

Package: kpcalg (via r-universe)

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Title Kernel PC Algorithm for Causal Structure Detection

Description Kernel PC (kPC) algorithm for causal structure learning and causal inference using graphical models. kPC is a version of PC algorithm that uses kernel based independence criteria in order to be able to deal with non-linear relationships and non-Gaussian noise.

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dcov.gamma	<i>Test to check the independence between two variables x and y using the Distance Covariance. The dcov.gamma() function, uses Distance Covariance independence criterion with gamma approximation to test for independence between two random variables.</i>
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Description

Test to check the independence between two variables x and y using the Distance Covariance. The dcov.gamma() function, uses Distance Covariance independence criterion with gamma approximation to test for independence between two random variables.

Usage

```
dcov.gamma(x, y, index = 1, numCol = 100)
```

Arguments

x	data of first sample
y	data of second sample
index	exponent on Euclidean distance, in (0,2]
numCol	Number of columns used in incomplete Singular Value Decomposition

Details

Let x and y be two samples of length n. Gram matrices K and L are defined as: $K_{i,j} = \|x_i - x_j\|^s$ and $L_{i,j} = \|y_i - y_j\|^s$, where $0 < s < 2$. $H_{i,j} = \delta_{i,j} - \frac{1}{n}$. Let $A = HKH$ and $B = HLH$, then $nV^2 = \frac{1}{n^2} \sum A_{i,j} B_{i,j}$. For more detail: [dcov.test](#) in package energy. Gamma test compares $nV_n^2(x, y)$ with the α quantile of the gamma distribution with mean and variance same as nV_n^2 under independence hypothesis.

Value

dcov.gamma() returns a list with class htest containing

method	description of test
statistic	observed value of the test statistic
estimate	$nV^2(x,y)$
estimates	a vector: [$nV^2(x,y)$, mean of $nV^2(x,y)$, variance of $nV^2(x,y)$]
replicates	replicates of the test statistic
p.value	approximate p-value of the test
data.name	description of data

Author(s)

Petras Verbyla (<petras.verbyla@mrc-bsu.cam.ac.uk>) and Nina Ines Bertille Desgranges

References

- A. Gretton et al. (2005). Kernel Methods for Measuring Independence. *JMLR* 6 (2005) 2075-2129.
- G. Szekely, M. Rizzo and N. Bakirov (2007). Measuring and Testing Dependence by Correlation of Distances. *The Annals of Statistics* 2007, Vol. 35, No. 6, 2769-2794.

See Also

[hsic.perm](#), [hsic.clust](#), [hsic.gamma](#), [dcov.test](#), [kernelCItest](#)

Examples

```
library(energy)
set.seed(10)
#independence
x <- runif(300)
y <- runif(300)

hsic.gamma(x,y)
hsic.perm(x,y)
dcov.gamma(x,y)
dcov.test(x,y)

#uncorelated but not dependent
z <- 10*(runif(300)-0.5)
w <- z^2 + 10*runif(300)

cor(z,w)
hsic.gamma(z,w)
hsic.perm(z,w)
dcov.gamma(z,w)
dcov.test(z,w)
```

frml.additive.smooth *Formula for GAM without crossterms*

Description

Creates a formula for [gam](#) to be used in [regrXonS](#). For data $X = (X_1, \dots, X_n, X_{n+1}, \dots, X_m)$, variable to be regressed X_i , $i=1\dots n$ and variables to regress on $S = X_{n+1}, \dots, X_m$ creates formula $X_i \sim s(X_{n+1}) + \dots + s(X_m)$.

Usage

```
frml.additive.smooth(target.ind, pred.inds, var.str = "x")
```

Arguments

target.ind	integer, number for the variable to be regressed
pred.inds	integer(s), number(s) for the variable(s) on which we regress
var.str	name of variables used to create formula, default is "x"

Value

formula.additive.smooth() returns a formula $X_i \sim s(X_{n+1}) + \dots + s(X_m)$

Author(s)

Petras Verbyla (<petras.verbyla@mrc-bsu.cam.ac.uk>)

See Also

[regrXonS](#)

frml.full.smooth *Formula for GAM with crossterms*

Description

Creates a formula for [gam](#) to be used in [regrXonS](#). For data $X = (X_1, \dots, X_n, X_{n+1}, \dots, X_m)$, variable to be regressed X_i , $i=1\dots n$ and variables to regress on $S = X_{n+1}, \dots, X_m$ creates formula $X_i \sim s(X_{n+1}, \dots, X_m)$.

