arguments with respect to GES: AGES uses data to initialize several scores taken as argument by GES. AGES modifies the forward and backward phases of GES performing single steps in either directions. For this reason, phase, iterate, and turning are not available arguments.

Value

ages returns a list with the following four 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.
CPDAGsList	A list of p*p matrices containing all CPDAGs considered by AGES in the aggregation processes
lambda	A vector containing the penalty parameter used to obtain the list of CPDAGs mentioned above. GES returns the list of CPDAGs when used with this vector of penalty parameters if used with phases = c("forward", "backward") and iterate = FALSE.

Author(s)

Marco Eigenmann (<eigenmann@stat.math.ethz.ch>)

References

D.M. Chickering (2002). Optimal structure identification with greedy search. *Journal of Machine Learning Research* **3**, 507–554

M.F. Eigenmann, P. Nandy, and M.H. Maathuis (2017). Structure learning of linear Gaussian structural equation models with weak edges. In *Proceedings of UAI 2017*

P. Nandy, A. Hauser and M.H. Maathuis (2018). High-dimensional consistency in score-based and hybrid structure learning. *Annals of Statistics*, to appear.

See Also

ges, EssGraph

Examples

```
## Example 1: ages adds correct orientations: Bar --> V6 and Bar --> V8

set.seed(77)

p <- 8
n <- 5000
## true DAG:
vars <- c("Author", "Bar", "Ctrl", "Goal", paste0("V",5:8))
```

```
gGtrue <- randomDAG(p, prob = 0.3, V = vars)
data = rmvDAG(n, gGtrue)


## Estimate the aggregated PDAG with ages
ages.fit <- ages(data = data)


## Estimate the essential graph with ges
## We specify the phases in order to have a fair comparison of the algorithms
## Without the phases specified it would be easy to find examples
## where each algorithm outperforms the other
score <- new("GaussL0penObsScore", data)
ges.fit <- ges(score, phase = c("forward","backward"), iterate = FALSE)

## Plots
if (require(Rgraphviz)) {
par(mfrow=c(1,3))
plot(ges.fit$essgraph, main="Estimated CPDAG with GES")
plot(ages.fit$essgraph, main="Estimated APDAG with AGES")
plot(gGtrue, main="TrueDAG")
}


## Example 2: ages adds correct orientations: Author --> Goal and Author --> V5

set.seed(50)

p <- 9
n <- 5000
## true DAG:
vars <- c("Author", "Bar", "Ctrl", "Goal", paste0("V",5:9))
gGtrue <- randomDAG(p, prob = 0.5, V = vars)
data = rmvDAG(n, gGtrue)


## Estimate the aggregated PDAG with ages
ages.fit <- ages(data = data)


## Estimate the essential graph with ges
## We specify the phases in order to have a fair comparison of the algorithms
## Without the phases specified it would be easy to find examples
## where each algorithm outperforms the other
score <- new("GaussL0penObsScore", data)
ges.fit <- ges(score, phase = c("forward","backward"), iterate = FALSE)

## Plots
if (require(Rgraphviz)) {
par(mfrow=c(1,3))
plot(ges.fit$essgraph, main="Estimated CPDAG with GES")
plot(ages.fit$essgraph, main="Estimated APDAG with AGES")
plot(gGtrue, main="TrueDAG")
```

```
}

## Example 3: ges and ages return the same graph

data(gmG)

data <- gmG8$x

## Estimate the aggregated PDAG with ages
ages.fit <- ages(data = data)


## Estimate the essential graph with ges
score <- new("GaussL0penObsScore", data)
ges.fit <- ges(score)


## Plots
if (require(Rgraphviz)) {
par(mfrow=c(1,3))
plot(ges.fit$essgraph, main="Estimated CPDAG with GES")
plot(ages.fit$essgraph, main="Estimated APDAG with AGES")
plot(gmG8$g, main="TrueDAG")
}
```

---

amatType *Types and Display of Adjacency Matrices in Package 'pcalg'*

Description

Two types of adjacency matrices are used in package **pcalg**: Type `amat.cpdag` for DAGs and CPDAGs and type `amat.pag` for MAGs and PAGs. The required type of adjacency matrix is documented in the help files of the respective functions or classes. If in some functions more detailed information on the graph type is needed (i.e. DAG or CPDAG; MAG or PAG) this information will be passed in a separate argument (see e.g. `gac` and the examples below).

Note that you get ('extract') such adjacency matrices as (S3) objects of `class "amat"` via the usual `as(., "<class>")` coercion,

```
as(from, "amat")
```

Arguments

`from`	an R object of class `pcAlgo`, as returned from `skeleton()` or `pc()` or an object of class `fciAlgo`, as from `fci()` (or `rfci`, `fciPlus`, and `dag2pag`), or an object of class `"LINGAM"` as returned from `lingam()`.

Details

Adjacency matrices are integer valued square matrices with zeros on the diagonal. They can have row- and columnnames; however, most functions will work on the (integer) column positions in the adjacency matrix.

Coding for type `amat.cpdag`**:**

`0`**:** No edge or tail

`1`**:** Arrowhead

Note that the edgemark-code refers to the *row* index (as opposed adjacency matrices of type mag or pag). E.g.:

```
amat[a,b] = 0  and  amat[b,a] = 1   implies a --> b.
amat[a,b] = 1  and  amat[b,a] = 0   implies a <-- b.
amat[a,b] = 0  and  amat[b,a] = 0   implies a     b.
amat[a,b] = 1  and  amat[b,a] = 1   implies a --- b.
```

Coding for type `amat.pag`**:**

`0`**:** No edge

`1`**:** Circle

`2`**:** Arrowhead

`3`**:** Tail

Note that the edgemark-code refers to the *column* index (as opposed adjacency matrices of type dag or cpdag). E.g.:

```
amat[a,b] = 2  and  amat[b,a] = 3   implies   a --> b.
amat[a,b] = 3  and  amat[b,a] = 2   implies   a <-- b.
amat[a,b] = 2  and  amat[b,a] = 2   implies   a <-> b.
amat[a,b] = 1  and  amat[b,a] = 3   implies   a --o b.
amat[a,b] = 0  and  amat[b,a] = 0   implies   a     b.
```

See Also

E.g. `gac` for a function which takes an adjacency matrix as input; `fciAlgo` for a class which has an adjacency matrix in one slot.

`getGraph(x)` extracts the `graph-class` object from `x`, whereas `as(*, "amat")` gets the corresponding adjacency matrix.

Examples

```
################################################
## Function gac() takes an adjecency matrix of
## any kind as input.  In addition to that, the
## precise type of graph (DAG/CPDAG/MAG/PAG) needs
## to be passed as a different argument
################################################
## Adjacency matrix of type 'amat.cpdag'
```

```
m1 <- matrix(c(0,1,0,1,0,0, 0,0,1,0,1,0, 0,0,0,0,0,1,
               0,0,0,0,0,0, 0,0,0,0,0,0, 0,0,0,0,0,0), 6,6)
## more detailed information on the graph type needed by gac()
gac(m1, x=1,y=3, z=NULL, type = "dag")

## Adjacency matrix of type 'amat.cpdag'
m2 <- matrix(c(0,1,1,0,0,0, 1,0,1,1,1,0, 0,0,0,0,0,1,
               0,1,1,0,1,1, 0,1,0,1,0,1, 0,0,0,0,0,0), 6,6)
## more detailed information on the graph type needed by gac()
gac(m2, x=3, y=6, z=c(2,4), type = "cpdag")

## Adjacency matrix of type 'amat.pag'
m3 <- matrix(c(0,2,0,0, 3,0,3,3, 0,2,0,3, 0,2,2,0), 4,4)
## more detailed information on the graph type needed by gac()
mg3 <- gac(m3, x=2, y=4, z=NULL, type = "mag")
pg3 <- gac(m3, x=2, y=4, z=NULL, type = "pag")

##############################################################
## as(*, "amat") returns an adjacency matrix incl. its type
##############################################################
## Load predefined data
data(gmG)
n <- nrow    (gmG8$x)
V <- colnames(gmG8$x)

## define sufficient statistics
suffStat <- list(C = cor(gmG8$x), n = n)
## estimate CPDAG
skel.fit <- skeleton(suffStat, indepTest = gaussCItest,
                     alpha = 0.01, labels = V)
## Extract the "amat" [and show nicely via  'print()' method]:
as(skel.fit, "amat")

################################################
## Function fci() returns an adjacency matrix
## of type amat.pag as one slot.
################################################
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, doPdsep = FALSE)
str(res)
## get the a(djacency) mat(rix)  and nicely print() it:
as(res, "amat")

################################################
## pcAlgo object
################################################
```

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

## define sufficient statistics
suffStat <- list(C = cor(gmG8$x), n = n)
## estimate CPDAG
skel.fit <- skeleton(suffStat, indepTest = gaussCItest,
                     alpha = 0.01, labels = V)
## Extract Adjacency Matrix - and print (via method 'print.amat'):
as(skel.fit, "amat")

pc.fit <- pc(suffStat, indepTest = gaussCItest,
             alpha = 0.01, labels = V)
pc.fit # (using its own print() method 'print.pcAlgo')

as(pc.fit, "amat")
```

---

backdoor *Find Set Satisfying the Generalized Backdoor Criterion (GBC)*

Description

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

Usage

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

Arguments

amat	adjacency matrix of type amat.cpdag or amat.pag.
x, y	(integer) position of variable X and Y, respectively, 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"); then the type of the adjacency matrix is assumed to be amat.cpdag. It can also be a MAG (type="mag"), or a PAG (type="pag"); then the type of the adjacency matrix is assumed to be amat.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 (2015).

The motivation to find a set W that satisfies the GBC 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 GBC 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 GBC (see Maathuis and Colombo, 2015). If the effect is not identifiable in this way, the output is NA. Otherwise, an explicit set W that satisfies the GBC 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 GBC, but the total causal effect might be identifiable via some other technique.

For the coding of the adjacency matrix see amatType.

Value

Either NA if the total causal effect is not identifiable via the GBC, or a set if the effect is identifiable via the GBC. 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

M.H. Maathuis and D. Colombo (2015). A generalized backdoor criterion. Annals of Statistics 43 1060-1088.

J. Pearl (1993). Comment: Graphical models, causality and intervention. *Statistical Science* **8**, 266–269.

See Also

gac for the Generalized Adjustment Criterion (GAC), which is a generalization of GBC; pc for estimating a CPDAG, dag2pag and fci for estimating a PAG, and pag2magAM for estimating a MAG.

Examples

```
##########################################################################
##DAG
##########################################################################
## Simulate the true DAG
suppressWarnings(RNGversion("3.5.0"))
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 set satisfying the GBC:
backdoor(true.amat, 5, 7, type="dag")

##########################################################################
##CPDAG
##########################################################################
#################################################
## Example not identifiable
## Maathuis and Colombo (2015), Fig. 3a, p.1072
#################################################
## create the graph
p <- 5
. <- 0
amat <- rbind(c(.,.,1,1,1),
              c(.,.,1,1,1),
              c(.,.,.,1,.),
              c(.,.,.,.,1),
              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=4,weights=c(1))
edL[[4]] <- list(edges=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 (2015), Fig. 3b, p.1072
################################################

## create the graph
p <- 6
amat <- rbind(c(0,0,1,1,0,1), c(0,0,1,1,0,1), c(0,0,0,0,1,0),
              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=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

## The effect is identifiable and the set satisfying GBC is:
backdoor(true.amat, 6, 3, type="cpdag")


#####################################################################
##PAG
#####################################################################
################################################
## Example identifiable
## Maathuis and Colombo (2015), Fig. 5a, p.1075
################################################

## create the graph
p <- 7
amat <- t(matrix(c(0,0,1,1,0,0,0, 0,0,1,1,0,0,0, 0,0,0,1,0,1,0,
                   0,0,0,0,0,0,1, 0,0,0,0,0,1,1, 0,0,0,0,0,0,0,
                   0,0,0,0,0,0,0),  7, 7))
colnames(amat) <- rownames(amat) <- as.character(1:7)
V <- as.character(1:7)
edL <- vector("list",length=7)
names(edL) <- V
edL[[1]] <- list(edges=c(3,4),weights=c(1,1))
edL[[2]] <- list(edges=c(3,4),weights=c(1,1))
edL[[3]] <- list(edges=c(4,6),weights=c(1,1))
```

```
edL[[4]] <- list(edges=7,weights=c(1))
edL[[5]] <- list(edges=c(6,7),weights=c(1,1))
g <- new("graphNEL", nodes=V, edgeL=edL, edgemode="directed")
L <- 5

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

## transform covariance matrix into a correlation matrix
true.corr <- cov2cor(cov.mat)
suffStat <- list(C=true.corr, n=10^9)
indepTest <- gaussCItest

## estimate the true PAG
true.pag <- dag2pag(suffStat, indepTest, g, L, alpha = 0.9999)@amat

## The effect is identifiable  and the backdoor set is:
backdoor(true.pag, 3, 5, type="pag")
```

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

Description

This function is DEPRECATED! Use `ida` instead.

Usage

```
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 call allDags is done
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

---

binCItest *G square Test for (Conditional) Independence of Binary Variables*

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, n.min = 10*df, 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.
n.min	the smallest n (number of observations, nrow(dm)) for which the G^2 test is computed; for smaller n, independence is assumed ($G^2 := 1$) with a warning. The default is $10m$, where m is the degrees of freedom assuming no structural zeros, $2^{\|S\|}$.
verbose	logical or integer indicating that increased diagnostic output is to be provided.
suffStat	a list with two elements, "dm", and "adaptDF" corresponding to the above two arguments of gSquareBin().

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

R.E. Neapolitan (2004). Learning Bayesian Networks. *Prentice Hall Series in Artificial Intelligence*. Chapter 10.3.1

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

```
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}

ftable(xtabs(~ x1+x2+x3))
dat <- cbind(x1,x2,x3)

## Test marginal and conditional independencies
gSquareBin(3,1,NULL,dat, verbose=TRUE)
gSquareBin(3,1, 2,  dat)
gSquareBin(1,3, 2,  dat) # the same
gSquareBin(1,3, 2,  dat, adaptDF=TRUE, verbose = 2)
```

checkTriple *Check Consistency of Conditional Independence for a Triple of Nodes*

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	(integer) position in adjacency matrix for 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.
maj.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

D. Colombo and M.H. Maathuis (2014).Order-independent constraint-based causal structure learning. *Journal of Machine Learning Research* **15** 3741-3782.

Examples

```
##################################################
## Using Gaussian Data
##################################################
## Load predefined data
data(gmG)
n <- nrow    (gmG8$x)
V <- colnames(gmG8$x)


## define independence test (partial correlations), and test level
indepTest <- gaussCItest
alpha <- 0.01
## define sufficient statistics
suffStat <- list(C = cor(gmG8$x), n = n)

## estimate CPDAG
pc.fit <- pc(suffStat, indepTest, alpha=alpha, labels = V, verbose = TRUE)

if (require(Rgraphviz)) {
  ## show estimated CPDAG
  par(mfrow=c(1,2))
  plot(pc.fit, main = "Estimated CPDAG")
  plot(gmG8$g, main = "True DAG")
}

a <- 6
```

```
b <- 1
c <- 8
checkTriple(a, b, c,
            nbrsA = c(1,5,7),
            nbrsC = c(1,5),
            sepsetA = pc.fit@sepset[[a]][[c]],
            sepsetC = pc.fit@sepset[[c]][[a]],
            suffStat=suffStat, indepTest=indepTest, alpha=alpha,
            version.unf = c(2,2),
            verbose = TRUE) -> ct
str(ct)
## List of 4
## $ decision: int 2
## $ version : int 1
## $ SepsetA : int [1:2] 1 5
## $ SepsetC : int 1

checkTriple(a, b, c,
            nbrsA = c(1,5,7),
            nbrsC = c(1,5),
            sepsetA = pc.fit@sepset[[a]][[c]],
            sepsetC = pc.fit@sepset[[c]][[a]],
            version.unf = c(1,1),
            suffStat=suffStat, indepTest=indepTest, alpha=alpha) -> c2
stopifnot(identical(ct, c2)) ## in this case,  'version.unf' had no effect
```

`compareGraphs` *Compare two graphs in terms of TPR, FPR and TDR*

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

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

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

```
## 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)) {
par(mfrow=c(2,1))
plot(gt) ; title("True graph")
plot(gl) ; title("Estimated graph")
(cg <- compareGraphs(gl,gt))

}
```

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`	(integer) position of variable X, Y and set of variables S, respectively, in the adjacency matrix. It is tested, whether `X` and `Y` are conditionally independent given the subset `S` of the remaining nodes.
`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 TRUE then it seems plausible, that x and y are conditionally independent given S. If 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

M. Kalisch and P. Buehlmann (2007). Estimating high-dimensional directed acyclic graphs with the PC-algorithm. *JMLR* **8** 613-636.

See Also

pcorOrder for computing a partial correlation given the correlation matrix in a recursive way.

dsepTest, disCItest and binCItest 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

```
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 <- qnorm(1-alpha/2)
(b1 <- 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))
   # -> 1 and 3 seem to be conditionally dependent given 2

## simulate another dep.case: x -> y -> z
```

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

## analyze data
suffStat <- list(C = cor(dat), n = nrow(dat))
gaussCItest(1,3,NULL, suffStat) ## dependent [highly signif.]
gaussCItest(1,3,  2,  suffStat) ## independent | S
```

---

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.

Value

Undirected correlation graph, a graph-class object (package **graph**); getGraph for the "fitted" graph.

Author(s)

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

Examples

```
## 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 function is a simple wrapper function for dag2essgraph which is more powerfull since it also allows the calculation of the Markov equivalence class in the presence of interventional data.

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 Alain Hauser(<alain.hauser@bfh.ch>)

References

C. Meek (1995). Causal inference and causal explanation with background knowledge. In *Proceedings of the Eleventh Conference on Uncertainty in Artificial Intelligence (UAI-95)*, pp. 403-411. Morgan Kaufmann Publishers, Inc.

P. Spirtes, C. Glymour and R. Scheines (2000) *Causation, Prediction, and Search*, 2nd edition, The MIT Press.

See Also

dag2essgraph, randomDAG, pc

Examples

```
## A -> B <- C
am1 <- matrix(c(0,1,0, 0,0,0, 0,1,0), 3,3)
colnames(am1) <- rownames(am1) <- LETTERS[1:3]
g1 <- as(t(am1), "graphNEL") ## convert to graph
cpdag1 <- dag2cpdag(g1)

if(requireNamespace("Rgraphviz")) {
    par(mfrow = c(1,2))
    plot(g1)
    plot(cpdag1)
}

## A -> B -> C
am2 <- matrix(c(0,1,0, 0,0,1, 0,0,0), 3,3)
colnames(am2) <- rownames(am2) <- LETTERS[1:3]
g2 <- as(t(am2), "graphNEL") ## convert to graph
cpdag2 <- dag2cpdag(g2)

if(requireNamespace("Rgraphviz")) {
    par(mfrow = c(1,2))
    plot(g2)
    plot(cpdag2)
}
```

---

dag2essgraph *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. Different representations are possible: dag can be an object of graphNEL (package **graph**) or an instance of a class derived from ParDAG.
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 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.

Value

Depending on the class of dag, the essential graph is returned as

- an instance of graphNEL, if dag is an instance of graphNEL,
- an instance of EssGraph, if dag is an instance of a class derived from ParDAG.

Author(s)

Alain Hauser (<alain.hauser@bfh.ch>)

References

A. Hauser and P. Bühlmann (2012). Characterization and greedy learning of interventional Markov equivalence classes of directed acyclic graphs. *Journal of Machine Learning Research* **13**, 2409–2464.

P. Spirtes, C.N. Glymour, and R. Scheines (2000). *Causation, Prediction, and Search*, MIT Press, Cambridge (MA).

See Also

dag2cpdag, Score, EssGraph

Examples

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

## Generate a random DAG
set.seed(42)
require(graph)
dag <- randomDAG(p, s)
nodes(dag) <- sprintf("V%d", 1:p)

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

## Different argument classes
res2 <- dag2essgraph(as(dag, "GaussParDAG"))
str(res2)

## Calculate interventional essential graph for intervention targets
## {1} and {3}
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

```
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 in $(0, 1)$ 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

```
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

Richardson, T. and Spirtes, P. (2002). Ancestral graph Markov models. *Ann. Statist.* **30**, 962–1030; Theorem 4.2., page 983.