Usage

```
frml.full.smooth(target.ind, pred.inds, var.str = "x")
```

Arguments

target.ind	integer, number for the variable to be regressed
pred.ind	integer(s), number(s) for the variable(s) on which we regress
var.str	name of variables used to create formula, default is "x"

Value

formula.full.smooth() returns a formula $X_i \sim s(X_{n+1}, \dots, X_m)$

Author(s)

Petras Verbyla (<petras.verbyla@mrc-bsu.cam.ac.uk>)

See Also

[regrXonS](#)

hsic.clust	<i>HSIC cluster permutation conditional independence test</i>
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Description

Conditional independence test using HSIC and permutation with clusters.

Usage

```
hsic.clust(x, y, z, sig = 1, p = 100, numCluster = 10, numCol = 50,
  eps = 0.1, paral = 1)
```

Arguments

x	first variable
y	second variable
z	set of variables on which we condition
sig	the with of the Gaussian kernel
p	the number of permutations
numCluster	number of clusters for clustering z
numCol	maximum number of columns that we use for the incomplete Cholesky decomposition
eps	normalization parameter for HSIC cluster test
paral	number of cores used

Details

Let x and y be two samples of length n . Gram matrices K and L are defined as: $K_{i,j} = \exp\left(\frac{(x_i - x_j)^2}{\sigma^2}\right)$, $L_{i,j} = \exp\left(\frac{(y_i - y_j)^2}{\sigma^2}\right)$ and $M_{i,j} = \exp\left(\frac{(z_i - z_j)^2}{\sigma^2}\right)$. $H_{i,j} = \delta_{i,j} - \frac{1}{n}$. Let $A = HKH$, $B = HLH$ and $C = HMMH$. $HSIC(X, Y|Z) = \frac{1}{n^2} \text{Tr}(AB - 2AC(C + \epsilon I)^{-2}CB + AC(C + \epsilon I)^{-2}CBC(C + \epsilon I)^{-2}C)$. Permutation test clusters Z and then permutes Y in the clusters of Z p times to get $Y_{(p)}$ and calculates $HSIC(X, Y_{(p)}|Z)$. $pval = \frac{1(HSIC(X, Y|Z) > HSIC(Z, Y_{(p)}|Z))}{p}$.

Value

hsic.clust() returns a list with class htest containing

method	description of test
statistic	observed value of the test statistic
estimate	HSIC(x,y)
estimates	a vector: [HSIC(x,y), mean of HSIC(x,y), variance of HSIC(x,y)]
replicates	replicates of the test statistic
p.value	approximate p-value of the test
data.name	description of data

Author(s)

Petrás Verbyla (<petras.verbyla@mrc-bsu.cam.ac.uk>) and Nina Ines Bertille Desgranges

References

Tillman, R. E., Gretton, A. and Spirtes, P. (2009). Nonlinear directed acyclic structure learning with weakly additive noise model. NIPS 22, Vancouver.

K. Fukumizu et al. (2007). Kernel Measures of Conditional Dependence. NIPS 20. <https://papers.nips.cc/paper/3340-kernel-measures-of-conditional-dependence.pdf>

See Also

[hsic.gamma](#), [hsic.perm](#), [kernelCItest](#)

Examples

```
library(energy)
set.seed(10)
# x and y dependent, but independent conditionally on z
z <- 10*runif(300)
x <- sin(z) + runif(300)
y <- cos(z) + runif(300)
plot(x,y)
hsic.gamma(x,y)
hsic.perm(x,y)
dcov.test(x,y)
hsic.clust(x,y,z)
```

 hsic.gamma

Hilber Schmidt Independence Criterion gamma test

Description

Test to check the independence between two variables x and y using HSIC. The `hsic.gamma()` function, uses Hilbert-Schmidt independence criterion to test for independence between random variables.

Usage

```
hsic.gamma(x, y, sig = 1, numCol = 100)
```

Arguments

<code>x</code>	data of first sample
<code>y</code>	data of second sample
<code>sig</code>	Gaussian kernel width for HSIC tests. Default is 1
<code>numCol</code>	maximum number of columns that we use for the incomplete Cholesky decomposition

Details

Let x and y be two samples of length n . Gram matrices K and L are defined as: $K_{i,j} = \exp\left(\frac{(x_i - x_j)^2}{\sigma^2}\right)$ and $L_{i,j} = \exp\left(\frac{(y_i - y_j)^2}{\sigma^2}\right)$. $H_{i,j} = \delta_{i,j} - \frac{1}{n}$. Let $A = HKH$ and $B = HLH$, then $HSIC(x, y) = \frac{1}{n^2} Tr(AB)$. Gamma test compares $HSIC(x, y)$ with the α quantile of the gamma distribution with mean and variance such as $HSIC$ under independence hypothesis.

Value

`hsic.gamma()` returns a list with class `hstest` containing

<code>method</code>	description of test
<code>statistic</code>	observed value of the test statistic
<code>estimate</code>	$HSIC(x, y)$
<code>estimates</code>	a vector: [$HSIC(x, y)$, mean of $HSIC(x, y)$, variance of $HSIC(x, y)$]
<code>replicates</code>	replicates of the test statistic
<code>p.value</code>	approximate p-value of the test
<code>data.name</code>	description of data

Author(s)

Petras Verbyla (<petras.verbyla@mrc-bsu.cam.ac.uk>) and Nina Ines Bertille Desgranges

References

A. Gretton et al. (2005). Kernel Methods for Measuring Independence. *JMLR* 6 (2005) 2075-2129.

See Also

[hsic.perm](#), [hsic.clust](#), [kernelCItest](#)

Examples

```
library(energy)
set.seed(10)
#independence
x <- runif(300)
y <- runif(300)

hsic.gamma(x,y)
hsic.perm(x,y)
dcov.gamma(x,y)
dcov.test(x,y)

#uncorelated but not dependent
z <- 10*(runif(300)-0.5)
w <- z^2 + 10*runif(300)

cor(z,w)
hsic.gamma(z,w)
hsic.perm(z,w)
dcov.gamma(z,w)
dcov.test(z,w)
```

hsic.perm

Hilber Schmidt Independence Criterion permutation test

Description

Test to check the independence between two variables x and y using HSIC. The `hsic.perm()` function, uses Hilbert-Schmidt independence criterion to test for independence between random variables.

Usage

```
hsic.perm(x, y, sig = 1, p = 100, numCol = 50)
```

Arguments

<code>x</code>	data of first sample
<code>y</code>	data of second sample
<code>sig</code>	Gaussian kernel width for HSIC tests. Default is 1

p	Number of permutations. Default is 100
numCol	maximum number of columns that we use for the incomplete Cholesky decomposition

Details

Let x and y be two samples of length n . Gram matrices K and L are defined as: $K_{i,j} = \exp \frac{(x_i - x_j)^2}{\sigma^2}$ and $L_{i,j} = \exp \frac{(y_i - y_j)^2}{\sigma^2}$. $H_{i,j} = \delta_{i,j} - \frac{1}{n}$. Let $A = HKH$ and $B = HLH$, then $HSIC(x, y) = \frac{1}{n^2} Tr(AB)$. Permutation test permutes y p times to get $y_{(p)}$ and calculates $HSIC(x, y_{(p)})$. $pval = \frac{1(HSIC(x, y) > HSIC(x, y_{(p)}))}{p}$.

Value

hsic.perm() returns a list with class htest containing

method	description of test
statistic	observed value of the test statistic
estimate	HSIC(x,y)
estimates	a vector: [HSIC(x,y), mean of HSIC(x,y), variance of HSIC(x,y)]
replicates	replicates of the test statistic
p.value	approximate p-value of the test
data.name	description of data

Author(s)

Petras Verbyla (<petras.verbyla@mrc-bsu.cam.ac.uk>) and Nina Ines Bertille Desgranges

References

A. Gretton et al. (2005). Kernel Methods for Measuring Independence. JMLR 6 (2005) 2075-2129.

See Also

[hsic.gamma](#), [hsic.clust](#), [kernelCItest](#)