See Also

fci, pc

Examples

```
## 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
## gaussCItest() with a large "virtual sample size" and a large alpha:
system.time(
true.pag <- dag2pag(suffStat = list(C = true.corr, n = 10^9),
                    indepTest = gaussCItest,
                    graph=g, L=L, alpha = 0.9999) )

### ---- Find PAG using fci-function --------------------------

## From trueCov(g), delete rows and columns belonging to latent variable L
true.cov1 <- cov.mat[-L,-L]
## transform covariance matrix into a correlation matrix
true.corr1 <- cov2cor(true.cov1)

## 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:
system.time(
true.pag1 <- fci(suffStat = list(C = true.corr1, n = 10^9),
                 indepTest = gaussCItest,
                 p = ncol(true.corr1), alpha = 0.9999) )

## confirm that the outputs are equal
stopifnot(true.pag@amat == true.pag1@amat)
```

`disCItest` *G square Test for (Conditional) Independence of Discrete Variables*

Description

G^2 test for (conditional) independence of *discrete* (each with a *finite* number of "levels") 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

```
gSquareDis(x, y, S, dm, nlev, adaptDF = FALSE, n.min = 10*df, verbose = FALSE)
disCItest (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 (rows: samples, columns: variables) with integer entries; the k levels for a given column must be coded by the integers 0,1,...,k-1. (see example)
nlev	optional vector with numbers of levels for each variable in `dm`.

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.
n.min	the smallest n (number of observations, nrow(dm)) for which the G^2 test is computed; for smaller n, independence is assumed ($G^2 := 1$) with a warning. The default is $10m$, where m is the degrees of freedom assuming no structural zeros, here, the product of all the number of levels (nlev[x]-1) * (nlev[y]-1) * prod(nlev[S]).
verbose	logical or integer indicating that increased diagnostic 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

R.E. Neapolitan (2004). Learning Bayesian Networks. *Prentice Hall Series in Artificial Intelligence*. Chapter 10.3.1

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

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

## Analyze data
gSquareDis(1,3, S=2, dat, nlev = c(3,4,2)) # but nlev is optional:
```

```
gSquareDis(1,3, S=2, dat, verbose=TRUE, adaptDF=TRUE)
## with too little data, gives a warning (and p-value 1):
gSquareDis(1,3, S=2, dat[1:60,], nlev = c(3,4,2))

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.

See p.136 of Sprirtes et al (2000) or Definition 4.1 of Maathuis and Colombo (2015).

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 of type amat.pag.
`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

P. Spirtes, C. Glymour and R. Scheines (2000) *Causation, Prediction, and Search*, 2nd edition, The MIT Press.

M.H. Maathuis and D. Colombo (2015). A generalized back-door criterion. *Annals of Statistics* **43** 1060-1088.

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, fci or fciPlus. dsepAM for a similar function for MAGs.

Examples

```
## 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)
```

---

dsepAM *Test for d-separation in a MAG*

Description

This function tests for d-separation (also known as m-separation) of nodes X and nodes Y given nodes S in a MAG.

Usage

```
dsepAM(X, Y, S = NULL, amat, verbose=FALSE)
```

Arguments

X	Vector of column numbers of nodes X in the adjacency matrix
Y	Vector of column numbers of nodes Y in the adjacency matrix
S	Vector of column numbers of nodes S in the adjacency matrix (may be empty)
amat	The Maximal Ancestral Graph encoded as adjacency matrix of type amatType
verbose	If true, more detailed output is provided.

Details

This function checks separation in the moralized graph as explained in Richardson and Spirtes (2002).

Value

TRUE if X and Y are d-separated by S in the MAG encoded by amat, otherwise FALSE.

Author(s)

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

References

T.S. Richardson and P. Spirtes (2002). Ancestral graph Markov models. *Annals of Statistics* **30** 962-1030.

See Also

`dsepAMTest` for a wrapper of this function that can easily be included into `skeleton`, `fci` or `fciPlus`. `dsep` for a similar function for DAGs.

Examples

```
# Y-structure MAG
# Encode as adjacency matrix
p <- 4 # total number of variables
V <- c("X1","X2","X3","X4") # variable labels
# amat[i,j] = 0 iff no edge btw i,j
# amat[i,j] = 1 iff i *-o j
# amat[i,j] = 2 iff i *-> j
# amat[i,j] = 3 iff i *-- j
amat <- rbind(c(0,0,2,0),
              c(0,0,2,0),
              c(3,3,0,2),
              c(0,0,3,0))
rownames(amat)<-V
colnames(amat)<-V

## d-separated
cat('X1 d-separated from X2? ', dsepAM(1,2,S=NULL,amat),'\n')
## not d-separated given node 3
cat('X1 d-separated from X2 given X4? ', dsepAM(1,2,S=4,amat),'\n')
## not d-separated by node 3 and 4
cat('X1 d-separated from X2 given X3 and X4? ', dsepAM(1,2,S=c(3,4),amat),'\n')
```

---

dsepAMTest *Test for d-separation in a MAG*

Description

This function tests for d-separation (also known as m-separation) of node `x` and node `y` given nodes `S` in a MAG. `dsepAMTest()` is written to be easily used in `skeleton`, `fci`, `fciPlus`.

Usage

```
dsepAMTest(x, y, S = NULL, suffStat)
```

Arguments

x	Column number of node x in the adjacency matrix
y	Column number of node y in the adjacency matrix
S	Vector of column numbers of nodes S in the adjacency matrix, may be empty
suffStat	a list with two elements, **amat** The Maximal Ancestral Graph encoded as adjacency matrix of type amatType **verbose** If true, more detailed output is provided.

Details

The function is a wrapper for dsepAM, which checks separation in the moralized graph as explained in Richardson and Spirtes (2002).

Value

Returns 1 if x and y are d-separated by S in the MAG encoded by amat, otherwise 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 MAG.

Author(s)

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

References

T.S. Richardson and P. Spirtes (2002). Ancestral graph Markov models. *Annals of Statistics* **30** 962-1030.

See Also

dsepTest for a similar function for DAGs. gaussCItest, disCItest and binCItest for similar functions for a conditional independence test for gaussian, discrete and binary variables, respectively.

Examples

```
# Y-structure MAG
# Encode as adjacency matrix
p <- 4 # total number of variables
V <- c("X1","X2","X3","X4") # variable labels
# amat[i,j] = 0 iff no edge btw i,j
# amat[i,j] = 1 iff i *-o j
# amat[i,j] = 2 iff i *-> j
# amat[i,j] = 3 iff i *-- j
amat <- rbind(c(0,0,2,0),
              c(0,0,2,0),
              c(3,3,0,2),
```

```
              c(0,0,3,0))
rownames(amat)<-V
colnames(amat)<-V

suffStat<-list(g=amat,verbose=FALSE)
## d-separated
cat('X1 d-separated from X2? ', dsepAMTest(1,2,S=NULL,suffStat),'\n')
## not d-separated given node 3
cat('X1 d-separated from X2 given X4? ',
dsepAMTest(1,2,S=4,suffStat),'\n')
## not d-separated by node 3 and 4
cat('X1 d-separated from X2 given X3 and X4? ', dsepAMTest(1,2,S=c(3,4),
suffStat),'\n')

# Derive PAG that represents the Markov equivalence class of the MAG with the FCI algorithm
# Make use of d-separation oracle as "independence test"
indepTest <- dsepAMTest
fci.pag <- fci(suffStat,indepTest,alpha = 0.5,labels = V,verbose=FALSE)
cat('True MAG:\n')
print(amat)
cat('PAG output by FCI:\n')
print(fci.pag@amat)
```

`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

```
dsepTest(x, y, S=NULL, 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.
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

dsepAMTest for a similar function for MAGs. gaussCItest, disCItest and binCItest for similar functions for a conditional independence test for gaussian, discrete and binary variables, respectively.

Examples

```
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 (observentional 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 $a \longrightarrow b$ 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.

Author(s)

Alain Hauser (<alain.hauser@bfh.ch>)

See Also

ParDAG

Examples

```
showClass("EssGraph")
```

---

fci *Estimate a PAG with the FCI Algorithm*

Description

Estimate a Partial Ancestral Graph (PAG) from observational data, using the FCI (Fast Causal Inference) algorithm, or from a combination of data from different (e.g., observational and interventional) contexts, using the FCI-JCI (Joint Causal Inference) extension.

Usage

```
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,
    numCores = 1, selectionBias = TRUE,
    jci = c("0","1","12","123"), contextVars = NULL,
    verbose = FALSE)
```

Arguments

suffStat	sufficient statistics: A named 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 with all relevant information, see above. The return value of indepTest() is the p-value of the test for conditional independence.
alpha	numeric significance level (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.

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 — 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 — 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) $\setminus$ $\{x, y\}$ 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 (2008).

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.

numCores — Specifies the number of cores to be used for parallel estimation of skeleton.

selectionBias — If TRUE, allow for selection bias. If FALSE, selection bias is excluded by assumption and hence rules R5-R7, as in Zhang (2008), are disabled.

jci	String specifying the JCI assumptions that are used. It can be one of: **"0"** No JCI assumption is made (default), **"1"** JCI assumption 1 (no system variable causes any context variable), **"12"** JCI assumptions 1 and 2 (no system variable causes any context variable, and no system variable is confounded with any context variable), **"123"** JCI assumptions 1, 2 and 3 (no system variable causes any context variable, no system variable is confounded with any context variable, and all context variables are confounded but are not direct causes of each other). For more information, see Mooij et al. (2020).
contextVars	Subset of variable indices {1,...,p} that will be treated as context variables in the JCI extension of FCI.
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. Under the assumption that the data are σ-faithful to a simple (possibly cyclic) SCM that allows for latent confounding (but selection bias is absent), the FCI algorithm estimates the σ-Markov equivalence class of the DMGs (directed mixed graphs) that describe the causal relations between the observed variables and the conditional independence relationships in the observed distribution through σ-separation (Mooij and Claassen, 2020). The FCI-JCI (Joint Causal Inference) extension allows the algorithm to combine data from different contexts, for example, observational and different types of interventional data (Mooij et al., 2020).

FCI estimates a **partial ancestral graph** (**PAG**). The PAG represents a Markov equivalence class of DAGs with latent and selection variables in the acyclic case (Zhang, 2008), and a Markov equivalence class of directed graphs with latent variables (but without selection variables) in the cyclic σ-separation case. A PAG contains the following types of edges: o-o, o–, o->, –>, <->, —. The bidirected edges come from latent confounders, and the undirected edges come from latent 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 (assuming the Markov property and faithfulness); (ii) a tail x `--*` y at x on an edge between x and y means that x is an ancestor of y or S; (iii) an arrowhead x `<-*` y at x on an edge between x and y means that x is not an ancestor of y, nor of S; (iv) a circle mark x `o-*` y at x on an edge between x and y means that there exists both a graph in the Markov equivalence class where x is ancestor of y or S, and one where x is not ancestor of y, nor of S. For further information on the interpretation of PAGs see e.g. (Zhang, 2008) and (Mooij and Claassen, 2020).

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 `skeleton(*, method="stable")` 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 `o-o` 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 o-o y` should be removed, one performs conditional indepedence 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 (2014). 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 (2008).

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, using the function `skeleton`, and the final skeleton, using the function `pdsep`. Thus, Anytime FCI performs fewer conditional independence tests than FCI. To use the Anytime algorithm, one sets `type = "anytime"` and needs to specify `m.max`, the maximum size of the conditioning sets.

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 (2014) 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, 2014). Colombo and Maathuis (2014) 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 (2014) for more details.

The FCI-JCI extension of FCI was introduced by Mooij et. al (2020). It is an implementation of

the *Joint Causal Inference* (JCI) framework that reduces causal discovery from several data sets corresponding to different contexts (e.g., observational and different interventional settings, or data measured in different labs or in different countries) to causal discovery from the pooled data (treated as a single 'observational' data set). Two types of variables are distinguished in the JCI framework: system variables (describing aspects of the system in some environment) and context variables (describing aspects of the environment of the system). Different assumptions regarding the causal relations between context variables and system variables can be made. The most common assumption (JCI Assumption 1: 'exogeneity') is that no system variable can affect any context variable. The second, less common, assumption (JCI Assumption 2: 'complete randomized context') is that there is no latent confounding between system and context. The third assumption (JCI Assumption 3: 'generic context model') is in fact a faithfulness assumption on the context distribution. The FCI-JCI extension can be used by specifying the subset of the variables that are designated as context variables with the `contextVars` argument, and by specifying the combination of JCI assumptions that is used with the `jci` argument. For the default values of these arguments, the JCI extension is not used. The only difference between the FCI-JCI extension and the standard FCI algorithm is that the background knowledge about the PAG implied by the JCI assumptions is exploited at several points in the FCI-JCI algorithm to enforce adjacencies between context variables (in case of JCI Assumption 3) and to orient certain edges adjacent to context variables (in case of JCI Assumptions 1, 2 or 3). The current JCI framework assumes that no selection bias is present, and therefore the FCI-JCI extension should be called with `selectionBias = FALSE`. For more details on FCI-JCI, and the general JCI framework, see Mooij et al. (2020).

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, Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Joris Mooij.

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See Also

`fciPlus` for a more efficient variation of FCI; `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`, `dsepTest` and `dsepAMTest` as examples for `indepTest`.

Examples

```
##################################################
## 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, doPdsep = FALSE)

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

## create the graph g
p <- 4
L <- 1 # '1' 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=3,weights=c(1))
edL[[3]] <- list(edges=5,weights=c(1))
edL[[4]] <- list(edges=5,weights=c(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 conditining 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
```

```
##################################################
## Joint Causal Inference Example
## Mooij et al. (2020), Fig. 43(a), p. 97
##################################################

# Encode MAG as adjacency matrix
p <- 8 # total number of variables
V <- c("Ca","Cb","Cc","X0","X1","X2","X3","X4") # 3 context variables, 5 system variables
# amat[i,j] = 0 iff no edge btw i,j
# amat[i,j] = 1 iff i *-o j
# amat[i,j] = 2 iff i *-> j
# amat[i,j] = 3 iff i *-- j
amat <- rbind(c(0,2,2,2,0,0,0,0),
              c(2,0,2,0,2,0,0,0),
              c(2,2,0,0,2,2,0,0),
              c(3,0,0,0,0,0,2,0),
              c(0,3,3,0,0,3,0,2),
              c(0,0,3,0,2,0,0,0),
              c(0,0,0,3,0,0,0,2),
              c(0,0,0,0,2,0,3,0))
rownames(amat)<-V
colnames(amat)<-V

# Make use of d-separation oracle as "independence test"
indepTest <- dsepAMTest
suffStat<-list(g=amat,verbose=FALSE)

# Derive PAG that represents the Markov equivalence class of the MAG with the FCI algorithm
# (assuming no selection bias)
fci.pag <- fci(suffStat, indepTest, alpha = 0.5, labels = V,
verbose=TRUE, selectionBias=FALSE)

# Derive PAG with FCI-JCI, the Joint Causal Inference extension of FCI
# (assuming no selection bias, and all three JCI assumptions)
fcijci.pag <- fci(suffStat, indepTest, alpha = 0.5, labels = V,
verbose=TRUE, contextVars=c(1,2,3), jci="123", selectionBias=FALSE)

# Report results
cat('True MAG:\n')
print(amat)
cat('PAG output by FCI:\n')
print(fci.pag@amat)
cat('PAG output by FCI-JCI:\n')
print(fcijci.pag@amat)

# Read off causal features from the FCI PAG
cat('Identified absence (-1) and presence (+1) of ancestral causal relations from FCI PAG:\n')
print(pag2anc(fci.pag@amat))
cat('Identified absence (-1) and presence (+1) of direct causal relations from FCI PAG:\n')
print(pag2edge(fci.pag@amat))
cat('Identified absence (-1) and presence (+1) of pairwise latent confounding from FCI PAG:\n')
print(pag2conf(fci.pag@amat))
```

```
# Read off causal features from the FCI-JCI PAG
cat('Identified absence (-1) and presence (+1) of ancestral causal relations from FCI-JCI PAG:\n')
print(pag2anc(fcijci.pag@amat))
cat('Identified absence (-1) and presence (+1) of direct causal relations from FCI-JCI PAG:\n')
print(pag2edge(fcijci.pag@amat))
cat('Identified absence (-1) and presence (+1) of pairwise latent confounding from FCI-JCI PAG:\n')
print(pag2conf(fcijci.pag@amat))
```

`fciAlgo-class` *Class "fciAlgo" of FCI Algorithm Results*

Description

This class of objects is returned by functions `fci()`, `rfci()`, `fciPlus`, and `dag2pag` and represent the estimated PAG (and sometimes properties of the algorithm). Objects of this class have methods for the functions `plot`, `show` and `summary`.

Usage

```
## S4 method for signature 'fciAlgo'
show(object)
## S3 method for class 'fciAlgo'
print(x, amat = FALSE, zero.print = ".", ...)

## S4 method for signature 'fciAlgo'
summary(object, amat = TRUE, zero.print = ".", ...)
## S4 method for signature 'fciAlgo,ANY'
plot(x, y, main = NULL, ...)
```

Arguments

`x, object`	a `"fciAlgo"` object.
`amat`	`logical` indicating if the adjacency matrix should be shown (printed) as well.
`zero.print`	string for printing `0` ('zero') entries in the adjacency matrix.
`y`	(generic `plot()` argument; unused).
`main`	main title, not yet supported.
`...`	optional further arguments (passed from and to methods).

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`: adjacency matrix; for the coding of the adjacency matrix see amatType

`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`, `fciPlus`, etc (see above); `pcAlgo`

Examples

```
## look at slots of the class
showClass("fciAlgo")

## Also look at the extensive examples in ?fci , ?fciPlus, etc !

## Not run:
## Suppose, fciObj is an object of class fciAlgo
## access slots by using the @ symbol
fciObj@amat   ## adjacency matrix
fciObj@sepset ## separation sets

## use show, summary and plot method
fciObj ## same as  show(fciObj)
show(fciObj)
summary(fciObj)
plot(fciObj)

## End(Not run)
```

`fciPlus` *Estimate a PAG with the FCI+ Algorithm*

Description

Estimate a Partial Ancestral Graph (PAG) from observational data, using the FCI+ (Fast Causal Inference) algorithm, or from a combination of data from different (e.g., observational and interventional) contexts, using the FCI+-JCI (Joint Causal Inference) extension.

Usage