Examples

```
library(energy)
set.seed(10)
#independence
x <- runif(300)
y <- runif(300)

hsic.gamma(x,y)
hsic.perm(x,y)
dcov.gamma(x,y)
dcov.test(x,y)
```

```
#uncorelated but not dependent
z <- 10*(runif(300)-0.5)
w <- z^2 + 10*runif(300)

cor(z,w)
hsic.gamma(z,w)
hsic.perm(z,w)
dcov.gamma(z,w)
dcov.test(z,w)
```

hsic.test

Hilber Schmidt Independence Criterion test

Description

Test to check the independence between two variables x and y using HSIC. The `hsic.test()` function, uses Hilbert-Schmidt independence criterion to test for independence between two random variables.

Usage

```
hsic.test(x, y, p = 0, hsic.method = c("gamma", "perm"), sig = 1,
  numCol = floor(length(x)/10))
```

Arguments

<code>x</code>	data of first sample
<code>y</code>	data of second sample
<code>p</code>	number of replicates, if 0
<code>hsic.method</code>	method for HSIC test, either gamma test hsic.gamma or permutation test hsic.perm
<code>sig</code>	Gaussian kernel width for HSIC. Default is 1
<code>numCol</code>	number of columns in the Incomplete Cholesky Decomposition of Gram matrices. Default is <code>floor(length(x)/10)</code>

Details

Let x and y be two samples of length n . Gram matrices K and L are defined as: $K_{i,j} = \exp \frac{(x_i - x_j)^2}{\sigma^2}$ and $L_{i,j} = \exp \frac{(y_i - y_j)^2}{\sigma^2}$. $H_{i,j} = \delta_{i,j} - \frac{1}{n}$. Let $A = HKH$ and $B = HLH$, then $HSIC(x, y) = \frac{1}{n^2} Tr(AB)$.

Value

`hsic.gamma()` returns a list with class `htest` containing

<code>method</code>	description of test
<code>statistic</code>	observed value of the test statistic

estimate	HSIC(x,y)
estimates	a vector: [HSIC(x,y), mean of HSIC(x,y), variance of HSIC(x,y)]
replicates	replicates of the test statistic
p.value	approximate p-value of the test
data.name	description of data

Author(s)

Petras Verbyla (<petras.verbyla@mrc-bsu.cam.ac.uk>) and Nina Ines Bertille Desgranges

References

A. Gretton et al. (2005). Kernel Methods for Measuring Independence. JMLR 6 (2005) 2075-2129.

See Also

[hsic.perm](#), [hsic.clust](#), [kernelCItest](#)

Examples

```
library(energy)
set.seed(10)
#independence
x <- runif(300)
y <- runif(300)

hsic.gamma(x,y)
hsic.perm(x,y)
dcov.gamma(x,y)
dcov.test(x,y)

#uncorelated but not dependent
z <- 10*(runif(300)-0.5)
w <- z^2 + 10*runif(300)

cor(z,w)
hsic.gamma(z,w)
hsic.perm(z,w)
dcov.gamma(z,w)
dcov.test(z,w)
```

kernelCItest

Kernel Conditional Independence test

Description

Test to check the (conditional) dependence between two variables x and y given a set of variables S , using independence criteria. The `kernelCItest()` function, uses Distance Covariance or Hilbert-Schmidt Independence Criterion to test for the (conditional) independence between random variables, with an interface that can easily be used in [skeleton](#), [pc](#) or [kpc](#).

Usage

```
kernelCItest(x, y, S = NULL, suffStat, verbose = FALSE, data,
            ic.method = NULL, p = NULL, index = NULL, sig = NULL, numCol = NULL,
            numCluster = NULL, eps = NULL, para1 = NULL)
```

Arguments

x, y, S	It is tested, whether x and y are conditionally independent given the subset S of the remaining nodes. x, y, S all are integers, corresponding to variable or node numbers.
suffStat	a list of parameters consisting of data, ic.method, p, index, sig, numCol, numCluster, eps, para1
verbose	a logical parameter, if TRUE, detailed output is provided.
data	numeric matrix with columns representing variables and rows representing samples
ic.method	Method for the (conditional) independence test: Distance Covariance (permutation or gamma test), HSIC (permutation or gamma test) or HSIC cluster
p	Number of permutations for Distance Covariance, HSIC permutation and HSIC cluster tests. Default is Distance Covariance
index	Number in (0,2] the power of the distance in the Distance Covariance
sig	Gaussian kernel width for HSIC tests. Default is 1
numCol	Number of columns used in the incomplete Cholesky decomposition. Default is 50
numCluster	Number of clusters for kPC clust algorithm
eps	Normalization parameter for kPC clust. Default is 0.1
para1	Number of cores to use for parallel calculations.