```
fciPlus(suffStat, indepTest, alpha, labels, p, verbose=TRUE,
 selectionBias = TRUE, jci = c("0","1","12","123"), contextVars = NULL)
```

Arguments

`suffStat`	sufficient statistics: A named `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 with all relevant information, see above. The return value of `indepTest()` is the p-value of the test for conditional independence.
`alpha`	numeric significance level (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`.
`selectionBias`	If `TRUE`, allow for selection bias. If `FALSE`, selection bias is excluded by assumption and hence rules R5-R7, as in Zhang (2008), are disabled.
`jci`	String specifying the JCI assumptions that are used. It can be one of: **"0"** No JCI assumption is made (default), **"1"** JCI assumption 1 (no system variable causes any context variable), **"12"** JCI assumptions 1 and 2 (no system variable causes any context variable, and no system variable is confounded with any context variable), **"123"** JCI assumptions 1, 2 and 3 (no system variable causes any context variable, no system variable is confounded with any context variable, and all context variables are confounded but are not direct causes of each other). For more information, see Mooij et al. (2020).
`contextVars`	Subset of variable indices {1,...,p} that will be treated as context variables in the JCI extension of FCI+.
`verbose`	logical indicating if progress of the algorithm should be printed. The default is true, which used to be hard coded previously.

Details

A (possibly much faster) variation of FCI (Fast Causal Inference). For details, please see the references, and also `fci`.

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)

Emilija Perkovic, Markus Kalisch (<kalisch@stat.math.ethz.ch>) and Joris Mooij.

References

T. Claassen, J. Mooij, and T. Heskes (2013). Learning Sparse Causal Models is not NP-hard. In *UAI 2013, Proceedings of the 29th Conference on Uncertainty in Artificial Intelligence*

See Also

`fci` for estimating a PAG using the FCI algorithm.

Examples

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

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

## find PAG using the FCI+ algorithm on "Oracle"
suffStat <- list(C = cov2cor(trueCov(myDAG)), n = 10^9)
m.fci <- fciPlus(suffStat, indepTest=gaussCItest,
                 alpha = 0.9999, p=p)
summary(m.fci)

if (require(Rgraphviz)) {
  par(mfrow=c(1,2))
plot(myDAG)
plot(m.fci)
}

################################################
## Joint Causal Inference Example
## Mooij et al. (2020), Fig. 43(a), p. 97
################################################
```

```
# Encode MAG as adjacency matrix
p <- 8 # total number of variables
V <- c("Ca","Cb","Cc","X0","X1","X2","X3","X4") # 3 context variables, 5 system variables
# amat[i,j] = 0 iff no edge btw i,j
# amat[i,j] = 1 iff i *-o j
# amat[i,j] = 2 iff i *-> j
# amat[i,j] = 3 iff i *-- j
amat <- rbind(c(0,2,2,2,0,0,0,0),
              c(2,0,2,0,2,0,0,0),
              c(2,2,0,0,2,2,0,0),
              c(3,0,0,0,0,0,2,0),
              c(0,3,3,0,0,3,0,2),
              c(0,0,3,0,2,0,0,0),
              c(0,0,0,3,0,0,0,2),
              c(0,0,0,0,2,0,3,0))
rownames(amat)<-V
colnames(amat)<-V

# Make use of d-separation oracle as "independence test"
indepTest <- dsepAMTest
suffStat<-list(g=amat,verbose=FALSE)

# Derive PAG that represents the Markov equivalence class of the MAG with the FCI+ algorithm
# (assuming no selection bias)
# fci.pag <- fciPlus(suffStat, indepTest, alpha = 0.5, labels = V,
# selectionBias=FALSE,verbose=TRUE)

# Derive PAG with FCI+-JCI, the Joint Causal Inference extension of FCI
# (assuming no selection bias, and all three JCI assumptions)
# fcijci.pag <- fciPlus(suffStat, indepTest, alpha = 0.5, labels = V,
# selectionBias=FALSE, contextVars=c(1,2,3), jci="123", verbose=TRUE)

# Report results
# cat('True MAG:\n')
# print(amat)
# cat('PAG output by FCI+:\n')
# print(fci.pag@amat)
# cat('PAG output by FCI+-JCI:\n')
# print(fcijci.pag@amat)

# Read off causal features from the FCI PAG
#cat('Identified absence (-1) and presence (+1) of ancestral causal relations from FCI+ PAG:\n')
#print(pag2anc(fci.pag@amat))
#cat('Identified absence (-1) and presence (+1) of direct causal relations from FCI+ PAG:\n')
#print(pag2edge(fci.pag@amat))
#cat('Identified absence (-1) and presence (+1) of pairwise latent confounding from FCI+ PAG:\n')
#print(pag2conf(fci.pag@amat))

# Read off causal features from the FCI-JCI PAG
#cat('Identified absence (-1) and presence (+1) of ancestral causal relations from FCI+-JCI PAG:\n')
#print(pag2anc(fcijci.pag@amat))
#cat('Identified absence (-1) and presence (+1) of direct causal relations from FCI+-JCI PAG:\n')
#print(pag2edge(fcijci.pag@amat))
```

```
#cat('Ident. absence (-1) and presence (+1) of pairwise latent confounding from FCI+-JCI PAG:\n')
#print(pag2conf(fcijci.pag@amat))
```

`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 of type amat.cpdag representing the skeleton; since a skeleton consists only of undirected edges, g must be symmetric.
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
g <- 1*(g != 0) # wgts --> 0/1; still lower triangular
print.table(g, zero.print=".")
skel <- g + t(g) ## adjacency matrix of skeleton

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

---

gac *Test If Set Satisfies Generalized Adjustment Criterion (GAC)*

Description

This function tests if z satisfies the Generalized Adjustment Criterion (GAC) relative to (x,y) in the graph represented by adjacency matrix amat and interpreted as type (DAG, maximal PDAG, CPDAG, MAG, PAG). If yes, z can be used in covariate adjustment for estimating causal effects of x on y.

Usage

```
gac(amat, x, y, z, type = "pag")
```

Arguments

amat	adjacency matrix of type amat.cpdag or amat.pag
x, y, z	(integer) positions of variables in x, y or z in the adjacency matrix. x, y and z can be vectors representing several nodes.
type	string specifying the type of graph of the adjacency matrix amat. It can be a DAG (type="dag"), a PDAG (type="pdag") or a CPDAG (type="cpdag"); then the type of the adjacency matrix is assumed to be amat.cpdag. It can also be a MAG (type="mag"), or a PAG (type="pag"); then the type of the adjacency matrix is assumed to be amat.pag.

Details

This work is a generalization of the work of Shpitser et al. (2012) (necessary and sufficient criterion in DAGs/ADMGs) and van der Zander et al. (2014) (necessary and sufficient criterion in MAGs). Moreover, it is a generalization of the Generalized Backdoor Criterion (GBC) of Maathuis and

Colombo (2013): While GBC is sufficient but not necessary, GAC is both sufficient and necessary for DAGs, CPDAGs, MAGs and PAGs. For more details see Perkovic et al. (2015, 2017a, 2017b).

The motivation to find a set z that satisfies the GAC with respect to (x,y) is the following:

A set of variables z *satisfies the GAC relative to* (x,y) *in the given graph, if and only if the causal effect of* x *on* y *is identifiable by covariate adjustment and is given by*

$$P(Y|do(X = x)) = \sum_{Z} P(Y|X, Z) \cdot P(Z),$$

(for any joint distribution "compatible" with the graph; the formula is for discrete variables with straightforward modifications for continuous variables). This result allows to write post-intervention densities (the one written using Pearl's do-calculus) using only observational densities estimated from the data.

For z to satisfy the GAC relative to (x,y) and the graph, the following three conditions must hold:

(0) The graph is adjustment amenable relative to (x,y).

(1) The intersection of z and the forbidden set (explained in Perkovic et al. (2015, 2017b) is empty.

(2) All proper definite status non-causal paths in the graph from x to y are blocked by z.

It is important to note that there can be x and y for which there is no set Z that satisfies the GAC, but the total causal effect might be identifiable via some technique other than covariate adjustment.

For details on the GAC for DAGs, CPDAGs, PAGs see Perkovic et. al (2015,2017a). For details on the GAC for MAGs see van der Zander et. al (2014) and for details on the GAC for maximal PDAGs see Perkovic et. al (2017b).

For the coding of the adjacency matrix see amatType. The input matrix can either be of class matrix or of class amat.

Value

A list with three components:

gac	logical; TRUE if z satisfies the GAC relative to (x,y) in the graph represented by amat and type
res	logical vector of length three indicating if each of the three conditions (0), (1) and (2) are true
f	node positions of nodes in the forbidden set (see Perkovic et al. (2015, 2017b)

Author(s)

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

References

E. Perkovic, J. Textor, M. Kalisch and M.H. Maathuis (2015). A Complete Generalized Adjustment Criterion. In *Proceedings of UAI 2015.*

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E. Perkovic, M. Kalisch and M.H. Maathuis (2017b). Interpreting and using CPDAGs with background knowledge. In *Proceedings of UAI 2017*.

I. Shpitser, T. VanderWeele and J.M. Robins (2012). On the validity of covariate adjustment for estimating causal effects. In *Proceedings of UAI 2010*.

B. van der Zander, M. Liskiewicz and J. Textor (2014). Constructing separators and adjustment sets in ancestral graphs. In *Proceedings of UAI 2014*.

M.H. Maathuis and D. Colombo (2013). A generalized backdoor criterion. *Annals of Statistics* 43 1060-1088.

See Also

backdoor for the Generalized Backdoor Criterion, pc for estimating a CPDAG and fci and fciPlus for estimating a PAG.

Examples

```
## We reproduce the four examples in Perkovic et. al (2015, 2017a)

##############################
## Example 4.1 in Perkovic et. al (2015), Example 2 in Perkovic et. al (2017a)
##############################
mFig1 <- matrix(c(0,1,1,0,0,0, 1,0,1,1,1,0, 0,0,0,0,0,1,
                  0,1,1,0,1,1, 0,1,0,1,0,1, 0,0,0,0,0,0), 6,6)
type <- "cpdag"
x <- 3; y <- 6
## Z satisfies GAC :
gac(mFig1, x,y, z=c(2,4),    type)
gac(mFig1, x,y, z=c(4,5),    type)
gac(mFig1, x,y, z=c(4,2,1),  type)
gac(mFig1, x,y, z=c(4,5,1),  type)
gac(mFig1, x,y, z=c(4,2,5),  type)
gac(mFig1, x,y, z=c(4,2,5,1),type)
## Z does not satisfy GAC :
gac(mFig1,x,y, z=2,    type)
gac(mFig1,x,y, z=NULL, type)

##############################
## Example 4.2 in Perkovic et. al (2015), Example 3 in Perkovic et. al (2017a)
##############################
mFig3a <- matrix(c(0,1,0,0, 1,0,1,1, 0,1,0,1, 0,1,1,0), 4,4)
mFig3b <- matrix(c(0,2,0,0, 3,0,3,3, 0,2,0,3, 0,2,2,0), 4,4)
mFig3c <- matrix(c(0,3,0,0, 2,0,3,3, 0,2,0,3, 0,2,2,0), 4,4)
type <- "pag"
x <- 2; y <- 4
## Z does not satisfy GAC
gac(mFig3a,x,y, z=NULL, type) ## not amenable rel. to (X,Y)
gac(mFig3b,x,y, z=NULL, type) ## not amenable rel. to (X,Y)
## Z satisfies GAC
gac(mFig3c,x,y, z=NULL, type) ## amenable rel. to (X,Y)

##############################
```

```
## Example 4.3 in Perkovic et. al (2015), Example 4 in Perkovic et. al (2017a)
##############################
mFig4a <- matrix(c(0,0,1,0,0,0, 0,0,1,0,0,0, 2,2,0,3,3,2,
                   0,0,2,0,2,2, 0,0,2,1,0,2, 0,0,1,3,3,0), 6,6)
mFig4b <- matrix(c(0,0,1,0,0,0, 0,0,1,0,0,0, 2,2,0,0,3,2,
                   0,0,0,0,2,2, 0,0,2,3,0,2, 0,0,2,3,2,0), 6,6)
type <- "pag"
x <- 3; y <- 4
## both PAGs are amenable rel. to (X,Y)
## Z satisfies GAC in Fig. 4a
gac(mFig4a,x,y, z=6, type)
gac(mFig4a,x,y, z=c(1,6), type)
gac(mFig4a,x,y, z=c(2,6), type)
gac(mFig4a,x,y, z=c(1,2,6), type)
## no Z satisfies GAC in Fig. 4b
gac(mFig4b,x,y, z=NULL, type)
gac(mFig4b,x,y, z=6, type)
gac(mFig4b,x,y, z=c(5,6), type)

##############################
## Example 4.4 in Perkovic et. al (2015), Example 8 in Perkovic et. al (2017a)
##############################
mFig5a <- matrix(c(0,1,0,0,0, 1,0,1,0,0, 0,0,0,0,1, 0,0,1,0,0, 0,0,0,0,0), 5,5)
type <- "cpdag"
x <- c(1,5); y <- 4
## Z satisfies GAC
gac(mFig5a,x,y, z=c(2,3), type)
## Z does not satisfy GAC
gac(mFig5a,x,y, z=2, type)

mFig5b <- matrix(c(0,1,0,0,0,0,0, 2,0,2,3,0,3,0, 0,1,0,0,0,0,0,
0,2,0,0,3,0,0, 0,0,0,2,0,2,3, 0,2,0,0,2,0,0, 0,0,0,0,2,0,0), 7,7)
type <- "pag"
x<-c(2,7); y<-6
## Z satisfies GAC
gac(mFig5b,x,y, z=c(4,5), type)
gac(mFig5b,x,y, z=c(4,5,1), type)
gac(mFig5b,x,y, z=c(4,5,3), type)
gac(mFig5b,x,y, z=c(1,3,4,5), type)
## Z does not satisfy GAC
gac(mFig5b,x,y, z=NULL, type)

##############################
## Example 4.7 in Perkovic et. al (2017b)
##############################
mFig3a <- matrix(c(0,1,0,0, 1,0,1,1, 0,1,0,1, 0,1,1,0), 4,4)
mFig3b <- matrix(c(0,1,0,0, 0,0,1,1, 0,0,0,1, 0,0,1,0), 4,4)
mFig3c <- matrix(c(0,0,0,0, 1,0,1,0, 0,1,0,1, 0,1,1,0), 4,4)
type <- "pdag"
x <- 2; y <- 4
## Z does not satisfy GAC
gac(mFig3a,x,y, z=NULL, type) ## not amenable rel. to (X,Y)
gac(mFig3c,x,y, z=NULL, type) ## amenable rel. to (X,Y), but no set can block X <- Y
```

```
## Z satisfies GAC
gac(mFig3b,x,y, z=NULL, type) ## amenable rel. to (X,Y)
```

---

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 maximal p-value of all conditional independence tests for edge $i - -j$.

Author(s)

Martin Maechler

See Also

"pcAlgo" and "fciAlgo".

Examples

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

GaussL0penIntScore-class

Class "GaussL0penIntScore"

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 ℓ_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 λ 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

```
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@bfh.ch>)

See Also

`gies`, `simy`, `GaussL0penObsScore`, `Score`

Examples

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

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

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

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

GaussL0penObsScore-class
Class "GaussL0penObsScore"

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 ℓ_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 λ 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

```
new("GaussL0penObsScore",
  data = matrix(1, 1, 1),
  lambda = 0.5*log(nrow(data)),
  intercept = TRUE,
  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@bfh.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.)
```

GaussParDAG-class *Class* "GaussParDAG" *of Gaussian Causal Models*

Description

The "GaussParDAG" class represents a Gaussian causal model.

Details

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@bfh.ch>)

References

A. Hauser and P. Bühlmann (2012). Characterization and greedy learning of interventional Markov equivalence classes of directed acyclic graphs. *Journal of Machine Learning Research* **13**, 2409–2464.

M. Kalisch and P. Buehlmann (2007). Estimating high-dimensional directed acyclic graphs with the PC-algorithm. *Journal of Machine Learning Research* **8**, 613–636.

K.B. Korb, L.R. Hope, A.E. Nicholson, and K. Axnick (2004). Varieties of causal intervention. *Proc. of the Pacific Rim International Conference on Artificial Intelligence (PRICAI 2004)*, 322–331

See Also

ParDAG

Examples

```
set.seed(307)
myDAG <- r.gauss.pardag(p = 5, prob = 0.4)
(wm <- myDAG$weight.mat())
m <- as(myDAG, "matrix") # TRUE/FALSE adjacency matrix
```

```
symnum(m)
stopifnot(identical(unname( m ),
                    unname(wm != 0)))
myDAG$err.var()
myDAG$intercept()
myDAG$set.intercept(runif(5, min=3, max=4))
myDAG$intercept()
if (require(Rgraphviz)) plot(myDAG)
```

---

gds *Greedy DAG Search to Estimate Markov Equivalence Class of DAG*

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(score, labels = score$getNodes(), targets = score$getTargets(),
    fixedGaps = NULL, phase = c("forward", "backward", "turning"),
    iterate = length(phase) > 1, turning = TRUE, maxDegree = integer(0),
    verbose = FALSE, ...)
```

Arguments

`score`	An instance of a class derived from `Score`.
`labels`	Node labels; by default, they are determined from the scoring object.
`targets`	A `list` of intervention targets (cf. details). A list of vectors, each vector listing the vertices of one intervention target.
`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.
`phase`	Character vector listing the phases that should be used; possible values: `forward`, `backward`, and `turning` (cf. details).
`iterate`	Logical indicating whether the phases listed in the argument `phase` should be iterated more than once (`iterate = TRUE`) or not.
`turning`	Setting `turning = TRUE` is equivalent to setting `phases = c("forward", "backward")` and `iterate = FALSE`; the use of the argument `turning` is deprecated.
`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

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 $a \longrightarrow b$ 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.

The phases that are actually run are specified with the argument `phase`. GDS cycles through the specified phases until no augmentation of the score is possible any more if `iterate = TRUE`. 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 straight-forward 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@bfh.ch>)

References

D.M. Chickering (2002). Optimal structure identification with greedy search. *Journal of Machine Learning Research* **3**, 507–554

A. Hauser and P. Bühlmann (2012). Characterization and greedy learning of interventional Markov equivalence classes of directed acyclic graphs. *Journal of Machine Learning Research* **13**, 2409–2464.

See Also

gies, ges, Score, EssGraph

Examples

```
## 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(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")
}
```

ges *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

```
ges(score, labels = score$getNodes(),
    fixedGaps = NULL, adaptive = c("none", "vstructures", "triples"),
    phase = c("forward", "backward", "turning"), iterate = length(phase) > 1,
    turning = NULL, maxDegree = integer(0), verbose = FALSE, ...)
```

Arguments

score	An instance of a class derived from Score which only accounts for observational data. If the dataset is high-dimensional (p>=n) ges might not be able to terminate.
labels	Node labels; by default, they are determined from the scoring object.
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.
adaptive	indicating whether constraints should be adapted to newly detected v-structures or unshielded triples (cf. details).
phase	Character vector listing the phases that should be used; possible values: forward, backward, and turning (cf. details).
iterate	Logical indicating whether the phases listed in the argument phase should be iterated more than once (iterate = TRUE) or not.
turning	Setting turning = TRUE is equivalent to setting phases = c("forward", "backward") and iterate = FALSE; the use of the argument turning is deprecated.
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 $a \longrightarrow b \longleftarrow c$). 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 $a \longrightarrow b$ 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.

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 if `iterate = TRUE`. Note that the turning phase 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. The original algorithm of Chickering (2002) is reproduced with `phase = c("forward", "backward")` and `iterate = FALSE`.

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.

Using the argument `fixedGaps`, one can make sure that certain edges will *not* be present in the resulting essential graph: if the entry `[i, j]` of the matrix passed to `fixedGaps` is `TRUE`, there will be no edge between nodes i and j. Using this argument can speed up the execution of GIES and allows the user to account for previous knowledge or other constraints. The argument `adaptive` can be used to relax the constraints encoded by `fixedGaps` according to a modification of GES called

ARGES (adaptively restricted greedy equivalence search) which has been presented in Nandy, Hauser and Maathuis (2015):

- When `adaptive = "vstructures"` and the algorithm introduces a new v-structure $a \longrightarrow b \longleftarrow c$ in the forward phase, then the edge $a - c$ is removed from the list of fixed gaps, meaning that the insertion of an edge between a and c becomes possible even if it was forbidden by the initial matrix passed to `fixedGaps`.
- When `adaptive = "triples"` and the algorithm introduces a new unshielded triple in the forward phase (i.e., a subgraph of three nodes a, b and c where a and b as well as b and c are adjacent, but a and c are not), then the edge $a - c$ is removed from the list of fixed gaps.

With one of the adaptive modifications, the successive application of a skeleton estimation method and GES restricted to an estimated skeleton still gives a *consistent* estimator of the DAG, which is not the case without the adaptive modification.

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@bfh.ch>)

References

D.M. Chickering (2002). Optimal structure identification with greedy search. *Journal of Machine Learning Research* **3**, 507–554

A. Hauser and P. Bühlmann (2012). Characterization and greedy learning of interventional Markov equivalence classes of directed acyclic graphs. *Journal of Machine Learning Research* **13**, 2409–2464.

P. Nandy, A. Hauser and M. Maathuis (2015). Understanding consistency in hybrid causal structure learning. *arXiv preprint* 1507.02608

P. Spirtes, C.N. Glymour, and R. Scheines (2000). *Causation, Prediction, and Search*, MIT Press, Cambridge (MA).

See Also

`pc`, `Score`, `EssGraph`

Examples

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

## Define the score (BIC)
score <- new("GaussL0penObsScore", gmG8$x)

## Estimate the essential graph
ges.fit <- ges(score)

## Plot the estimated essential graph and the true DAG
if (require(Rgraphviz)) {
  par(mfrow=c(1,2))
  plot(ges.fit$essgraph, main = "Estimated CPDAG")
  plot(gmG8$g, main = "True DAG")
  str(ges.fit, max=2)
}
## alternative:
if (require(Matrix)) {
  as(as(ges.fit$essgraph,"graphNEL"),"Matrix")
}
```

---

getGraph *Get the "graph" Part or Aspect of R Object*

Description

Get the graph-class 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-class 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

See Also

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

Examples

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

---

getNextSet *Iteration through a list of all combinations of choose(n,k)*

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

```
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:

nextSet	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

```
## 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(score, labels = score$getNodes(), targets = score$getTargets(),
     fixedGaps = NULL, adaptive = c("none", "vstructures", "triples"),
     phase = c("forward", "backward", "turning"), iterate = length(phase) > 1,
     turning = NULL, maxDegree = integer(0), verbose = FALSE, ...)
```

Arguments

score	An R object inheriting from Score.
labels	Node labels; by default, they are determined from the scoring object.
targets	A list of intervention targets (cf. details). A list of vectors, each vector listing the vertices of one intervention target.
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.
adaptive	indicating whether constraints should be adapted to newly detected v-structures or unshielded triples (cf. details).
phase	Character vector listing the phases that should be used; possible values: forward, backward, and turning (cf. details).
iterate	Logical indicating whether the phases listed in the argument phase should be iterated more than once (iterate = TRUE) or not.
turning	Setting turning = TRUE is equivalent to setting phases = c("forward", "backward") and iterate = FALSE; the use of the argument turning is deprecated.
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 $r \cdot n_v$, 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

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 $a \longrightarrow b$ 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.

The phases that are actually run are specified with the argument `phase`. GIES cycles through the specified phases until no augmentation of the score is possible any more if `iterate = TRUE`. 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.

Using the argument `fixedGaps`, one can make sure that certain edges will *not* be present in the resulting essential graph: if the entry `[i, j]` of the matrix passed to `fixedGaps` is `TRUE`, there will be no edge between nodes i and j. Using this argument can speed up the execution of GIES and allows the user to account for previous knowledge or other constraints. The argument `adaptive` can be used to relax the constraints encoded by `fixedGaps` as follows:

- When `adaptive = "vstructures"` and the algorithm introduces a new v-structure $a \longrightarrow b \longleftarrow c$ in the forward phase, then the edge $a - c$ is removed from the list of fixed gaps, meaning that the insertion of an edge between a and c becomes possible even if it was forbidden by the initial matrix passed to `fixedGaps`.
- When `adaptive = "triples"` and the algorithm introduces a new unshielded triple in the forward phase (i.e., a subgraph of three nodes a, b and c where a and b as well as b and c are adjacent, but a and c are not), then the edge $a - c$ is removed from the list of fixed gaps.

This modifications of the forward phase of GIES are inspired by the analog modifications in the forward phase of GES, which makes the successive application of a skeleton estimation method and GES restricted to an estimated skeleton a *consistent* estimator of the DAG (cf. Nandy, Hauser and Maathuis, 2015).

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@bfh.ch>)

References

D.M. Chickering (2002). Optimal structure identification with greedy search. *Journal of Machine Learning Research* **3**, 507–554

A. Hauser and P. Bühlmann (2012). Characterization and greedy learning of interventional Markov equivalence classes of directed acyclic graphs. *Journal of Machine Learning Research* **13**, 2409–2464.

P. Nandy, A. Hauser and M. Maathuis (2015). Understanding consistency in hybrid causal structure learning. *arXiv preprint* 1507.02608

See Also

`ges`, `Score`, `EssGraph`

Examples

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

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

## Estimate the essential graph
gies.fit <- gies(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")
}
```

gmB *Graphical Model 5-Dim Binary Example Data*

Description

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

gmD *Graphical Model Discrete 5-Dim Example Data*

Description

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

Usage

```
data(gmD)
```

Format

A list of two components

x: a data.frame with 5 columns X1 .. X5 each coding a discrete variable (aka factor) with interagesInt [1:10000, 1:5] 2 2 1 1 1 2 2 0 2 0 ...

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

where x is the data matrix and g is the DAG from which the data were generated.

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

```
data(gmD)
str(gmD, max=1)
if(require("Rgraphviz"))
  plot(gmD$ g, main = "gmD $ g --- the DAG of the gmD (10'000 x 5 discrete data)")
## >>>  1 --> 3 <-- 2 --> 4 --> 5
str(gmD$x)
## The number of unique values of each variable:
sapply(gmD$x, function(v) nlevels(as.factor(v)))
## X1 X2 X3 X4 X5
##  3  2  3  4  2
lapply(gmD$x, table) ## the (marginal) empirical distributions
## $X1
##    0    1    2
## 1933 3059 5008
##
## $X2
##    0    1
## 8008 1992
##
## $X3
## .....
```

---

gmG *Graphical Model 8-Dimensional Gaussian Example Data*

Description

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

Usage

```
data(gmG)
```

Format

gmG and gmG8 are each a list of two components

x: a numeric matrix 5000×8.

g: a graph, i.e., of formal class "graphNEL" from package **graph** with 6 slots
.. ..@ nodes : chr [1:8] "1" "2" "3" "4" ...
.. ..@ edgeL :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 gmG: In the previous version, the data generation wgtMatrix had the non-zero weights in reversed order for each node. On the other hand, for gmG8, the correct weights were used in all cases

Source

The data set is identical to the one generated by

```
## 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.compatible=TRUE), g = gGtrue)
gmG8 <- list(x = rmvDAG(n, gGtrue),                       g = gGtrue)
```

Examples

```
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
  if (require(Rgraphviz)) plot(gmG$g)
  pairs(gmG$x, gap = 0,
 panel=function(...) smoothScatter(..., add=TRUE))
}
```

gmI *Graphical Model 7-dim IDA Data Examples*

Description

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

Usage

```
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

```
## 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

```
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
  if (require(Rgraphviz)) plot(gmI $ g)
  pairs(gmI$x, 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.

g: 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

```
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

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

---

gmL *Latent Variable 4-Dim Graphical Model Data Example*

Description

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

Usage

```
data(gmL)
```

Format

The format is a list of 2 components

x: $ x: 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: $ 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 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

```
## 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

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

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

pairs(gmL $x) # the data
```

---

ida *Estimate Multiset of Possible Joint Total Causal Effects*

Description

`ida()` estimates the multiset of possible joint total causal effects of variables (`X`) onto variables (`Y`) from observational data via adjustment.

Usage

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

Arguments

`x.pos`, `x`	Positions of variables `X` in the covariance matrix.
`y.pos`, `y`	Positions of variables `Y` in the covariance matrix.
`mcov`	Covariance matrix that was used to estimate `graphEst`.
`graphEst`	Estimated CPDAG or PDAG. The CPDAG is typically from `pc()`: If the result of `pc` is `pc.fit`, the estimated CPDAG can be obtained by `pc.fit@graph`. A PDAG can be obtained from the CPDAG by adding background knowledge using `addBgKnowledge()`.

`method` Character string specifying the method with default `"local"`.

`"global"`: The algorithm considers all undirected edges in the CPDAG or PDAG, using the possible parents as adjustment sets to estimate *all* possible causal effects. It is hence *slow* and can only be applied to singleton `X`.

`"local"`: The algorithm only considers edges in the neighborhood of `X` in the CPDAG or PDAG, using the possible parents as adjustment sets to estimate the *unique* possible causal effects. It is hence much *faster* than `"global"` and can only be applied to singleton `X`.

`"optimal"`: The algorithm considers only those edges necessary to compute the possible optimal valid adjustment sets, using these as adjustment sets to estimate the *unique* possible causal effects. It is hence *faster* than the `"global"` option but also slower than `"local"`. It provides more efficient estimates than both alternatives but is also more sensitive to faulty graph estimates. Can be applied to sets `X`.

See details below.

`y.notparent` Logical; for singleton `X` and `Y`. If true, any edge between `X` and `Y` is assumed to be of the form `X->Y`. Not implemented for the `method="optimal"`

`verbose` If TRUE, details on the regressions are printed.

`all.dags` All DAGs in the equivalence class represented by the CPDAG or PDAG can be precomputed by `pdag2allDags()` and passed via this argument. In that case, `pdag2allDags(..)` is not called internally. This option is only relevant when using `method="global"`.

`type` Type of graph `"graphEst"`; can be of type `"cpdag"` or `"pdag"` (e.g. a CPDAG with background knowledge from Meek, 1995)

Details

It is assumed that we have observational data from a multivariate Gaussian distribution faithful to the true (but unknown) underlying causal DAG (without hidden variables). Under these assumptions, this function estimates the multiset of possible total joint effects of `X` on `Y`. Here the total joint effect of $\mathtt{X} = (X_1, X_2)$ on `Y` is defined via Pearl's do-calculus as the vector $(E[Y|do(X_1 = x_1 + 1, X_2 = x_2)] - E[Y|do(X_1 = x_1, X_2 = x_2)], E[Y|do(X_1 = x_1, X_2 = x_2 + 1)] - E[Y|do(X_1 = x_1, X_2 = x_2)])$, with a similar definition for more than two variables. These values are equal to the partial derivatives (evaluated at x_1, x_2) of $E[Y|do(X = x_1', X_2 = x_2')]$ with respect to x_1' and x_2'. Moreover, under the Gaussian assumption, these partial derivatives do not depend on the values at which they are evaluated.

We estimate a *set* of possible joint total causal effects instead of the unique joint 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 `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 adjusting for a valid adjustment set.

For example, if `X` and `Y` are singleton and `Y` is not a parent of `X`, we can take the regression coefficient of `X` in the regression `lm(Y ~ X + pa(X,G))`, where `pa(X,G)` denotes the parents of `X` in the DAG G; if `Y` is a parent of `X` in G, we can 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 possible total joint 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 `method="global"`, the method as described above is carried out, where all DAGs in the equivalene class of the estimated CPDAG or PDAG `graphEst` are computed using the function `pdag2allDags`. The parent set for each DAG is then used to estimate the corresponding possible total causal effect. This method is suitable for small graphs (say, up to 10 nodes) and can only be used for singleton X.

If `method="local"`, we only consider all valid possible directions of undirected edges that have X as an endpoint.

In the case of a CPDAG, we consider all possible directions of undirected edges that have X as an endpoint, such that no new v-structure is created. Maathuis, Kalisch and Buehlmann (2009) showed that there is at least one DAG in the equivalence class for each such local configuration. Hence, the procedure is truly local in this setting.

In the case of a PDAG, we need to verify for all possible directions whether they lead to an amenable max. PDAG if we apply Meek's orientation rules. In this setting the complexity of the `"local"` method is similar to the `"optimal"` one and it is not truly local. For details see Section 4.2 in Perkovic, Kalisch and Maathuis (2017).

We estimate the total causal effect of X on Y for each valid configuration as above, using linear regression adjusting for the correspoding possible parents. As we adjust for the same sets as in the `"global"` method, it follows that the multisets of total causal effects of the two methods have the same unique values. They may, however, have different multiplicities.

Since the parents of X are usually an inefficient valid adjustment set we provide a third method, that uses different adjustment sets.

If `method="optimal"`, we do not determine all DAGs in the equivalence class of the CPDAG or PDAG. Instead, we only direct edges until obtaining an amenable PDAG, which is sufficient for computing the optimal valid adjustment set. Each amenable PDAG can be obtained by orienting the neighborhood of X and then applying Meek's orientation rules, similar to the `"local"` method for PDAGs. This can be done faster than the `"global"` method but is slower than the `"local"` method, especially for CPDAGs. For details see Witte, Henckel, Maathuis and Didelez (2019).

For each amenable PDAG the corresponding optimal valid adjustment set is computed. The optimal set is a valid adjustment set irrespectively of whether X is a singleton. Hence, as opposed to the other two, this method can be applied to sets X. Sometimes, however, a joint total causal effect cannot be estimated via adjustment. In these cases we recommend use of the pcalg function `jointIda`.

We then estimate the joint total causal effect of X on Y for each valid configuration with linear regression, adjusting for the possible optimal sets. If the estimated graph is correct, each of these regressions is guaranteed to be more efficient than the corresponding linear regression with any other valid adjustment set (see Henckel, Perkovic and Maathuis (2019) for more details). The estimates are, however, more sensitive to graph estimation errors than the ones obtained with the other two methods. If X is a singleton, the output of this method is a multiset of the same size as the output of the `"local"` method.

For example, a CPDAG may represent eight DAGs, and the "global" method may produce an estimate of the multiset of possible total effects {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" and "optimal" methods, on the other hand, may prodcue estimates of the set {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 for all three methods are identical implies that summary measures of the multiset that only depend on the unique values (such as the minimum absolute value) can be estimated with all three.

Value

A list of length |Y| of matrices, each containing the possible joint total causal effect of X on one node in Y.

Author(s)

Markus Kalisch (<kalisch@stat.math.ethz.ch>), Emilija Perkovic and Leonard Henckel

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See Also

jointIda for estimating the multiset of possible total *joint* effects; idaFast for faster estimation of the multiset of possible total causal effects for several target variables.

pc for estimating a CPDAG. addBgKnowledge for obtaining a PDAG from CPDAG and background knowledge.

Examples

```
## Simulate the true DAG
suppressWarnings(RNGversion("3.5.0"))
set.seed(123)
p <- 10
myDAG <- randomDAG(p, prob = 0.2) ## true DAG
myCPDAG <- dag2cpdag(myDAG) ## true CPDAG
myPDAG <- addBgKnowledge(myCPDAG,2,3) ## true PDAG with background knowledge 2 -> 3
covTrue <- trueCov(myDAG) ## true covariance matrix

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

## estimate CPDAG and PDAG -- see  help(pc)
suffStat <- list(C = cor(dat), n = n)
pc.fit <- pc(suffStat, indepTest = gaussCItest, p=p, alpha = 0.01)
pc.fit.pdag <- addBgKnowledge(pc.fit@graph,2,3)

if (require(Rgraphviz)) {
  ## plot the true and estimated graphs
  par(mfrow = c(1,3))
  plot(myDAG, main = "True DAG")
  plot(pc.fit, main = "Estimated CPDAG")
  plot(pc.fit.pdag, main = "Max. PDAG")
}

## Supppose that we know the true CPDAG and covariance matrix
(l.ida.cpdag <- ida(3,10, covTrue, myCPDAG, method = "local", type = "cpdag"))
(o.ida.cpdag <- ida(3,10, covTrue, myCPDAG, method = "optimal", type = "cpdag"))
## Not run: (g.ida.cpdag <- ida(3,10, covTrue, myCPDAG, method = "global", type = "cpdag"))
## All three methods produce the same unique values.

## Supppose that we know the true PDAG and covariance matrix
(l.ida.pdag <- ida(3,10, covTrue, myPDAG, method = "local", type = "pdag"))
(o.ida.pdag <- ida(3,10, covTrue, myPDAG, method = "optimal", type = "pdag"))
## Not run: (g.ida.pdag <- ida(3,10, covTrue, myPDAG, method = "global", type = "pdag"))
## All three methods produce the same unique values.

## From the true DAG, we can compute the true causal effect of 3 on 10
(ce.3.10 <- causalEffect(myDAG, 10, 3))
## Indeed, this value is contained in the values found by all methods

## When working with data we have to use the estimated CPDAG and
## the sample covariance matrix
(l.ida.est.cpdag <- ida(3,10, cov(dat), pc.fit@graph, method = "local", type = "cpdag"))
(o.ida.est.cpdag <- ida(3,10, cov(dat), pc.fit@graph, method = "optimal", type = "cpdag"))
## Not run: (g.ida.est.cpdag <- ida(3,10, cov(dat), pc.fit@graph,
method = "global", type = "cpdag"))
## End(Not run)
## The unique values of the local and the global method are still identical.
## While not identical, the values of the optimal method are very similar.
```

```
## The true causal effect is contained in all three sets, up to a small
## estimation error (0.118 vs. 0.112 with true value 0.114)

## Similarly, when working with data and background knowledge we have to use the estimated PDAG and
## the sample covariance matrix
(l.ida.est.pdag <- ida(3,10, cov(dat), pc.fit.pdag, method = "local", type = "pdag"))
(o.ida.est.pdag <- ida(3,10, cov(dat), pc.fit.pdag, method = "optimal", type = "pdag"))
## Not run: (g.ida.est.pdag <- ida(3,10, cov(dat), pc.fit.pdag, method = "global", type = "pdag"))
## The unique values of the local and the global method are still identical.
## While not necessarily identical, the values of the optimal method will be similar.

## The true causal effect is contained in both sets, up to a small estimation error

## All three can also be applied to sets y.
(l.ida.cpdag.2 <- ida(3,c(6,10), cov(dat), pc.fit@graph, method = "local", type = "cpdag"))
(o.ida.cpdag.2 <- ida(3,c(6,10), cov(dat), pc.fit@graph, method = "optimal", type = "cpdag"))
## Not run: (g.ida.cpdag.2 <- ida(3,c(6,10), cov(dat), pc.fit@graph,
method = "global", type = "cpdag"))
## End(Not run)
## For the methods local and global we recommend use of idaFast in this case for better performance.

## Note that only the optimal method can be appplied to sets x.
(o.ida.cpdag.2 <- ida(c(2,3),10, cov(dat), pc.fit@graph, method = "optimal", type = "cpdag"))
```

`idaFast` *Multiset of Possible Total Causal Effects for Several Target Var.s*

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

```
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

```
## 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)

## estimate CPDAG (see help on the function "pc")
suffStat <- list(C = cor(dat), n = n)
pc.fit <- pc(suffStat, indepTest = gaussCItest, 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 combinded 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 `fciAlgo` objects, as those need different edge marks.

Author(s)

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See Also

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

Examples

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

## define sufficient statistics
suffStat <- list(C = cor(gmG8$x), n = n)
## estimate CPDAG
pc.fit <- pc(suffStat, indepTest = gaussCItest,
             alpha = 0.01, labels = V, verbose = TRUE)

## Edge list
showEdgeList(pc.fit)

## Adjacency matrix
showAmat(pc.fit)

## Plot using package igraph; show estimated CPDAG:
iplotPC(pc.fit)
```

---

isValidGraph *Check for a DAG, CPDAG or a maximally oriented PDAG*

Description

Check whether the adjacency matrix `amat` matches the specified `type`.

Usage

```
isValidGraph(amat, type = c("pdag", "cpdag", "dag"), verbose = FALSE)
```

Arguments

`amat`	adjacency matrix of type `amat.cpdag` (see `amatType`)
`type`	string specifying the type of graph of the adjacency matrix amat. It can be a DAG (`type="dag"`), a CPDAG (`type="cpdag"`) or a maximally oriented PDAG (`type="pdag"`) from Meek (1995).
`verbose`	If TRUE, detailed output on why the graph might not be valid is provided.

Details

For a given adjacency matrix `amat` and graph `type`, this function checks whether the two match.

For `type = "dag"` we require that `amat` does NOT contain directed cycles.

For `type = "cpdag"` we require that `amat` does NOT contain directed or partially directed cycles. We also require that the undirected part of the CPDAG (represented by `amat`) is made up of chordal components and that our graph is maximally oriented according to rules from Meek (1995).

For type = "pdag" we require that amat does NOT contain directed cycles. We also require that the PDAG is maximally oriented according to rules from Meek (1995). Additionally, we require that the adjacency matrix amat1 of the CPDAG corresponding to our PDAG (represented by amat), satisfies isValidGraph(amat = amat1, type = "cpdag") == TRUE and that there is no mismatch in the orientations implied by amat and amat1. We obtain amat1 by extracting the skeleton and v-structures from amat and then closing the orientation rules from Meek (1995).

Value

TRUE, if the adjacency matrix amat is of the type specified and FALSE, otherwise.

Author(s)

Emilija Perkovic and Markus Kalisch

References

C. Meek (1995). Causal inference and causal explanation with background knowledge, In Proceedings of UAI 1995, 403-410.

Examples

```
## a -> b -> c
amat <- matrix(c(0,1,0, 0,0,1, 0,0,0), 3,3)
colnames(amat) <- rownames(amat) <- letters[1:3]
## graph::plot(as(t(amat), "graphNEL"))
isValidGraph(amat = amat, type = "dag") ## is a valid DAG
isValidGraph(amat = amat, type = "cpdag") ## not a valid CPDAG
isValidGraph(amat = amat, type = "pdag") ## is a valid PDAG

## a -- b -- c
amat <- matrix(c(0,1,0, 1,0,1, 0,1,0), 3,3)
colnames(amat) <- rownames(amat) <- letters[1:3]
## plot(as(t(amat), "graphNEL"))
isValidGraph(amat = amat, type = "dag") ## not a valid DAG
isValidGraph(amat = amat, type = "cpdag") ## is a valid CPDAG
isValidGraph(amat = amat, type = "pdag") ## is a valid PDAG

## a -- b -- c -- d -- a
amat <- matrix(c(0,1,0,1, 1,0,1,0, 0,1,0,1, 1,0,1,0), 4,4)
colnames(amat) <- rownames(amat) <- letters[1:4]
## plot(as(t(amat), "graphNEL"))
isValidGraph(amat = amat, type = "dag") ## not a valid DAG
isValidGraph(amat = amat, type = "cpdag") ## not a valid CPDAG
isValidGraph(amat = amat, type = "pdag") ## not a valid PDAG
```

jointIda *Estimate Multiset of Possible Total Joint Effects*

Description

jointIda() estimates the multiset of possible total joint effects of a set of intervention variables (X) on another variable (Y) from observational data. This is a version of ida that allows multiple simultaneous interventions.