Value

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

Author(s)

Petras Verbyla (<petras.verbyla@mrc-bsu.cam.ac.uk>) and Nina Ines Bertille Desgranges

References

- G. Székely, M. Rizzo and N. Bakirov (2007). Measuring and Testing Dependence by Correlation of Distances. *The Annals of Statistics* 2007, Vol. 35, No. 6, 2769-2794.
- A. Gretton et al. (2005). Kernel Methods for Measuring Independence. *JMLR* 6 (2005) 2075-2129.
- R. Tillman, A. Gretton and P. Spirtes (2009). Nonlinear directed acyclic structure learning with weakly additive noise model. *NIPS* 22, Vancouver.

Examples

```

set.seed(10)
library(pcalg)
z <- 10*runif(300)
w <- 10*runif(300)
x <- sin(z) + runif(300)
y <- cos(z) + runif(300)

data <- cbind(x,y,z,w)

#conditionally independent
test1a <- kernelCItest(x=1,y=2,S=c(3),suffStat = list(data=data,ic.method="dcc.gamma"))
test2a <- kernelCItest(x=1,y=2,S=c(3),suffStat = list(data=data,ic.method="dcc.perm"))
test3a <- kernelCItest(x=1,y=2,S=c(3),suffStat = list(data=data,ic.method="hsic.gamma"))
test4a <- kernelCItest(x=1,y=2,S=c(3),suffStat = list(data=data,ic.method="hsic.perm"))
test5a <- kernelCItest(x=1,y=2,S=c(3),suffStat = list(data=data,ic.method="hsic.clust"))
test6a <- gaussCItest( x=1,y=2,S=c(3),suffStat = list(C=cor(data),n=4))

test1a
test2a
test3a
test4a
test5a
test6a

#dependent
test1b <- kernelCItest(x=1,y=2,S=c(4),suffStat = list(data=data,ic.method="dcc.gamma"))
test2b <- kernelCItest(x=1,y=2,S=c(4),suffStat = list(data=data,ic.method="dcc.perm"))
test3b <- kernelCItest(x=1,y=2,S=c(4),suffStat = list(data=data,ic.method="hsic.gamma"))
test4b <- kernelCItest(x=1,y=2,S=c(4),suffStat = list(data=data,ic.method="hsic.perm"))
test5b <- kernelCItest(x=1,y=2,S=c(4),suffStat = list(data=data,ic.method="hsic.clust"))
test6b <- gaussCItest( x=1,y=2,S=c(4),suffStat = list(C=cor(data),n=4))

test1b
test2b
test3b
test4b
test5b
test6b

```

Description

Estimates the weakly additive noise partially directed acyclic graph (WAN-PDAG) from observational data, using the kPC algorithm. This is a version of `pc` from `pcalg` package, that uses HSIC (`hsic.gamma`, `hsic.perm` or `hsic.clust`) or distance covariance (`dcov.test` or `dcov.gamma`) independence tests and `udag2wanpdag` instead of `udag2pdag` in the last step.

Usage

```
kpc(suffStat, indepTest, alpha, labels, p, fixedGaps = NULL,
    fixedEdges = NULL, NAdelate = TRUE, m.max = Inf, u2pd = c("relaxed",
    "rand", "retry"), skel.method = c("stable", "original", "stable.fast"),
    conservative = FALSE, maj.rule = FALSE, solve.conf1 = FALSE,
    verbose = FALSE)
```