Usage

```
jointIda(x.pos, y.pos, mcov, graphEst = NULL, all.pasets = NULL,
         technique = c("RRC", "MCD"), type = c("pdag", "cpdag", "dag"))
```

Arguments

x.pos	(integer vector) positions of the intervention variables X in the covariance matrix.
y.pos	(integer) position of variable Y in the covariance matrix. (y.pos can also be an integer vector, see Note.)
mcov	(estimated) covariance matrix.
graphEst	(graphNEL object) Estimated CPDAG or PDAG. The CPDAG is typically from pc(): If the result of pc is pc.fit, the estimated CPDAG can be obtained by pc.fit@graph. The PDAG can be obtained from CPDAG by adding background knowledge using addBgKnowledge(). graphEst can only be considered if all.pasets is NULL.
all.pasets	(an optional argument and the default is NULL) A list where each element is a list of size length(x.pos). Each sub-list all.pasets[[i]] contains possible parent sets of x.pos in the same order, i.e., all.pasets[[i]][[j]] is a possible parent set of x.pos[j]. This option can be used if possible parent sets of the intervention variables are known.
technique	character string specifying the technique that will be used to estimate the total joint causal effects (given the parent sets), see details below. "RRC": Recursive regressions for causal effects. "MCD": Modifying the Cholesky decomposition.
type	Type of graph "graphEst"; can be of type "cpdag", "pdag" (e.g. a CPDAG with background knowledge from Meek, 1995) or "dag".

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 joint effects of X on Y. Here the total joint effect of $X = (X_1, X_2)$ on Y is defined via Pearl's do-calculus as the vector $(E[Y|do(X_1 = x_1 + 1, X_2 = x_2)] - E[Y|do(X_1 = x_1, X_2 = x_2)], E[Y|do(X_1 = x_1, X_2 = x_2 + 1)] - E[Y|do(X_1 = x_1, X_2 = x_2)])$, with a similar definition for more than two variables. These values are equal to the partial

derivatives (evaluated at (x_1, x_2)) of $E[Y|do(X = x_1', X_2 = x_2')]$ with respect to x_1' and x_2'. Moreover, under the Gaussian assumption, these partial derivatives do not depend on the values at which they are evaluated.

We estimate a *multiset* of possible total joint effects instead of the unique total joint 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 CPDAG or PDAG based on the data. The CPDAG represents the equivalence class of DAGs and can be estimated from observational data with the function pc (see the help file of this function).

The PDAG contains more orientations than the CPDAG and thus, represents a smaller equivalence class of DAGs, compared to the CPDAG. We can obtain a PDAG if we have background knowledge of, for example, certain edge orientations of undirected edges in the CPDAG. We obtain the PDAG by adding these orientations to the CPDAG using the function addBgKnowledge (see the help file of this function).

Then using the CPDAG or PDAG we extract a collection of "jointly valid" parent sets of the intervention variables from the estimated CPDAG. For each set of jointly valid parent sets we apply RRC (recursive regressions for causal effects) or MCD (modifying the Cholesky decomposition) to estimate the total joint effect of `X` on `Y` from the sample covariance matrix (see Section 3 of Nandy et. al, 2015).

Value

A matrix representing the multiset containing the estimated possible total joint effects of `X` on `Y`. The number of rows is equal to `length(x.pos)`, i.e., each column represents a vector of possible joint causal effects.

Note

For a single variable `X`, `jointIda()` estimates the same quantities as `ida()`. If `graphEst` is of `type = "cpdag"`, `jointIda()` obtains `all.pasets` by using the semi-local approach described in Section 5 in Nandy et. al, (2015). Nandy et. al, (2015) show that `jointIda()` yields correct multiplicities of the distinct elements of the resulting multiset (in the sense that it matches `ida()` with `method="global"` up to a constant factor).

If `graphEst` is of `type = "pdag"`, `jointIda()` obtains `all.pasets` by using the semi-local approach described in Algorithm 2, Section 4.2 in Perkovic et. al (2017). For this case, `jointIda()` does not necessarily yield the correct multiplicities of the distinct elements of the resulting multiset (it behaves similarly to `ida()` with `method="local"`).

`jointIda()` (like idaFast) also allows direct computation of the total joint effect of a set of intervention variables `X` on another set of target variables `Y`. In this case, `y.pos` must be an integer vector containing positions of the target variables `Y` in the covariance matrix and the output is a list of matrices that correspond to the variables in `Y` in the same order. This method is slightly more efficient than looping over `jointIda()` with single target variables, if `all.pasets` is not specified.

Author(s)

Preetam Nandy, Emilija Perkovic

References

P. Nandy, M.H. Maathuis and T.S. Richardson (2017). Estimating the effect of joint interventions from observational data in sparse high-dimensional settings. In *Annals of Statistics*.

E. Perkovic, M. Kalisch and M.H. Maathuis (2017). Interpreting and using CPDAGs with background knowledge. In *Proceedings of UAI 2017*.

See Also

ida, the simple version; pc for estimating a CPDAG.

Examples

```
## Create a weighted DAG
p <- 6
V <- as.character(1:p)
edL <- list(
  "1" = list(edges=c(3,4), weights=c(1.1,0.3)),
  "2" = list(edges=c(6),  weights=c(0.4)),
  "3" = list(edges=c(2,4,6),weights=c(0.6,0.8,0.9)),
  "4" = list(edges=c(2),weights=c(0.5)),
  "5" = list(edges=c(1,4),weights=c(0.2,0.7)),
  "6" = NULL)
myDAG <- new("graphNEL", nodes=V, edgeL=edL, edgemode="directed") ## true DAG
myCPDAG <- dag2cpdag(myDAG) ## true CPDAG
myPDAG <- addBgKnowledge(myCPDAG,1,3) ## true PDAG with background knowledge 1 -> 3
covTrue <- trueCov(myDAG) ## true covariance matrix

n <- 1000
## simulate Gaussian data from the true DAG
dat <- if (require("mvtnorm")) {
  set.seed(123)
  rmvnorm(n, mean=rep(0,p), sigma=covTrue)
} else readRDS(system.file(package="pcalg", "external", "N_6_1000.rds"))

## estimate CPDAG and PDAG -- see  help(pc), help(addBgKnoweldge)
suffStat <- list(C = cor(dat), n = n)
pc.fit <- pc(suffStat, indepTest = gaussCItest, p = p, alpha = 0.01, u2pd="relaxed")
pc.fit.pdag <- addBgKnowledge(pc.fit@graph,1,3)

if (require(Rgraphviz)) {
  ## plot the true and estimated graphs
  par(mfrow = c(1,3))
  plot(myDAG, main = "True DAG")
  plot(pc.fit, main = "Estimated CPDAG")
  plot(pc.fit.pdag, main = "Estimated PDAG")
}

## Suppose that we know the true CPDAG and covariance matrix
jointIda(x.pos=c(1,2), y.pos=6, covTrue, graphEst=myCPDAG, technique="RRC", type = "cpdag")
jointIda(x.pos=c(1,2), y.pos=6, covTrue, graphEst=myCPDAG, technique="MCD", type = "cpdag")
```

```
## Suppose that we know the true PDAG and covariance matrix
jointIda(x.pos=c(1,2), y.pos=6, covTrue, graphEst=myPDAG, technique="RRC", type = "pdag")
jointIda(x.pos=c(1,2), y.pos=6, covTrue, graphEst=myPDAG, technique="MCD", type = "pdag")

## Instead of knowing the true CPDAG or PDAG, it is enough to know only
## the jointly valid parent sets of the intervention variables
## to use RRC or MCD
## all.jointly.valid.pasets:
ajv.pasets <- list(list(5,c(3,4)),list(integer(0),c(3,4)),list(3,c(3,4)))
jointIda(x.pos=c(1,2), y.pos=6, covTrue, all.pasets=ajv.pasets, technique="RRC")
jointIda(x.pos=c(1,2), y.pos=6, covTrue, all.pasets=ajv.pasets, technique="MCD")

## From the true DAG, we can compute the true total joint effects
## using RRC or MCD
cat("Dim covTrue: ", dim(covTrue),"\n")
jointIda(x.pos=c(1,2), y.pos=6, covTrue, graphEst=myDAG, technique="RRC", type = "dag")
jointIda(x.pos=c(1,2), y.pos=6, covTrue, graphEst=myDAG, technique="MCD", type = "dag")


## When working with data, we have to use the estimated CPDAG or PDAG
## and the sample covariance matrix
jointIda(x.pos=c(1,2), y.pos=6, cov(dat), graphEst=pc.fit@graph, technique="RRC", type = "cpdag")
jointIda(x.pos=c(1,2), y.pos=6, cov(dat), graphEst=pc.fit@graph, technique="MCD", type = "cpdag")

jointIda(x.pos=c(1,2), y.pos=6, cov(dat), graphEst=pc.fit.pdag, technique="RRC", type = "pdag")
jointIda(x.pos=c(1,2), y.pos=6, cov(dat), graphEst=pc.fit.pdag, technique="MCD", type = "pdag")
## RRC and MCD can produce different results when working with data

## jointIda also works when x.pos has length 1 and in the following example
## it gives the same result as ida() (see Note)
##
## When the CPDAG is known
jointIda(x.pos=1, y.pos=6, covTrue, graphEst=myCPDAG, technique="RRC", type = "cpdag")
ida(x.pos=1, y.pos=6, covTrue, graphEst=myCPDAG, method="global", type = "cpdag")

## When the PDAG is known
jointIda(x.pos=1, y.pos=6, covTrue, graphEst=myPDAG, technique="RRC", type = "pdag")
ida(x.pos=1, y.pos=6, covTrue, graphEst=myPDAG, method="global", type = "pdag")

## When the DAG is known
jointIda(x.pos=1, y.pos=6, covTrue, graphEst=myDAG, technique="RRC", type = "dag")
ida(x.pos=1, y.pos=6, covTrue, graphEst=myDAG, method="global")
## Note that, causalEffect(myDAG,y=6,x=1) does not give the correct value in this case,
## since this function requires that the variables are in a causal order.
```

---

legal.path *Check if a 3-node-path is Legal*

Description

Check if the path $a - -b - -c$ is legal.

A 3-node path $a - -b - -c$ is "legal" iff either b is a collider or $a - -b - -c$ 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 -> b)

Value

TRUE if path is legal, otherwise FALSE.

Note

Prerequisite: $a - -b - -c$ *must* be in a path (and this is *not* checked by 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)
```

LINGAM *Linear non-Gaussian Acyclic Models (LiNGAM)*

Description

Fits a Linear non-Gaussian Acyclic Model (LiNGAM) to the data and returns the corresponding DAG.

For details, see the reference below.

Usage

```
lingam(X, verbose = FALSE)

## For back-compatibility; this is *deprecated*
LINGAM(X, verbose = FALSE)
```

Arguments

X	n x p data matrix (n: sample size, p: number of variables).
verbose	logical or integer indicating that increased diagnostic output is to be provided.

Value

`lingam()` returns an R object of (S3) class "LINGAM", basically a `list` with components

Bpruned	a $p \times p$ matrix B of linear coefficients, where $B_{i,j}$ corresponds to a directed edge from j to i.
stde	a vector of length p with the standard deviations of the estimated residuals
ci	a vector of length p with the intercepts of each equation
	.....

`LINGAM()` — *deprecated now* — returns a `list` with components

Adj	a $p \times p$ 0/1 adjacency matrix A. `A[i,j] == 1` corresponds to a directed edge from i to j.
B	$p \times p$ matrix of corresponding linear coefficients. Note it corresponds to the *transpose* of `Adj`, i.e., `identical( Adj, t(B) != 0 )` is true.

Author(s)

Of `LINGAM()` and the underlying functionality, Patrik Hoyer <patrik.hoyer@helsinki.fi>, Doris Entner <entnerd@hotmail.com>, Antti Hyttinen <antti.hyttinen@cs.helsinki.fi> and Jonas Peters <jonas.peters@tuebingen.mpg.de>.

References

S. Shimizu, P.O. Hoyer, A. Hyv\"arinen, A. Kerminen (2006) A Linear Non-Gaussian Acyclic Model for Causal Discovery; *Journal of Machine Learning Research* **7**, 2003–2030.

See Also

`fastICA` from package **fastICA** is used.

Examples

```
################################################
## Exp 1
################################################
set.seed(1234)
n <- 500
eps1 <- sign(rnorm(n)) * sqrt(abs(rnorm(n)))
eps2 <- runif(n) - 0.5

x2 <- 3 + eps2
x1 <- 0.9*x2 + 7 + eps1
```

```
#truth: x1 <- x2
trueDAG <- cbind(c(0,1),c(0,0))

X <- cbind(x1,x2)
res <- lingam(X)

cat("true DAG:\n")
show(trueDAG)

cat("estimated DAG:\n")
as(res, "amat")

cat("\n true constants:\n")
show(c(7,3))
cat("estimated constants:\n")
show(res$ci)

cat("\n true (sample) noise standard deviations:\n")
show(c(sd(eps1), sd(eps2)))
cat("estimated noise standard deviations:\n")
show(res$stde)


################################################
## Exp 2
################################################
set.seed(123)
n <- 500
eps1 <- sign(rnorm(n)) * sqrt(abs(rnorm(n)))
eps2 <- runif(n) - 0.5
eps3 <- sign(rnorm(n)) * abs(rnorm(n))^(1/3)
eps4 <- rnorm(n)^2

x2 <-                eps2
x1 <-   0.9*x2     + eps1
x3 <-   0.8*x2     + eps3
x4 <- -x1  -0.9*x3 + eps4

X <- cbind(x1,x2,x3,x4)

trueDAG <- cbind(x1 = c(0,1,0,0),
                 x2 = c(0,0,0,0),
                 x3 = c(0,1,0,0),
                 x4 = c(1,0,1,0))
## x4 <- x3 <- x2 -> x1 -> x4
## adjacency matrix:
## 0 0 0 1
## 1 0 1 0
## 0 0 0 1
## 0 0 0 0

res1 <- lingam(X, verbose = TRUE)# details on LINGAM
res2 <- lingam(X, verbose = 2)   # details on LINGAM and fastICA
```

```
## results are the same, of course:
stopifnot(identical(res1, res2))
cat("true DAG:\n")
show(trueDAG)

cat("estimated DAG:\n")
as(res1, "amat")
```

`mat2targets` *Conversion between an intervention matrix and a list of intervention targets*

Description

In a data set with n measurements of p variables, intervened variables can be specified in two ways:

- with a `logical` intervention matrix of dimension $n \times p$, where the entry `[i, j]` indicates whether variable j has been intervened in measurement i; or
- with a list of (unique) intervention targets and a p-dimensional vector indicating the indices of the intervention targets of the p measurements.

The function `mat2targets` converts the first representation to the second one, the function `targets2mat` does the reverse conversion. The second representation 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)
targets2mat(p, targets, target.index)
```

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`.
`p`	Number of variables
`targets`	List of unique intervention targets
`target.index`	Vector of intervention target indices. The intervention target of data point `i` is encoded as `targets[[target.index[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 `targets[[target.index[i]]]`.

Author(s)

Alain Hauser (<alain.hauser@bfh.ch>)

See Also

Score, gies, simy

Examples

```
## 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]]])

## Convert back to matrix representation
all(A == targets2mat(p, target.list$targets, target.list$target.index))
```

---

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

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

Arguments

dm	numeric data matrix; rows are observiations ("samples"), columns are variables.
method	a string; "standard" (default), "Qn", "QnStable", "ogkQn" and "shrink" envokes standard, elementwise robust (based on Q_n scale estimator, see Qn), robust (Q_n 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 estimte. "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

```
## 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
```

---

opt.target *Get an optimal intervention target*

Description

Given a (observational or interventional) essential graph (or "CPDAG"), find the optimal intervention target that maximizes the number of edges that can be oriented after the intervention.

Usage

```
opt.target(essgraph, max.size, use.node.names = TRUE)
```

Arguments

essgraph	An EssGraph or graphNEL object representing a (observational or interventional) essential graph (or "CPDAG").
max.size	Maximum size of the intervention target. Only 1 and the number of vertices of essgraph are allowed; the latter means no size limit is applied (the default if the parameter is missing).
use.node.names	Indicates if the intervention target should be returned as a list of node names (if TRUE) or indices (if FALSE).

Details

This function implements active learning strategies for structure learning from interventional data, one that calculates an optimal single-vertex intervention target, and one that calculates an optimal intervention target of arbitrary size. "Optimal" means the proposed intervention target guarantees the highest number of edges that can be oriented after performing the intervention, assuming the essential graph provided as input is the true essential graph under the currently available interventional data (i.e., neglecting possible estimation errors).

Implementation corresponds to algorithms "OptSingle" and "OptUnb" published in Hauser and Bühlmann (2012).

Value

A character vector of node names (if use.node.names = TRUE), or an integer vector of node indices (if use.node.names = FALSE) indicating the optimal intervention target.

Author(s)

Alain Hauser (<alain.hauser@math.ethz.ch>)

References

A. Hauser and P. Bühlmann (2012). Two optimal strategies for active learning of causal models from interventions. *Proceedings of the 6th European Workshop on Probabilistic Graphical Models (PGM-2012)*, 123–130

See Also

EssGraph

Examples

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

## Define the score (BIC)
```

```
score <- new("GaussL0penObsScore", gmG8$x)

## Estimate the essential graph using GES
ges.fit <- ges(score)
essgraph <- ges.fit$essgraph

## Plot the estimated essential graph
if (require(Rgraphviz)) {
  plot(essgraph, main = "Estimated CPDAG")
}
## The CPDAG has 1 unoriented component with 3 edges (Author <-> Bar, Bar <->
## Ctrl, Bar <-> V5)

## Get optimal single-vertex and unbounded intervention target
opt.target(essgraph, max.size = 1)
opt.target(essgraph, max.size = essgraph$node.count())
```

`optAdjSet` *Compute the optimal adjustment set*

Description

`optAdjSet` computes the optimal valid adjustment set relative to the variables (`X`,`Y`) in the given graph.

Usage

```
optAdjSet(graphEst,x.pos,y.pos)
```

Arguments

`graphEst`	graphNel object or adjacency matrix of type amat.cpdag.
`x.pos`, `x`	Positions of variables `X` in the covariance matrix.
`y.pos`, `y`	Positions of variables `Y` in the covariance matrix.

Details

Suppose we have data from a linear SEM compatible with a known causal graph `G` and our aim is to estimate the total joint effect of `X` on `Y`. Here the total joint effect of $\mathtt{X} = (X_1, X_2)$ on `Y` is defined via Pearl's do-calculus as the vector $(E[Y|do(X_1 = x_1 + 1, X_2 = x_2)] - E[Y|do(X_1 = x_1, X_2 = x_2)], E[Y|do(X_1 = x_1, X_2 = x_2 + 1)] - E[Y|do(X_1 = x_1, X_2 = x_2)])$, with a similar definition for more than two variables. These values are equal to the partial derivatives (evaluated at x_1, x_2) of $E[Y|do(X = x_1', X_2 = x_2')]$ with respect to x_1' and x_2'. Moreover, under the linearity assumption, these partial derivatives do not depend on the values at which they are evaluated.

It is possible to estimate the total joint effect of `X` on `Y` with a simple linear regression of the form `lm(Y ~ X + Z)`, if and only if the covariate set `Z` is a valid adjustment set (see Perkovic et al. (2018)). Often, however, there are multiple such valid adjustment sets, providing total effect estimates with varying accuracies. Suppose that there exists a valid adjustment set relative to (`X`,`Y`) in causal graph

G, and each node in Y is a descendant of X, then there exists a valid adjustment which provides the total effect estimate with the optimal asymptotic variance, which we will refer to as O(X,Y,G) (Henckel et al., 2019). This function returns this optimal valid adjustment set O(X,Y,G).

The restriction that each node in Y be a descendant of the node set X is not notable, as the total effect of the node set X on a non-descendant is always 0. If provided with a node set Y that does not fulfill this condition this function computes a pruned node set Y2 by removing all nodes from Y that are not descendants of X and returns O(X,Y2,G) instead. The user will be alerted to this and given the pruned set Y2.

Value

A vector with the positions of the nodes of the optimal set O(X,Y,G).

Author(s)

Leonard Henckel

References

E. Perković, J. Textor, M. Kalisch and M.H. Maathuis (2018). Complete graphical characterization and construction of adjustment sets in Markov equivalence classes of ancestral graphs. *Journal of Machine Learning Research.* **18**(220) 1–62,

L. Henckel, E. Perkovic and M.H. Maathuis (2019). Graphical criteria for efficient total effect estimation via adjustment in causal linear models. *Working Paper.*

Examples

```
## Simulate a true DAG, its CPDAG and an intermediate max. PDAG
suppressWarnings(RNGversion("3.5.0"))
set.seed(123)
p <- 10
## true DAG
myDAG <- randomDAG(p, prob = 0.3)
## true CPDAG
myCPDAG <- dag2cpdag(myDAG)
## true PDAG with added background knowledge 5 -> 6
myPDAG <- addBgKnowledge(myCPDAG,5,6)
if (require(Rgraphviz)) {
par(mfrow = c(1,3))
plot(myDAG)
plot(myPDAG)
plot(myCPDAG) ## plot of the graphs
}

## if the CPDAG C is amenable relative to (X,Y),
## the optimal set will be the same for all DAGs
## and any max. PDAGs obtained by adding background knowledge to C
(optAdjSet(myDAG,3,10))
(optAdjSet(myPDAG,3,10))
(optAdjSet(myCPDAG,3,10))
```

```
## the optimal adjustment set can also be compute for sets X and Y
(optAdjSet(myDAG,c(3,4),c(9,10)))
(optAdjSet(myPDAG,c(3,4),c(9,10)))
(optAdjSet(myCPDAG,c(3,4),c(9,10)))

## The only restriction is that it requires all nodes in Y to be
## descendants of X.
## However, if a node in Y is non-descendant of X the lowest variance
## partial total effect estimate is simply 0.
## Hence, we can proceed with a pruned Y. This function does this automatically!
optAdjSet(myDAG,1,c(3,9))

## Note that for sets X there may be no valid adjustment set even
## if the PDAG is is amenable relative to (X,Y).
## Not run: optAdjSet(myPDAG,c(4,9),7)
```

---

pag2anc *Reads off identifiable ancestors and non-ancestors from a directed PAG*

Description

Constructs a matrix which contains identifiable ancestral and non-ancestral relations in the Markov equivalence class represented by a directed partial ancestral graph.

Usage

```
pag2anc(P,verbose=FALSE)
```

Arguments

P	Adjacency matrix of type amat.pag, which should encode a directed PAG (i.e., it should not contain any undirected edges of the form x --- y or any circle-tail edges of the form x o-- y).
verbose	If true, more detailed output is provided.

Details

We say that node i is ancestor of node j in a directed mixed graph (DMG) iff there exists a directed path from i to j in that graph. If the directed mixed graph has a causal interpretation (for example, if it is the graph of a simple SCM) then ancestral relations coincide (generically) with causal relations.

This function implements the sufficient conditions (Propositions 4 and 5) in Mooij and Claassen (2020) for concluding whether an ancestral relation between two nodes must be present or absent in all directed mixed graphs in the Markov equivalence class represented by the directed PAG P. It applies to both the acyclic case as well as the cyclic (simple SCM) case, assuming the d-separation resp. σ-separation Markov property.

The output is a matrix containing for each ordered pair of nodes whether the presence of an ancestral relation was identified, or the absence, or neither.

It is not known whether these sufficient conditions for identifiability are complete. Hence, zero entries in the result indicate that the sufficient condition gives no conclusion, rather than that the Markov equivalence class represented by the directed PAG necessarily contains DMGs where an ancestral relation is present as well as DMGs where it is absent.

`P` should be an adjacency matrix of type amat.pag that contains no undirected and circle-tail edges.

Value

Matrix `A`, where entry `A[i,j]` equals

1 if node `i` is an identifiable ancestor of node `j`,

-1 if node `i` is an identifiable non-ancestor of node `j`,

0 in case the ancestral relationship between nodes `i` and `j` is unknown.

Author(s)

Joris Mooij.

References

J. M. Mooij and T. Claassen (2020). Constraint-Based Causal Discovery using Partial Ancestral Graphs in the presence of Cycles. *In Proc. of the 36th Conference on Uncertainty in Artificial Intelligence (UAI-20)*, 1159-1168.

Examples

```
################################################
## Mooij et al. (2020), Fig. 43(a), p. 97
################################################

# Encode ADMG as adjacency matrix
p <- 8 # total number of variables
V <- c("Ca","Cb","Cc","X0","X1","X2","X3","X4") # 3 context variables, 5 system variables
# amat[i,j] = 0 iff no edge btw i,j
# amat[i,j] = 1 iff i *-o j
# amat[i,j] = 2 iff i *-> j
# amat[i,j] = 3 iff i *-- j
amat <- rbind(c(0,2,2,2,0,0,0,0),
              c(2,0,2,0,2,0,0,0),
              c(2,2,0,0,2,2,0,0),
              c(3,0,0,0,0,0,2,0),
              c(0,3,3,0,0,3,0,2),
              c(0,0,3,0,2,0,0,0),
              c(0,0,0,3,0,0,0,2),
              c(0,0,0,0,2,0,3,0))
rownames(amat)<-V
colnames(amat)<-V
```

```
# Make use of d-separation oracle as "independence test"
indepTest <- dsepAMTest
suffStat<-list(g=amat,verbose=FALSE)

# Derive PAG that represents the Markov equivalence class of the ADMG with the FCI algorithm
# (assuming no selection bias)
fci.pag <- fci(suffStat,indepTest,alpha = 0.5,labels = V,verbose=TRUE,selectionBias=FALSE)

# Read off causal features from the FCI PAG
cat('Identified absence (-1) and presence (+1) of ancestral causal relations from FCI PAG:\n')
print(pag2anc(fci.pag@amat))
```

`pag2conf` *Reads off identifiable unconfounded node pairs from a directed PAG*

Description

Constructs a matrix which contains identifiably unconfounded node pairs in the Markov equivalence class represented by a directed partial ancestral graph.

Usage

```
pag2conf(P)
```

Arguments

`P`	Adjacency matrix of type amat.pag, which should encode a directed PAG (i.e., it should not contain any undirected edges of the form `x --- y` or any circle-tail edges of the form `x o-- y`).

Details

We say that nodes `i` and `j` are confounded in a directed mixed graph (DMG) iff there exists a bidirected edge `i<->j` in that graph. If the directed mixed graph has a causal interpretation (for example, if it is the graph of a simple SCM) then the presence of a bidirected edge coincides (generically) with the presence of a confounder, i.e., a latent common cause (relative to the variables in the graph).

This function implements the sufficient condition (Proposition 6) in Mooij and Claassen (2020) for concluding whether two nodes are unconfounded in all directed mixed graphs in the Markov equivalence class represented by the directed PAG `P`. It applies to both the acyclic case as well as the cyclic (simple SCM) case, assuming the d-separation resp. σ-separation Markov property.

The output is a (symmetric) matrix containing for each ordered pair of nodes whether the two nodes are identifiably unconfounded.

It is not known whether these sufficient conditions for identifiability are complete. Hence, zero entries in the result indicate that the sufficient condition gives no conclusion, rather than that the Markov equivalence class represented by the directed PAG necessarily contains DMGs where a bidirected edge is present.

`P` should be an adjacency matrix of type amat.pag that contains no undirected and circle-tail edges.

Value

Matrix `A`, where entry `A[i,j]` equals

-1 if nodes `i` and `j` are identifiably unconfounded,

0 in case it is unknown whether nodes `i` and `j` are confounded or not.

Author(s)

Joris Mooij.

References

J. M. Mooij and T. Claassen (2020). Constraint-Based Causal Discovery using Partial Ancestral Graphs in the presence of Cycles. *In Proc. of the 36th Conference on Uncertainty in Artificial Intelligence (UAI-20)*, 1159-1168.

Examples

```
################################################
## Mooij et al. (2020), Fig. 43(a), p. 97
################################################

# Encode ADMG as adjacency matrix
p <- 8 # total number of variables
V <- c("Ca","Cb","Cc","X0","X1","X2","X3","X4") # 3 context variables, 5 system variables
# amat[i,j] = 0 iff no edge btw i,j
# amat[i,j] = 1 iff i *-o j
# amat[i,j] = 2 iff i *-> j
# amat[i,j] = 3 iff i *-- j
amat <- rbind(c(0,2,2,2,0,0,0,0),
              c(2,0,2,0,2,0,0,0),
              c(2,2,0,0,2,2,0,0),
              c(3,0,0,0,0,0,2,0),
              c(0,3,3,0,0,3,0,2),
              c(0,0,3,0,2,0,0,0),
              c(0,0,0,3,0,0,0,2),
              c(0,0,0,0,2,0,3,0))
rownames(amat)<-V
colnames(amat)<-V

# Make use of d-separation oracle as "independence test"
indepTest <- dsepAMTest
suffStat<-list(g=amat,verbose=FALSE)


# Derive PAG that represents the Markov equivalence class of the ADMG with the FCI algorithm
# (assuming no selection bias)
fci.pag <- fci(suffStat,indepTest,alpha = 0.5,labels = V,verbose=TRUE,selectionBias=FALSE)

# Read off causal features from the FCI PAG
cat('Identified absence (-1) and presence (+1) of pairwise latent confounding from FCI PAG:\n')
```

```
print(pag2conf(fci.pag@amat))
```

`pag2edge` *Reads off identifiable parents and non-parents from a directed PAG*

Description

Constructs a matrix which contains identifiable parental and non-parental relations in the Markov equivalence class represented by a directed partial ancestral graph.

Usage

```
pag2edge(P)
```

Arguments

`P`	Adjacency matrix of type amat.pag, which should encode a directed PAG (i.e., it should not contain any undirected edges of the form `x --- y` or any circle-tail edges of the form `x o-- y`).

Details

We say that node `i` is parent of node `j` in a directed mixed graph (DMG) iff there exists a directed edge `i-->j` in that graph. If the directed mixed graph has a causal interpretation (for example, if it is the graph of a simple SCM) then parental relations coincide (generically) with direct causal relations (relative to the variables in the graph).

This function implements the sufficient conditions (Propositions 7 and 8) in Mooij and Claassen (2020) for concluding whether a parental relation between two nodes must be present or absent in all directed mixed graphs in the Markov equivalence class represented by the directed PAG `P`. It applies to both the acyclic case as well as the cyclic (simple SCM) case, assuming the d-separation resp. σ-separation Markov property.

The output is a matrix containing for each ordered pair of nodes whether the presence of a parental relation was identified, or the absence, or neither.

It is not known whether these sufficient conditions for identifiability are complete. Hence, zero entries in the result indicate that the sufficient condition gives no conclusion, rather than that the Markov equivalence class represented by the directed PAG necessarily contains DMGs where a parental relation is present as well as DMGs where it is absent.

`P` should be an adjacency matrix of type amat.pag that contains no undirected and circle-tail edges.

Value

Matrix `A`, where entry `A[i,j]` equals

1 if node `i` is an identifiable parent of node `j`,

-1 if node `i` is an identifiable non-parent of node `j`,

0 in case the parental relationship between nodes `i` and `j` is unknown.

Author(s)

Joris Mooij.

References

J. M. Mooij and T. Claassen (2020). Constraint-Based Causal Discovery using Partial Ancestral Graphs in the presence of Cycles. *In Proc. of the 36th Conference on Uncertainty in Artificial Intelligence (UAI-20)*, 1159-1168.

Examples

```
################################################
## Mooij et al. (2020), Fig. 43(a), p. 97
################################################

# Encode ADMG as adjacency matrix
p <- 8 # total number of variables
V <- c("Ca","Cb","Cc","X0","X1","X2","X3","X4") # 3 context variables, 5 system variables
# amat[i,j] = 0 iff no edge btw i,j
# amat[i,j] = 1 iff i *-o j
# amat[i,j] = 2 iff i *-> j
# amat[i,j] = 3 iff i *-- j
amat <- rbind(c(0,2,2,2,0,0,0,0),
              c(2,0,2,0,2,0,0,0),
              c(2,2,0,0,2,2,0,0),
              c(3,0,0,0,0,0,2,0),
              c(0,3,3,0,0,3,0,2),
              c(0,0,3,0,2,0,0,0),
              c(0,0,0,3,0,0,0,2),
              c(0,0,0,0,2,0,3,0))
rownames(amat)<-V
colnames(amat)<-V

# Make use of d-separation oracle as "independence test"
indepTest <- dsepAMTest
suffStat<-list(g=amat,verbose=FALSE)


# Derive PAG that represents the Markov equivalence class of the ADMG with the FCI algorithm
# (assuming no selection bias)
fci.pag <- fci(suffStat,indepTest,alpha = 0.5,labels = V,verbose=TRUE,selectionBias=FALSE)

# Read off causal features from the FCI PAG
cat('Identified absence (-1) and presence (+1) of direct causal relations from FCI PAG:\n')
print(pag2edge(fci.pag@amat))
```

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

```
pag2magAM(amat.pag, x, max.chordal = 10, verbose = FALSE)
```

Arguments

amat.pag	Adjacency matrix of type amat.pag
x	(integer) position in adjacency matrix of 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 (2015) for details.

Value

The output is an adjacency matrix of type amat.pag representing a valid MAG that belongs to the Markov equivalence class represented by the given PAG.

Author(s)

Diego Colombo, Markus Kalisch and Martin Maechler.

References

M.H. Maathuis and D. Colombo (2015). A generalized back-door criterion. *Annals of Statistics* **43** 1060-1088.

Zhang, J. (2006). Causal Inference and Reasoning in Causally Insufficient Systems. Ph. D. thesis, Carnegie Mellon University.

See Also

fci, dag2pag, backdoor

Examples

```
## 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
```

ParDAG-class *Class* "ParDAG" *of Parametric Causal Models*

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.

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@bfh.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,
   u2pd = c("relaxed", "rand", "retry"),
   skel.method = c("stable", "original", "stable.fast"),
   conservative = FALSE, maj.rule = FALSE, solve.confl = FALSE,
   numCores = 1, 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 (integer) column positions 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.
numCores	Specifies the number of cores to be used for parallel estimation of skeleton.
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.
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	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 $i \longrightarrow j$ 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 $i \longrightarrow j$ and there is at least one DAG in the Markov equivalence class with edge $i \longleftarrow j$.

The CPDAG is estimated using the PC algorithm (named after its inventors **P**eter Spirtes and **C**lark Glymour). The skeleton is estimated by the function skeleton which uses a modified version of the original PC algorithm (see Colombo and Maathuis (2014) 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 (2014) 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 ($a \longrightarrow b \longleftarrow c$) 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 $a \longrightarrow b \longleftarrow c$ 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 (conservative = 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 (2014) 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, 2014). 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 $b \longleftarrow c$ in v-structure $a \longrightarrow b \longleftarrow c$, while it should be directed as $b \longrightarrow c$ in v-structure $b \longrightarrow c \longleftarrow d$. With the option solve.confl = FALSE, in such cases, we simply overwrite the directions of the conflicting edge. In the example above this means that we obtain $a \longrightarrow b \longrightarrow c \longleftarrow d$ if $a - b - c$ was visited first, and $a \longrightarrow b \longleftarrow c \longleftarrow d$ 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 solve.confl = TRUE (which is only supported with option u2pd = "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 $b \leftrightarrow c$ 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 to be interpreted causally. The useage 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 (2014) for more details.

Note that calling (conservative = TRUE), or maj.rule = TRUE, together with solve.confl = TRUE

produces a fully order-independent output, see Colombo and Maathuis (2014).

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 $a \longrightarrow b \longleftarrow c \longleftarrow d$. In this case, `u2pd` is not used.

Using the function `isValidGraph` one can check if the final output is indeed a valid CPDAG.

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

D. Colombo and M.H. Maathuis (2014).Order-independent constraint-based causal structure learning. *Journal of Machine Learning Research* **15** 3741-3782.

M. Kalisch, M. Maechler, D. Colombo, M.H. Maathuis and P. Buehlmann (2012). Causal Inference Using Graphical Models with the R Package pcalg. *Journal of Statistical Software* **47(11)** 1–26, doi:10.18637/jss.v047.i11.

M. Kalisch and P. Buehlmann (2007). Estimating high-dimensional directed acyclic graphs with the PC-algorithm. *JMLR* **8** 613-636.

J. Ramsey, J. Zhang and P. Spirtes (2006). Adjacency-faithfulness and conservative causal inference. In *Proceedings of the 22nd Annual Conference on Uncertainty in Artificial Intelligence*. AUAI Press, Arlington, VA.

P. Spirtes, C. Glymour and R. Scheines (2000). *Causation, Prediction, and Search*, 2nd edition. The MIT Press.

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`. `isValidGraph` for testing whether the output is a valid CPDAG.

Examples

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

## estimate CPDAG
pc.fit <- pc(suffStat = list(C = cor(gmG8$x), n = n),
             indepTest = gaussCItest, ## indep.test: partial correlations
             alpha=0.01, labels = V, verbose = TRUE)
if (require(Rgraphviz)) {
  ## show estimated CPDAG
  par(mfrow=c(1,2))
  plot(pc.fit, main = "Estimated CPDAG")
  plot(gmG8$g, main = "True DAG")
}
################################################
## Using d-separation oracle
################################################
## define sufficient statistics (d-separation oracle)
suffStat <- list(g = gmG8$g, jp = RBGL::johnson.all.pairs.sp(gmG8$g))
## 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(gmG8$g, 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,
           ## independence test: G^2 statistic
           indepTest = disCItest, alpha = 0.01, labels = V, verbose = TRUE)
if (require(Rgraphviz)) {
  ## show estimated CPDAG
  par(mfrow = c(1,2))
  plot(pc.D, main = "Estimated CPDAG")
  plot(gmD$g, main = "True DAG")
}
```

```
################################################
## Using binary data
################################################
## Load binary data
data(gmB)
V <- colnames(gmB$x)
## estimate CPDAG
pc.B <- pc(suffStat = list(dm = gmB$x, adaptDF = FALSE),
           indepTest = binCItest, alpha = 0.01, labels = V, verbose = TRUE)
pc.B
if (require(Rgraphviz)) {
  ## show estimated CPDAG
  plot(pc.B, main = "Estimated CPDAG")
  plot(gmB$g, main = "True DAG")
}

################################################
## Detecting ambiguities due to sampling error
################################################
## Load predefined data
data(gmG)
n <- nrow    (gmG8$ x)
V <- colnames(gmG8$ x) # labels aka node names

## estimate CPDAG
pc.fit <- pc(suffStat = list(C = cor(gmG8$x), n = n),
             indepTest = gaussCItest, ## indep.test: partial correlations
             alpha=0.01, labels = V, verbose = TRUE)

## due to sampling error, some edges were overwritten:
isValidGraph(as(pc.fit, "amat"), type = "cpdag")

## re-fit with solve.confl = TRUE
pc.fit2 <- pc(suffStat = list(C = cor(gmG8$x), n = n),
             indepTest = gaussCItest, ## indep.test: partial correlations
             alpha=0.01, labels = V, verbose = TRUE,
             solve.confl = TRUE)

## conflicting edge is V5 - V6
as(pc.fit2, "amat")
```

`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

```
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 intitial 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 indicatin 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, 2014): 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

D. Colombo and M.H. Maathuis (2014).Order-independent constraint-based causal structure learning. *Journal of Machine Learning Research* **15** 3741-3782.

J. Ramsey, J. Zhang and P. Spirtes (2006). Adjacency-faithfulness and conservative causal inference. In *Proceedings of the 22nd Annual Conference on Uncertainty in Artificial Intelligence*, Arlington, VA. AUAI Press.

See Also

skeleton, pc, fci

---

pcalg2dagitty *Transform the adjacency matrix from* **pcalg** *into a* **dagitty** *object*

Description

Transform the adjacency matrix of type amat.cpdag or amat.pag (for details on coding see amatType).

Usage

```
pcalg2dagitty(amat, labels, type = "cpdag")
```

Arguments

amat	adjacency matrix of type amat.cpdag or amat.pag
labels	character vector of variable (or "node") names.
type	string specifying the type of graph of the adjacency matrix amat. It can be a DAG (type="dag"), a CPDAG (type="cpdag") or a maximally oriented PDAG (type="pdag") from Meek (1995); then the type of adjacency matrix is assumed to be amat.cpdag. It can also be a MAG (type = "mag") or a PAG (type="pag"); then the type of the adjacency matrix is assumed to be amat.pag.

Details

For a given adjacency matrix `amat` the form `amat.cpdag` or `amat.pag` and a specified graph `type`, this function returns a dagitty object corresponding to the graph structure specified by `amat`, `labels` and `type`. The resulting object is compatible with the **dagitty** package.

Value

A dagitty graph (see the **dagitty** package).

Author(s)

Emilija Perkovic and Markus Kalisch

Examples

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

amat <- wgtMatrix(gmG8$g)
amat[amat != 0] <- 1
if(requireNamespace("dagitty", quietly = TRUE)) {
dagitty_dag1 <- pcalg2dagitty(amat,V,type="dag")
}
```

---

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

```
pcAlgo(dm = NA, C = NA, n=NA, alpha, corMethod = "standard",
       verbose=FALSE, directed=FALSE, G=NULL, datatype = "continuous",
       NAdelete=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 speciyfing 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)
datatype	Distinguish between discrete and continuous data
NAdelete	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 weigths) 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

P. Spirtes, C. Glymour and R. Scheines (2000) *Causation, Prediction, and Search*, 2nd edition, The MIT Press.

Kalisch M. and P. B\"uhlmann (2007) *Estimating high-dimensional directed acyclic graphs with the PC-algorithm*; JMLR, Vol. 8, 613-636, 2007.

---

pcAlgo-class *Class "pcAlgo" of PC Algorithm Results, incl. Skeleton*

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.

Usage

```
## S4 method for signature 'pcAlgo,ANY'
plot(x, y, main = NULL,
     zvalue.lwd = FALSE, lwd.max = 7, labels = NULL, ...)
## S3 method for class 'pcAlgo'
print(x, amat = FALSE, zero.print = ".", ...)