Arguments

suffStat	a list of sufficient statistics, containing all necessary elements for the conditional independence decisions in the function <code>indepTest</code>
indepTest	A function for testing conditional independence. It is internally called as <code>indepTest(x,y,S,suffStat)</code> , and tests conditional independence of <code>x</code> and <code>y</code> given <code>S</code> . Here, <code>x</code> and <code>y</code> are variables, and <code>S</code> is a (possibly empty) vector of variables (all variables are denoted by their column numbers in the adjacency matrix). <code>suffStat</code> is a list, see the argument above. The return value of <code>indepTest</code> is the p-value of the test for conditional independence. Default is kernelCItest .
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 <code>p</code> .
p	(optional) number of variables (or nodes). May be specified if labels are not, in which case labels is set to 1:p.
fixedGaps	A logical matrix of dimension $p \times p$. If entry <code>[i,j]</code> or <code>[j,i]</code> (or both) are TRUE, the edge <code>i-j</code> is removed before starting the algorithm. Therefore, this edge is guaranteed to be absent in the resulting graph.
fixedEdges	A logical matrix of dimension $p \times p$. If entry <code>[i,j]</code> or <code>[j,i]</code> (or both) are TRUE, the edge <code>i-j</code> is never considered for removal. Therefore, this edge is guaranteed to be present in the resulting graph.
NAdelate	If <code>indepTest</code> 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 <code>skeleton</code> .
conservative	Logical indicating if the conservative PC is used. In this case, only option <code>u2pd = "relaxed"</code> 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.conf1	If TRUE, the orientation of the v-structures and the orientation rules work with lists for candidate sets and allow bi-directed edges to resolve conflicting edge orientations. In this case, only option <code>u2pd = relaxed</code> 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.
verbose	If TRUE, detailed output is provided.

Details

For more information: [pc](#).

Value

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

Author(s)

Petras Verbyla (<petras.verbyla@mrc-bsu.cam.ac.uk>)

References

Tillman, R. E., Gretton, A. and Spirtes, P. (2009). Nonlinear directed acyclic structure learning with weakly additive noise model. NIPS 22, Vancouver.

Examples

```
## Not run:
library(pcalg)
set.seed(4)
n <- 300
data <- NULL
x1 <- 2*(runif(n)-0.5)
x2 <- x1 + runif(n)-0.5
x3 <- x1^2 + 0.6*runif(n)
x4 <- rnorm(n)
x5 <- x3 + x4^2 + 2*runif(n)
x6 <- 10*(runif(n)-0.5)
x7 <- x6^2 + 5*runif(n)
x8 <- 2*x7^2 + 1.5*rnorm(n)
x9 <- x7 + 4*runif(n)
data <- cbind(x1,x2,x3,x4,x5,x6,x7,x8,x9)
true <- matrix(0,9,9)
true[c(1),c(2,3)]<-true[c(3,4),5]<-true[c(6),c(7)]<-true[c(7),c(8)]<-true[7,9]<-1

pc <- pc(suffStat = list(C = cor(data), n = 9),
        indepTest = gaussCItest,
        alpha = 0.9,
        labels = colnames(data),
        u2pd = "relaxed",
        skel.method = "stable",
```

```

      verbose = TRUE)
kpc1 <- kpc(suffStat = list(data=data, ic.method="dcc.perm"),
           indepTest = kernelCItest,
           alpha = 0.1,
           labels = colnames(data),
           u2pd = "relaxed",
           skel.method = "stable",
           verbose = TRUE)
kpc2 <- kpc(suffStat = list(data=data, ic.method="hsic.gamma"),
           indepTest = kernelCItest,
           alpha = 0.1,
           labels = colnames(data),
           u2pd = "relaxed",
           skel.method = "stable",
           verbose = TRUE)
kpc3 <- kpc(suffStat = list(data=data, ic.method="hsic.perm"),
           indepTest = kernelCItest,
           alpha = 0.1,
           labels = colnames(data),
           u2pd = "relaxed",
           skel.method = "stable",
           verbose = TRUE)
kpc4 <- kpc(suffStat = list(data=data, ic.method="hsic.clust"),
           indepTest = kernelCItest,
           alpha = 0.1,
           labels = colnames(data),
           u2pd = "relaxed",
           skel.method = "stable",
           verbose = TRUE)

if (require(Rgraphviz)) {
  par(mfrow=c(2,3))
  plot(pc,main="pc")
  plot(kpc1,main="dpc.perm")
  plot(kpc2,main="kpc.gamma")
  plot(kpc3,main="kpc.perm")
  plot(kpc4,main="kpc.clust")
  plot(as(true,"graphNEL"),main="True DAG")
}

## End(Not run)

```

regrVonPS

Check if variable can be regressed to independence on its parents

Description

Uses the generalised additive model [gam](#) to non-linearly and non-parametrically regress variable V on its parents and set of variables S.