## S4 method for signature 'pcAlgo'
summary(object, amat = TRUE, zero.print = ".", ...)
## S4 method for signature 'pcAlgo'
show(object)
```

Arguments

x, object	a "pcAlgo" object.
y	(generic plot() argument; unused).
main	main title for the plot (with an automatic default).
zvalue.lwd	logical indicating if the line width (lwd) of the edges should be made proportional to the entries of matrix zMin (originally) or derived from matrix pMax.
lwd.max	maximal lwd to be used, if zvalue.lwd is true.
labels	if non-NULL, these are used to define node attributes nodeAttrs and attrs, passed to agopen() from package **Rgraphviz**.
amat	logical indicating if the adjacency matrix should be shown (printed) as well.
zero.print	string for printing 0 ('zero') entries in the adjacency matrix.
...	optional further arguments (passed from and to methods).

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-class": the undirected or partially directed graph that was estimated.

zMin: Deprecated.

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, fciAlgo

Examples

```
  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 = gaussCItest, alpha = 0.01, p = p)

## use methods of class pcAlgo
show(pc.fit)
if(require(Rgraphviz))
  plot(pc.fit, main = "Fitted graph")
summary(pc.fit)

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

---

pcorOrder *Compute Partial Correlations*

Description

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

Usage

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

Arguments

i, j	(integer) position of variable i and j, respectively, in correlation matrix.
k	(integer) positions of zero or more conditioning variables in the correlation matrix.
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 recusive 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 pseudoinverse() from package **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

condIndFisherZ for testing zero partial correlation.

Examples

```
## 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

```
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	a string determining the method for correlation estimation via `mcor()`; specifically any of the `mcor(*, method = "..")` can be used, e.g., `"Qn"` for one kind of robust correlation estimate.
verbose	`logical` or in $\{0, 1, 2\}$; **FALSE, 0:** No output, **TRUE, 1:** Little output, **2:** Detailed output. Note that such diagnostic output may make the function considerably 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

Buehlmann, P., Kalisch, M. and Maathuis, M.H. (2010). Variable selection for high-dimensional linear models: partially faithful distributions and the PC-simple algorithm. *Biometrika* **97**, 261–278.

See Also

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

Examples

```
p <- 10
## generate and draw random DAG :
suppressWarnings(RNGversion("3.5.0"))
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]
(pcS <- pcSelect(d.mat[,10], d.mat[,-10], alpha=0.05))
## You see, that variable 4,5,6 are considered as important
## By inspecting zMin,
with(pcS, zMin[G])
## you can also see that the influence of variable 6
## is most evident from the data (its zMin is 18.64, so quite large - as
## a rule of thumb for judging what is large, you could use quantiles
## of the Standard Normal Distribution)
```

---

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

```
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

```
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)
```

---

pdag2allDags *Enumerate All DAGs in a Markov Equivalence Class*

Description

pdag2allDags computes all DAGs in the Markov Equivalence Class Represented by a Given Partially Directed Acyclic Graph (PDAG).

Usage

```
pdag2allDags(gm, verbose = FALSE)
```

Arguments

gm	adjacency matrix of type amat.cpdag
verbose	logical; if true, some output is produced during computation

Details

All DAGs extending the given PDAG are computing while avoiding new v-structures and cycles. If no DAG is found, the function returns NULL.

Value

List with two elements:

dags:	Matrix; every row corresponds to a DAG; every column corresponds to an entry in the adjacency matrix of this DAG. Thus, the adjacency matrix (of type amat.cpdag) contained in the i-th row of matrix dags can be obtained by calling matrix(dags[i,],p,p, byrow = TRUE) (assuming the input PDAG has p nodes).
nodeNms	Node labels of the input PDAG.

Author(s)

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

Examples

```
## Example 1
gm <- rbind(c(0,1),
            c(1,0))
colnames(gm) <- rownames(gm) <- LETTERS[1:2]
res1 <- pdag2allDags(gm)
## adjacency matrix of first DAG in output
amat1 <- matrix(res1$dags[1,],2,2, byrow = TRUE)
colnames(amat1) <- rownames(amat1) <- res1$nodeNms
amat1 ## A --> B

## Example 2
gm <- rbind(c(0,1,1),
            c(1,0,1),
            c(1,1,0))
colnames(gm) <- rownames(gm) <- LETTERS[1:ncol(gm)]
res2 <- pdag2allDags(gm)
## adjacency matrix of first DAG in output
amat2 <- matrix(res2$dags[1,],3,3, byrow = TRUE)
colnames(amat2) <- rownames(amat2) <- res2$nodeNms
amat2

## Example 3
gm <- rbind(c(0,1,1,0,0),
            c(1,0,0,0,0),
            c(1,0,0,0,0),
            c(0,1,1,0,1),
            c(0,0,0,1,0))
colnames(gm) <- rownames(gm) <- LETTERS[1:ncol(gm)]
res3 <- pdag2allDags(gm)
## adjacency matrix of first DAG in output
amat3 <- matrix(res3$dags[1,],5,5, byrow = TRUE)
colnames(amat3) <- rownames(amat3) <- res3$nodeNms
amat3

if (require(Rgraphviz)) {
## for convenience a simple plotting function
## for the function output
plotAllDags <- function(res) {
    require(graph)
    p <- sqrt(ncol(res$dags))
    nDags <- ceiling(sqrt(nrow(res$dags)))
    par(mfrow = c(nDags, nDags))
    for (i in 1:nrow(res$dags)) {
        tmp <- matrix(res$dags[i,],p,p)
        colnames(tmp) <- rownames(tmp) <- res$nodeNms
        plot(as(tmp, "graphNEL"))
    }
}
plotAllDags(res1)
amat1 ## adj.matrix corresponding to the first plot for expl 1
plotAllDags(res2)
```

```
amat2 ## adj.matrix corresponding to the first plot for expl 2
plotAllDags(res3)
amat3 ## adj.matrix corresponding to the first plot for expl 3
}
```

---

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

```
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.

Author(s)

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

References

D.Dor, M.Tarsi (1992). A simple algorithm to construct a consistent extension of a partially oriented graph. Technicial Report R-185, Cognitive Systems Laboratory, UCLA

Examples

```
p <- 10 # number of random variables
n <- 10000 # number of samples
s <- 0.4 # sparsness 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))
```

---

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 and that is not flagged as fixed by the `fixedEdges` argument, 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

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

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$(x, G) \setminus \{x, y\}$, 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**.

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.

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 (2014)).

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

P. Spirtes, C. Glymour and R. Scheines (2000). *Causation, Prediction, and Search*, 2nd edition. The MIT Press.

D. Colombo, M.H. Maathuis, M. Kalisch and T.S. Richardson (2012). Learning high-dimensional directed acyclic graphs with latent and selection variables. *Annals of Statistics* **40**, 294–321.

D. Colombo and M.H. Maathuis (2014). Order-independent constraint-based causal structure learning. *Journal of Machine Learning Research* **15** 3741-3782.

See Also

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

Examples

```
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
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

`fci`

---

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,
       plot = requireNamespace("Rgraphviz"), main = ,
       cex.main = 1.25, font.main = par("font.main"), col.main=par("col.main"),
       ...)
```

Arguments

graphObj	An R object of class graph.
y	(integer) position of the starting node in the adjacency matrix.
dist	Distance of nodes included in subgraph from starting node y.
amat	Precomputed adjacency matrix of type amat.cpdag (optional)
directed	logical indicating if the subgraph should be directed.
plot	logical indicating if the subgraph should be plotted (or just returned). Defaults to true when **Rgraphviz** is installed.
main	title to be used, with a sensible default; see title.
cex.main, font.main, col.main	optional settings for the main title; see title.
...	optional arguments passed to the plot() from package **Rgraphviz**.

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. Note that the neighbourhood does *not* depend on edge directions. If directed is true (as per default), the orientation of the edges is taken from the initial graph.

For the plotting, the package **Rgraphviz** must be installed.

Value

the desired subgraph is returned; invisibly, i.e., via invisible, if plot is true.

Author(s)

Daniel Stekhoven, then Martin Maechler.

Examples

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

if(requireNamespace("Rgraphviz")) {
  ## 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
  par(op)
} else { ## without 'Rgraphviz'
  sg2d <- plotSG(myDAG, 8, 2, directed = TRUE,  plot=FALSE)
  sg2u <- plotSG(myDAG, 8, 2, directed = FALSE, plot=FALSE)
}
```

---

possAn *Find possible ancestors of given node(s).*

Description

In a DAG, CPDAG, MAG or PAG determine which nodes are (possible) ancestors of x on definite status or just any paths potentially avoiding given nodes on the paths.

Usage

```
possAn(m, x, y = NULL, possible = TRUE, ds = TRUE,
type = c("cpdag", "pdag", "dag", "mag", "pag"))
```

Arguments

m	Adjacency matrix in coding according to type.
x	Node positions of starting nodes.
y	Node positions of nodes through which a path must not go.
possible	If TRUE, possible ancestors are returned.
ds	If TRUE, only paths of definite status are considered.
type	Type of adjacency matrix in m. The coding is according to amatType.

Details

Not all possible combinations of the arguments are currently implemented and will issue an error if called.

Value

Vector of all node positions found as (possible) ancestors of the nodes in x.

Author(s)

Markus Kalisch

See Also

amatType

Examples

```
## a -- b -> c
amat <- matrix(c(0,1,0, 1,0,1, 0,0,0), 3,3)
colnames(amat) <- rownames(amat) <- letters[1:3]
if (require(Rgraphviz)) plot(as(t(amat), "graphNEL"))

possAn(m = amat, x = 3, possible = TRUE, ds = FALSE, type = "pdag") ## all nodes
possAn(m = amat, x = 3, y = 2, possible = TRUE, ds = FALSE, type = "pdag") ## only node 1
```

---

possDe *Find possible descendants of given node(s).*

Description

In a DAG, CPDAG, MAG or PAG determine which nodes are (possible) descendants of x on definite status or just any paths potentially avoiding given nodes on the paths.

Usage

```
possDe(m, x, y = NULL, possible = TRUE, ds = TRUE,
type = c("cpdag", "pdag", "dag", "mag", "pag"))
```

Arguments

m	Adjacency matrix in coding according to type.
x	Node positions of starting nodes.
y	Node positions of nodes through which a path must not go.
possible	If TRUE, possible descendents are returned.
ds	If TRUE, only paths of definite status are considered.
type	Type of adjacency matrix in m. The coding is according to amatType.

Details

Not all possible combinations of the arguments are currently implemented and will issue an error if called.

Value

Vector of all node positions found as (possible) descendents of the nodes in x.

Author(s)

Markus Kalisch

See Also

amatType

Examples

```
## a -> b -- c
amat <- matrix(c(0,1,0, 0,0,1, 0,1,0), 3,3)
colnames(amat) <- rownames(amat) <- letters[1:3]
if (require(Rgraphviz)) plot(as(t(amat), "graphNEL"))

possDe(m = amat, x = 1, possible = TRUE, ds = FALSE, type = "pdag") ## all nodes
possDe(m = amat, x = 1, possible = FALSE, ds = FALSE, type = "pdag") ## only nodes 1 and 2
possDe(m = amat, x = 1, y = 2, possible = TRUE, ds = FALSE, type = "pdag") ## only node 1
```

---

possibleDe *[DEPRECATED] Find possible descendants on definite status paths.*

Description

This function is DEPRECATED! Use possDe instead.

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

Usage

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

Arguments

amat	adjacency matrix of type amat.pag
x	(integer) position of node x (node of interest) in the adjacency matrix.

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 (2015), 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

M.H. Maathuis and D. Colombo (2015). A generalized back-door criterion. *Annals of Statistics* **43** 1060-1088.

See Also

backdoor, amatType

Examples

```
amat <- matrix( c(0,3,0,0,0,0, 2,0,2,0,0,0, 0,3,0,0,0,0, 0,0,0,0,1,0,
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 *Compute Possible-D-SEP(x,G) of a node x in a PDAG G*

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.

See Spirtes et al (2000) or Definition 3.3 of Colombo et al (2012).

Usage

```
qreach(x, amat, verbose = FALSE)
```

Arguments

x	(integer) position of vertex x in the adjacency matrix of which Possible-D-SEP set is to be computed.
amat	Adjacency matrix of type amat.pag.
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

P. Spirtes, C. Glymour and R. Scheines (2000). *Causation, Prediction, and Search*, 2nd edition, The MIT Press.

D. Colombo, M.H. Maathuis, M. Kalisch, T.S. Richardson (2012). Learning high-dimensional directed acyclic graphs with latent and selection variables. *Annals of Statistics* **40**, 294–321.

See Also

`fci` and `pdsep` which both use this function.

---

r.gauss.pardag *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, labels = as.character(1:p),
               lbv = 0.5, ubv = 1)
```

Arguments

`p`	the 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.
`labels`	(optional) character vector of variable (or "node") names.
`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@bfh.ch>)

References

P. Erdős and A. Rényi (1960). On the evolution of random graphs. *Publications of the Mathematical Institute of the Hungarian Academy of Sciences* **5**, 17–61.

A. Hauser and P. Bühlmann (2012). Characterization and greedy learning of interventional Markov equivalence classes of directed acyclic graphs. *Journal of Machine Learning Research* **13**, 2409–2464.

See Also

GaussParDAG, randomDAG

Examples

```
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 weigths 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$weight.mat()
V <- myDAG$err.var()
any((B > 0 & B < 0.1) | B > 1)
any(V < 0.5 | V > 1.5)
diag(myDAG$cov.mat())
```

---

randDAG *Random DAG Generation*

Description

Generating random directed acyclic graphs (DAGs) with fixed expected number of neighbours. Several different methods are provided, each intentionally biased towards certain properties. The methods are based on the analogue `*.game` functions in the **igraph** package.

Usage

```
randDAG(n, d, method ="er", par1=NULL, par2=NULL,
        DAG = TRUE, weighted = TRUE, wFUN = list(runif, min=0.1, max=1))
```

Arguments

`n`	integer, at least 2, indicating the number of nodes in the DAG.
`d`	a positive number, corresponding to the expected number of neighbours per node, more precisely the expected sum of the in- and out-degree.
`method`	a string, specifying the method used for generating the random graph. See details below.
`par1`, `par2`	optional additional arguments, dependent on the method. See details.
`DAG`	logical, if `TRUE`, labelled graph is directed to a labelled acyclic graph.
`weighted`	logical indicating if edge weights are computed according to `wFUN`.

wFUN — a function for computing the edge weights in the DAG. It takes as first argument a number of edges m for which it returns a vector of length m containing the weights. Alternatively, wFUN can be a list consisting of the function in the first entry and of further arguments of the function in the additional entries. The default (only if weighted is true) is a uniform weight in $[0.1, 1]$. See the examples for more.

Details

A (weighted) random graph with n nodes and expected number of neighbours d is constructed. For DAG=TRUE, the graph is oriented to a DAG. There are eight different random graph models provided, each selectable by the parameters method, par1 and par2, with method, a string, taking one of the following values:

regular: Graph where every node has exactly d incident edges. par1 and par2 are not used.

watts: Watts-Strogatz graph that interpolates between the regular (par1->0) and Erdoes-Renyi graph (par1->1). The parameter par1 is per default 0.5 and has to be in (0,1). par2 is not used.

er: Erdoes-Renyi graph where every edge is present independently. par1 and par2 are not used.

power: A graph with power-law degree distribution with expectation d.par1 and par2 are not used.

bipartite: Bipartite graph with at least par1*n nodes in group 1 and at most (1-par1)*n nodes in group 2. The argument par1 has to be in [0,1] and is per default 0.5. par2 is not used.

barabasi: A graph with power-law degree distribution and preferential attachement according to parameter par1. It must hold that par1 >= 1 and the default is par1=1. par2 is not used.

geometric: A geometric random graph in dimension par1, where par1 can take values from {2,3,4,5} and is per default 2. If par2="geo" and weighted=TRUE, then the weights are computed according to the Euclidean distance. There are currently no other option for par2 implemented.

interEr: A graph with par1 islands of Erdoes-Renyi graphs, every pair of those connected by a certain number of edges proportional to par2 (fraction of inter-connectivity). It is required that n/s be integer and par2 in $(0, 1)$. Defaults are par1=2 and par2=0.25, respectively.

Value

A graph object of class graphNEL.

Note

The output is *not* topologically sorted (as opposed to the output of randomDAG).

Author(s)

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

References

These methods are mainly based on the analogue functions in the **igraph** package.

See Also

the package **igraph**, notably help pages such as sample_k_regular or sample_smallworld;

unifDAG from package **unifDAG** for generating uniform random DAGs.

randomDAG a limited and soon deprecated version of randDAG; rmvDAG for generating multivariate data according to a DAG.

Examples

```
set.seed(38)
dag1 <- randDAG(10, 4, "regular")
dag2 <- randDAG(10, 4, "watts")
dag3 <- randDAG(10, 4, "er")
dag4 <- randDAG(10, 4, "power")
dag5 <- randDAG(10, 4, "bipartite")
dag6 <- randDAG(10, 4, "barabasi")
dag7 <- randDAG(10, 4, "geometric")
dag8 <- randDAG(10, 4, "interEr", par2 = 0.5)

if (require(Rgraphviz)) {
  par(mfrow=c(4,2))
  plot(dag1,main="Regular graph")
  plot(dag2,main="Watts-Strogatz graph")
  plot(dag3,main="Erdoes-Renyi graph")
  plot(dag4,main="Power-law graph")
  plot(dag5,main="Bipartite graph")
  plot(dag6,main="Barabasi graph")
  plot(dag7,main="Geometric random graph")
  plot(dag8,main="Interconnected island graph")
}

set.seed(45)
dag0 <- randDAG(6,3)
dag1 <- randDAG(6,3, weighted=FALSE)
dag2 <- randDAG(6,3, DAG=FALSE)
if (require(Rgraphviz)) {
  par(mfrow=c(1,2))
  plot(dag1)
  plot(dag2)      ## undirected graph
}
dag0@edgeData   ## note the uniform weights between 0.1 and 1
dag1@edgeData   ## note the constant weights

wFUN <- function(m,lB,uB) { runif(m,lB,uB) }
dag <- randDAG(6,3,wFUN=list(wFUN,1,4))
dag@edgeData   ## note the uniform weights between 1 and 4
```

---

randomDAG *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, lB = 0.1, 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 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 graph-class from package **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

randDAG for a more elaborate version of this function; rmvDAG for generating data according to a DAG; compareGraphs for comparing the skeleton of a DAG with some other undirected graph (in terms of TPR, FPR and TDR).

Examples

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

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

Description

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

Usage

```
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,
     numCores = 1, 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.
numCores	Specifies the number of cores to be used for parallel estimation of skeleton.
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 o-o 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$(d, c) \setminus \{f1, f2\}$. 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 (2014) 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, 2014).