Usage

```
regrVonPS(G, V, S, suffStat, indepTest = kernelCitest, alpha = 0.2)
```

Arguments

G	adjacency matrix, for the graph
V	integer, node which we regress
S	integer(s), set we regress on
suffStat	sufficient statistics to perform the independence test kernelCitest
indepTest	independence test to check for dependence between residuals of V and S
alpha	numeric cutoff for significance level of individual partial correlation tests

Value

regrVonPS() returns the number of p-values smaller than the cutoff, i.e 0 means residuals of V are independent of all variables in S

Author(s)

Petras Verbyla (<petras.verbyla@mrc-bsu.cam.ac.uk>)

```
regrXonS
```

Regress set of variables on its parents

Description

Uses the generalised additive model [gam](#) to non-linearly and non-parametrically regress set of variables X on a set of variables S and returns residuals of X.

Usage

```
regrXonS(X, S)
```

Arguments

X	numeric matrix, set of variables to be regressed. Each column represents separate variable
S	numeric matrix, set of variables we will regress on. Each column represents separate variable

Details

If the number of variables in S is ≤ 5 we use [frml.full.smooth](#) as formula for [gam](#) to regress X on S, otherwise we use [frml.additive.smooth](#).

Value

regrXonS() returns the residuals of X regressed on S.

Author(s)

Petras Verbyla (<petras.verbyla@mrc-bsu.cam.ac.uk>)

See Also

[kernelCItest](#)

Examples

```
set.seed(10)
library(energy)
z <- 10*runif(300)
w <- 10*runif(300)
x <- sin(z) + runif(300)
y <- cos(z) + runif(300)
data <- cbind(x,y,z,w)

hsic.gamma(x,y)
hsic.perm(x,y)
dcov.test(x,y)

resid <- regrXonS(cbind(x,y),cbind(z,w))

hsic.gamma(resid[,1],resid[,2])
hsic.perm(resid[,1],resid[,2])
dcov.test(resid[,1],resid[,2])
```

udag2wanpdag

Last kPC Algorithm Step: Extend Object with Skeleton to Completed PDAG

Description

This function performs the last (generalised transitive) step in the [kpc](#) algorithm. It transforms an object of the class "pcAlgo" containing a skeleton and corresponding conditional independence information into a weakly additive noise directed acyclic graph (CPDAG). The functions first determine the v-structures in the collider step, and then performs the Generalised Transitive Step as described in Tillman et al (2009) to orient as many of the remaining edges as possible.

Usage

```
udag2wanpdag(gInput, suffStat, indepTest = kernelCItest, alpha = 0.2,
  verbose = FALSE, unfVect = NULL, solve.conf1 = FALSE,
  orientCollider = TRUE, rules = rep(TRUE, 3))
```

Arguments

<code>gInput</code>	"pcAlgo"-object containing skeleton and conditional independence information.
<code>suffStat</code>	a list of sufficient statistics, containing all necessary elements for the conditional independence decisions in the function <code>indepTest</code> .
<code>indepTest</code>	A function for testing conditional independence. It is internally called as <code>indepTest(x,y,S,suffStat)</code> . Default is <code>kernelCItest</code> .
<code>alpha</code>	significance level (number in (0,1) for the individual conditional independence tests.
<code>verbose</code>	0: No output; 1: Details
<code>unfVect</code>	vector containing numbers that encode ambiguous triples (as returned by <code>pc.cons.intern</code>). This is needed in the conservative and majority rule PC algorithms.
<code>solve.confl</code>	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.
<code>orientCollider</code>	if TRUE, collider are oriented.
<code>rules</code>	Array of length 3 containing TRUE or FALSE for each rule. TRUE in position <code>i</code> means that rule <code>i</code> (R_i) will be applied. By default, all rules are used. <code>gInput</code>

Details

First we perform a collider step, that is orienting triples $a-b-c$ as $a \rightarrow b \leftarrow c$ iff b is not in separating set of a and c . Then we orient edges $a-S$ as $a \rightarrow S$ if b_r is independent of a set S , where b_r are the residuals of b non parametrically regressed on S and parents of b and none of the edges S_i-a can be oriented as $S_i \rightarrow a$, that is residuals S_i_r would be independent of a .

Value

An oriented object of class "pcAlgo".

References

Tillman, R. E., Gretton, A. and Spirtes, P. (2009). Nonlinear directed acyclic structure learning with weakly additive noise model. NIPS 22, Vancouver.

Examples

```
## Not run:
library(pcalg)
set.seed(4)
n <- 300
data <- NULL
x1 <- 2*(runif(n)-0.5)
x2 <- x1 + runif(n)-0.5
x3 <- x1^2 + 0.6*runif(n)
x4 <- rnorm(n)
x5 <- x3 + x4^2 + 2*runif(n)
```

```

x6 <- 10*(runif(n)-0.5)
x7 <- x6^2 + 10*runif(n)
x8 <- 2*x7^2 + rnorm(n)
x9 <- x7 + 5*runif(n)
data <- cbind(x1,x2,x3,x4,x5,x6,x7,x8,x9)
true <- matrix(0,9,9)
true[c(1),c(2,3)]<-true[c(3,4),5]<-true[c(6),c(7)]<-true[c(7),c(8)]<-true[7,9]<-1
## estimate skeleton
resU1 <- skeleton(suffStat = list(data=data, ic.method="dcc.perm", p=200),
                 indepTest = kernelCItest,
                 verbose = TRUE, alpha = 0.1, p=9)

resU2 <- skeleton(suffStat = list(data=data, ic.method="hsic.gamma",
                                 sig=1, numCol = 50),
                 indepTest = kernelCItest,
                 verbose = TRUE, alpha = 0.1, p=9)

resU3 <- skeleton(suffStat = list(data=data, ic.method="hsic.perm",
                                 sig=1, numCol = 50, p=200),
                 indepTest = kernelCItest,
                 verbose = TRUE, alpha = 0.1, p=9)

resU4 <- skeleton(suffStat = list(data=data, ic.method="hsic.clust",
                                 p=200, sig=1, numCluster=100, numCol = 50,
                                 eps = 0.1, paral = 1),
                 indepTest = kernelCItest,
                 verbose = TRUE, alpha = 0.1, p=9)

resU5 <- skeleton(suffStat = list(C = cor(data), n = n),
                 indepTest = gaussCItest,
                 verbose = TRUE, alpha = 0.1, p=9)

if (require(Rgraphviz)) {
  par(mfrow=c(2,3))
  plot(resU1,main="dpc")
  plot(resU2,main="kpc-resid-gamma")
  plot(resU3,main="kpc-resid-perm")
  plot(resU4,main="kpc-clust")
  plot(resU5,main="pc")
  plot(as(true,"graphNEL"),main="True DAG")
}

## orient edges using three different methods
resD1 <- udag2wanpdag(gInput = resU1,
                    suffStat = list(data=data, ic.method="dcc.perm", sig=1, numCol = 50, p=200),
                    indepTest = kernelCItest,
                    verbose = TRUE, alpha = 0.1)
resD2 <- udag2wanpdag(gInput = resU1,
                    suffStat = list(data=data, ic.method="hsic.gamma", sig=1, numCol = 50),
                    indepTest = kernelCItest,
                    verbose = TRUE, alpha = 0.1)
resD3 <- udag2wanpdag(gInput = resU1,
                    suffStat = list(data=data, ic.method="hsic.perm", sig=1, numCol = 50, p=200),

```

```
                indepTest = kernelCitest,
                verbose = TRUE, alpha = 0.1)
resD4 <- udag2pdagRelaxed(gInput = resU1, verbose = T)
if (require(Rgraphviz)) {
  par(mfrow=c(2,3))
  plot(resD1,main="dpc")
  plot(resD2,main="kpc-resid-gamma")
  plot(resD3,main="kpc-resid-perm")
  plot(resD4,main="pc")
  plot(as(true,"graphNEL"),main="True DAG")
}

## End(Not run)
```

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