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 (2014).

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

D. Colombo and M.H. Maathuis (2014).Order-independent constraint-based causal structure learning. *Journal of Machine Learning Research* **15** 3741-3782.

D. Colombo, M. H. Maathuis, M. Kalisch, T. S. Richardson (2012). Learning high-dimensional directed acyclic graphs with latent and selection variables. *Ann. Statist.* **40**, 294-321.

See Also

`fci` and `fciPlus` 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`, `disCItest`, `binCItest` and `dsepTest` as examples for `indepTest`.

Examples

```
##################################################
## 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 RFCI algorithm
suffStat <- list(C = cov2cor(trueCov(myDAG)), n = 10^9)
indepTest <- gaussCItest
res <- rfci(suffStat, indepTest, alpha = 0.9999, p=p, verbose=TRUE)

################################################%  --------------
## 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=3,weights=c(1))
edL[[3]] <- list(edges=5,weights=c(1))
edL[[4]] <- list(edges=5,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 RFCI 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(1,0,0,2),
                  c(0,3,3,0))
## check that estimated and correct PAG are in agreement:
stopifnot(corr.pag == rfci.pag@amat)
```

---

rmvDAG *Generate Multivariate Data according to a DAG*

Description

Generate multivariate data with dependency structure specified by a (given) DAG (**D**irected **A**cyclic **G**raph) with nodes corresponding to random variables. The DAG has to be **topologically ordered**.

Usage

```
rmvDAG(n, dag,
       errDist = c("normal", "cauchy", "t4", "mix", "mixt3", "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", "mixt3" 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", "mixt3", "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 distributuion, `mix` specifies the fraction of "outlier" samples (i.e., Cauchy, t_3 or $N(0, 100)$).
`errMat`	numeric $n * p$ matrix specifiying 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

$$X_i = w_1 * X_1 + \ldots + w_k * X_k + E_i.$$

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

Value

A $n * p$ 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

```
## 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@bfh.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, GaussL0penIntScore and GaussL0penObsScore.

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.

.nodes: Node labels. They are passed to causal inference methods by default to label the nodes of the resulting graph.

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.

.pardag.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

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

nodes Node labels

... 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.fit(vertex, parents, ...)` Calculates a local model fit of a vertex and its parents, e.g. by MLE. 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.fit(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@bfh.ch>)

References

T. Silander and P. Myllymäki (2006). A simple approach for finding the globally optimal Bayesian network structure. *Proceedings of the 22nd Conference on Uncertainty in Artificial Intelligence (UAI 2006)*, 445–452

See Also

`ges`, `gies`, `simy`, `GaussL0penIntScore`, `GaussL0penObsScore`

`searchAM` *Search for certain nodes in a DAG/CPDAG/MAG/PAG*

Description

Searches for all ancestors, descendants, anteriors, spouses, neighbors, parents, children or possible descendants of a (set of) node(s) in a DAG, CPDAG, MAG or PAG.

Usage

```
searchAM(amat,x,
  type = c("an", "de", "ant", "sp", "nb", "pa", "ch", "pde"))
```

Arguments

`amat`	Adjacency matrix of type amat.pag.
`x`	Target node(s), given as (a vector of) column number(s) of the node(s) in the adjacency matrix.
`type`	Character string specifying which relation to the target nodes in `x` is asked for. It can be one of:
	"an" ancestors: nodes `y` s.t. `y-->...-->x`;

"de" descendants: nodes y s.t. y<--...<--x;

"ant" anteriors: nodes y s.t. y---...---z-->...-->x, i.e. there is an undirected path from y to a node z followed by a directed path from z to x;

"sp" spouses: nodes y s.t. y<->x;

"nb" neighbors: nodes y s.t. y---x;

"pa" parents: nodes y s.t. y-->x;

"ch" children: nodes y s.t. y<--x;

"pde" possible descendants: nodes y s.t. there is a possibly directed path from y to x: y {o,-}--{o,>} ... {o,-}--{o,>} x.

For the precise definitions of these concepts, see the references.

Details

This function performs a search for nodes related to the set of target nodes x in the way specified by type in adjacency matrix amat of type amat.pag.

Value

Vector of column numbers of the nodes related to x as specified by type.

Author(s)

Joris Mooij.

References

T.S. Richardson and P. Spirtes (2002). Ancestral graph Markov models. *Annals of Statistics* **30** 962-1030.

J. Zhang (2008). Causal Reasoning with Ancestral Graphs. *Journal of Machine Learning Research* **9** 1437-1474.

Examples

```
# Y-structure MAG
# Encode as adjacency matrix
p <- 10 # total number of variables
V <- c("X1","X2","X3","X4","X5","X6","X7","X8","X9","X10") # variable labels
# amat[i,j] = 0 iff no edge btw i,j
# amat[i,j] = 1 iff i *-o j
# amat[i,j] = 2 iff i *-> j
# amat[i,j] = 3 iff i *-- j
amat <- rbind(c(0,3,0,0,0,0,0,0,0,0),
              c(3,0,3,0,0,0,0,0,0,0),
              c(0,3,0,2,0,0,0,0,0,0),
              c(0,0,3,0,2,0,0,0,0,0),
              c(0,0,0,3,0,2,0,2,2,1),
              c(0,0,0,0,3,0,2,0,0,0),
              c(0,0,0,0,0,3,0,0,0,0),
              c(0,0,0,0,2,0,0,0,0,0),
```

```
              c(0,0,0,0,1,0,0,0,0,0),
              c(0,0,0,0,1,0,0,0,0,0))
rownames(amat)<-V
colnames(amat)<-V

stopifnot(all.equal(searchAM(amat,5,type = "an"), c(3,4,5))) # ancestors of X5
stopifnot(all.equal(searchAM(amat,5,type = "de"), c(5,6,7))) # descendants of X5
stopifnot(all.equal(searchAM(amat,5,type = "ant"), c(1,2,3,4,5))) # anteriors of X5
stopifnot(all.equal(searchAM(amat,5,type = "sp"), c(8))) # spouses of X5
stopifnot(all.equal(searchAM(amat,2,type = "nb"), c(1,3))) # neighbors of X2
stopifnot(all.equal(searchAM(amat,c(4,6),type = "pa"), c(3,5))) # parents of {X4,X6}
stopifnot(all.equal(searchAM(amat,c(3,5),type = "ch"), c(4,6))) # children of {X3,X5}
stopifnot(all.equal(searchAM(amat,5,type = "pde"), c(5,6,7,9,10))) # possible descendants of X5
```

---

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

```
shd(g1,g2)
```

Arguments

g1	Graph object
g2	Graph object

Value

The value of the SHD (numeric).

Author(s)

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

References

I. Tsamardinos, L.E. Brown and C.F. Aliferis (2006). The Max-Min Hill-Climbing Bayesian Network Structure Learning Algorithm. *JMLR* **65**, 31–78.

Examples

```
## generate two graphs
g1 <- randomDAG(10, prob = 0.2)
g2 <- randomDAG(10, prob = 0.2)
## compute SHD
(shd.val <- shd(g1,g2))
```

---

showAmat *Show Adjacency Matrix of pcAlgo object*

Description

This function is deprecated - Use `as(*, "amat")` instead !

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

Usage

```
showAmat(object)
```

Arguments

object	an R object of class pcAlgo, as returned from skeleton() or pc().

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().

showEdgeList *Show Edge List of pcAlgo object*

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

none; 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().

simy *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

```
simy(score, labels = score$getNodes(), targets = score$getTargets(),
    verbose = FALSE, ...)
```

Arguments

score	An instance of a class derived from Score.
labels	Node labels; by default, they are determined from the scoring object.
targets	A list of intervention targets (cf. details). A list of vectors, each vector listing the vertices of one intervention target.
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 $a \longrightarrow b$ 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.

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@bfh.ch>)

References

T. Silander and P. Myllymäki (2006). A simple approach for finding the globally optimal Bayesian network structure. *Proceedings of the 22nd Conference on Uncertainty in Artificial Intelligence (UAI 2006)*, 445–452

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(score)
eDAG <- simy.fit$essgraph
as(eDAG, "graph")

## Look at the graph incidence matrix (a "sparseMatrix"):
if(require(Matrix))
  show( as(as(eDAG, "graphNEL"), "Matrix") )


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

---

skeleton — *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,
         numCores = 1, 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.
`numCores`	number of processor cores to use for parallel computation. Only available for `method = "stable.fast"`.
`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 indepedence 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 (2014) 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 (2014) 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 ($m = 0, 1, \dots$) 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
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.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 (2014). 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 (2014)).

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, Alain Hauser, and Diego Colombo.

References

D. Colombo and M.H. Maathuis (2014).Order-independent constraint-based causal structure learning. *Journal of Machine Learning Research* **15** 3741-3782.

D. Colombo, M. H. Maathuis, M. Kalisch, T. S. Richardson (2012). Learning high-dimensional directed acyclic graphs with latent and selection variables. *Ann. Statist.* **40**, 294-321.

M. Kalisch and P. Buehlmann (2007). *Estimating high-dimensional directed acyclic graphs with the PC-algorithm*, JMLR **8** 613-636.

P. Spirtes, C. Glymour and R. Scheines (2000). *Causation, Prediction, and Search*, 2nd edition, MIT Press.

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

```
##################################################
## Using Gaussian Data
##################################################
## Load predefined data
data(gmG)
n <- nrow    (gmG8$x)
V <- colnames(gmG8$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
data(gmB)
X <- gmB$x

## estimate Skeleton
skel.fm2 <- skeleton(suffStat = list(dm = X, adaptDF = FALSE),
                     indepTest = binCItest, alpha = 0.01,
                     labels = colnames(X), verbose = TRUE)
if (require(Rgraphviz)) {
  ## show estimated Skeleton
  par(mfrow = c(1,2))
  plot(skel.fm2, main = "Binary Data 'gmB': Estimated Skeleton")
```

```
  plot(gmB$g, main = "True DAG")
}
```

`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

```
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)
```

---

udag2apag *Last step of RFCI algorithm: Transform partially oriented graph into RFCI-PAG*

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

```
udag2apag(apag, suffStat, indepTest, alpha, sepset,
          rules = rep(TRUE, 10), unfVect = NULL, verbose = FALSE)
```

Arguments

apag	Adjacency matrix of type amat.pag
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. Each separation set is a vector with (integer) positions of variables in the adjacency matrix. 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 addiitonal 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 unambigous 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 (2014).

Value

apag	Final adjacency matrix of type amat.pag
sepset	Updated list of separating sets

Author(s)

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

References

D. Colombo and M.H. Maathuis (2014).Order-independent constraint-based causal structure learning. *Journal of Machine Learning Research* **15** 3741-3782.

D. Colombo, M. H. Maathuis, M. Kalisch, T. S. Richardson (2012). Learning high-dimensional directed acyclic graphs with latent and selection variables. *Ann. Statist.* **40**, 294–321.

J. Zhang (2008). On the completeness of orientation rules for causal discovery in the presence of latent confounders and selection bias. *Artificial Intelligence* **172**, 1873–1896.

See Also

rfci, udag2pag, dag2pag, udag2pdag, udag2pdagSpecial, udag2pdagRelaxed

Examples

```
################################################%  --------       -----------
## 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, 0,0,0,1,0, 0,0,0,0,0, 0,0,0,1,0),5,5))
V <- LETTERS[1:5]
colnames(amat) <- rownames(amat) <- V
edL <- setNames(vector("list",length=5), V)
edL[[1]] <- list(edges= c(2,4),weights=c(1,1))
edL[[2]] <- list(edges= 3,     weights=c(1))
edL[[3]] <- list(edges= 5,     weights=c(1))
edL[[4]] <- list(edges= 5,     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)

n <- 100000
alpha <- 0.01
p <- ncol(true.corr)

if (require("MASS")) {
  ## generate 100000 samples of DAG using standard normal error distribution
  set.seed(289)
  d.mat <- mvrnorm(n, mu = 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")
```

```
  print(u.t <- find.unsh.triple(amat.resD)) # four of them

  ## check and orient v-structures
  vstrucs <- rfci.vStruc(suffStat, indepTest, alpha=alpha,
    sepset = resD@sepset, g.amat = amat.resD,
    unshTripl= u.t$unshTripl, unshVect = u.t$unshVect,
    verbose = TRUE)

  ## Estimate the final skeleton and extend it into a PAG
  ## (using all 10 rules, as per default):
  resP <- udag2apag(vstrucs$amat, suffStat, indepTest=indepTest, alpha=alpha,
      sepset=vstrucs$sepset, verbose = TRUE)
  print(Amat <- resP$graph)
} # only if "MASS" is there
```

---

udag2pag *Last steps of FCI algorithm: Transform Final Skeleton into FCI-PAG*

Description

This function performs the last steps of the FCI algorithm, as it transforms an unoriented final skeleton into a Partial Ancestral Graph (PAG). The final skeleton must have been estimated with pdsep() or fciplus.intern(). The result is an adjacency matrix indicating also the edge marks.

Usage

```
udag2pag(pag, sepset, rules = rep(TRUE, 10), unfVect = NULL,
  jci = c("0","1","12","123"), contextVars = NULL, verbose = FALSE,
  orientCollider = TRUE)
```

Arguments

pag	Adjacency matrix of type amat.pag
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. Each separation set is a vector with (integer) positions of variables in the adjacency matrix. This object is thought to be obtained from a pcAlgo-object.
rules	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.
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.
orientCollider	if TRUE, colliders are oriented.
jci	String specifying the JCI assumptions that are used. It can be one of:

"0" No JCI assumption is made (default),

"1" JCI assumption 1 (no system variable causes any context variable),

"12" JCI assumptions 1 and 2 (no system variable causes any context variable, and no system variable is confounded with any context variable),

"123" JCI assumptions 1, 2 and 3 (no system variable causes any context variable, no system variable is confounded with any context variable, and all context variables are confounded but are not direct causes of each other).

`contextVars` Subset of variable indices {1,...,p} that will be treated as context variables in the JCI extension.

Details

The skeleton is transformed into an FCI-PAG using rules by Zhang (2008). When using the JCI extension, additional adjacency and orientation rules incorporate the JCI background knowledge regarding the causal relations of the context variables; for details, see Mooij et al. (2020).

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 unambigous 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 (2014).

Value

Adjacency matrix of type amat.pag.

Author(s)

Diego Colombo and Markus Kalisch (<kalisch@stat.math.ethz.ch>); JCI extension by Joris Mooij.

References

D. Colombo and M.H. Maathuis (2014).Order-independent constraint-based causal structure learning. *Journal of Machine Learning Research* **15** 3741-3782.

D. Colombo, M. H. Maathuis, M. Kalisch, T. S. Richardson (2012). Learning high-dimensional directed acyclic graphs with latent and selection variables. *Ann. Statist.* **40**, 294–321.

J. M. Mooij, S. Magliacane, T. Claassen (2020). Joint Causal Inference from Multiple Contexts. *Journal of Machine Learning Research* **21**(99), 1–108.

J. Zhang (2008). On the completeness of orientation rules for causal discovery in the presence of latent confounders and selection bias. *Artificial Intelligence* **172**, 1873–1896.

See Also

fci, fciPlus, udag2apag, 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, 0,0,0,1,0, 0,0,0,0,0, 0,0,0,1,0),5,5))
V <- as.character(1:5)
colnames(amat) <- rownames(amat) <- V
edL <- vector("list",length=5)
names(edL) <- V
edL[[1]] <- list(edges= c(2,4),weights=c(1,1))
edL[[2]] <- list(edges= 3,     weights=c(1))
edL[[3]] <- list(edges= 5,     weights=c(1))
edL[[4]] <- list(edges= 5,     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
true.cov <- cov.mat[-L,-L]

## transform it in a correlation matrix
true.corr <- cov2cor(true.cov)

if (require("MASS")) {
  ## generate 100000 samples of DAG using standard normal error distribution
  n <- 100000
  alpha <- 0.01
  set.seed(314)
  d.mat <- mvrnorm(n, mu = rep(0,dim(true.corr)[1]), Sigma = true.cov)

  ## estimate the skeleton of given data
  suffStat <- list(C = cor(d.mat), n = n)
  indepTest <- gaussCItest
  resD <- skeleton(suffStat, indepTest, p=dim(true.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(true.corr)[2],
      resD@sepset, alpha = alpha, m.max = Inf,
      pMax = resD@pMax)

  ## extend the skeleton into a PAG using all 10 rules
  resP <- udag2pag(pag = pdsepRes$G, pdsepRes$sepset, rules = rep(TRUE,10),
     verbose = TRUE)
  colnames(resP) <- rownames(resP) <- as.character(2:5)
  print(resP)

} # only if "MASS" is there
```

---

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 indepedence tests or violations of the faithfulness assumption. The three functions deal with such conflicts in different ways, as described in Details.

Usage

```
udag2pdag       (gInput, verbose)
udag2pdagRelaxed(gInput, verbose, unfVect=NULL, solve.confl=FALSE,
  orientCollider = TRUE, rules = rep(TRUE, 3))
udag2pdagSpecial(gInput, verbose, n.max=100)
```

Arguments

gInput	"pcAlgo"-object containing skeleton and conditional indepedence 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.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. 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.
orientCollider	if TRUE, collider are oriented.
rules	Array of length 3 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.

Details

for udag2pdag**:** 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 udag2pdag 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 udag2pdagSpecial**:** If the graph after orienting the v-structures as in udag2pdag 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 udag2pdag 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 udag2pdagRelaxed**:** 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 unambigous 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.confl = FALSE`, earlier edge orientations are overwritten by later ones as in `udag2pdag` and `udag2pdagSpecial`.

If `solv.confl = 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 (2014)).

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 (type amat.cpdag) .

amat1 Adjacency matrix of final graph with v-structures after changing the ordering in which the v-structures are considered (type amat.cpdag) .

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

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P. Spirtes, C. Glymour and R. Scheines (2000) *Causation, Prediction, and Search*, 2nd edition, The MIT Press.

J. Pearl (2000), *Causality*, Cambridge University Press.

D. Colombo and M.H. Maathuis (2014).Order-independent constraint-based causal structure learning. *Journal of Machine Learning Research* **15** 3741-3782.

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
d.mat <- rmvDAG(n, myDAG, errDist = "normal")

## estimate skeleton
resU <- skeleton(suffStat = list(C = cor(d.mat), n = n),
                 indepTest = gaussCItest, ## (partial correlations)
                 alpha = 0.05, p=p)

## orient edges using three different methods
resD1 <- udag2pdagRelaxed(resU, verbose=0)
resD2 <- udag2pdagSpecial(resU, verbose=0, n.max=100)
resD3 <- udag2pdag       (resU, verbose=0)
```

---

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 of type amat.pag
x, z	(integer) position of variable x and z, respectively, in the adjacency matrix.

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 (2015), Def. 3.1)

Value

TRUE if edge is visible, otherwise FALSE.

Author(s)

Diego Colombo

References

M.H. Maathuis and D. Colombo (2015). A generalized backdoor criterion. Annals of Statistics 43 1060-1088.

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 *Weight Matrix of a Graph, e.g., a simulated DAG*

Description

Given a graph object g, as generated e.g., by randomDAG, return the matrix of its edge weights, the "weight matrix".

Usage

```
wgtMatrix(g, transpose = TRUE)
```

Arguments

g	graph object (package **graph**) of, say, p nodes, e.g. containing a DAG.
transpose	logical indicating if the weight matrix should be transposed (t(.), 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, M[i,j] is the weight of the edge from i to j.

Nowadays, this is a trivial wrapper around `as(g, "matrix")` using the (`coerce`) method provided by the **graph** package.

Value

The $p \times p$ weight matrix `M`.

Note

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

```
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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