Package 'CopulaREMADA'

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Title Copula Mixed Effect Models for Bivariate and Trivariate Meta-Analysis of Diagnostic Test Accuracy Studies

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Depends R (>= 2.0.0), statmod, matlab, tensor

Description It has functions to implement the copula mixed models for bivariate and trivariate meta-analysis of diagnostic test accuracy studies.

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NeedsCompilation no

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R topics documented:

`betaDG` *The beta-D-Glucan-data*

Description

Data on 8 cohort studies inthemeta-analysis inKarageorgopouloset al.(2011). The interes there is to assess $beta$-D-Glucan as aserum or plasma marker for the presence of invasive fungal infections.

Usage

```
data(betaDG)
```

Format

A data frame with 8 observations on the following 4 variables.

TP the number of true positives

FN the number of false negatives

FP the number of false positives

TN the number of true negatives

References

Karageorgopoulos DE, Vouloumanou EK, Ntziora F, Michalopoulos A, Rafailidis PI, Falagas ME. (2011) $beta$-D-Glucan assay for the diagnosis of invasive fungal infections: a meta-analysis. *Clinical Infectious Diseases*, 52(6):750–770.

`CopulaREMADA` *Maximum likelihood estimation for copula mixed models for diagnostic test accurracy studies*

Description

For copula mixed models for diagnostic test accuracy studies numerical evaluation of the MLE is easily done with the following steps:

1. Calculate Gauss-Legendre quadrature points gl$nodes and weights gl$weights.

2. Convert from independent uniform quadrature points to dependent uniform quadrature points that have distribution 'cop'. The inverse of the conditional distribution qcondcop corresponding to the copula 'cop' is used to achieve this.

3. Numerically evaluate the joint probability mass function with the bivariate integral in a double sum.

With Gauss-Legendre quadrature, the same nodes and weights are used for different functions; this helps in yielding smooth numerical derivatives for numerical optimization via quasi-Newton. Our comparisons show that $n_q = 15$ is adequate with good precision to at least at four decimal places.

Usage

```
CopulaREMADA.norm(TP,FN,FP,TN,gl,mgrid,qcond,tau2par)
CopulaREMADA.beta(TP,FN,FP,TN,gl,mgrid,qcond,tau2par)
countermonotonicCopulaREMADA.norm(TP,FN,FP,TN,gl,mgrid)
countermonotonicCopulaREMADA.beta(TP,FN,FP,TN,gl,mgrid)
```

Arguments

TP	the number of true positives
FN	the number of false negatives
FP	the number of false positives
TN	the number of true negatives
gl	a list containing the components of Gauss-Legendre nodes gl$nodes and weights gl$weights
mgrid	a list containing two matrices with the rows of the output matrix x are copies of the vector gl$nodes; columns of the output matrix y are copies of the vector gl$nodes. For more details see also meshgrid
qcond	function for conditional copula cdf
tau2par	function for maping Kendall's tau to copula parameter

Value

A list containing the following components:

minimum	the value of the estimated minimum of the negative log-likelihood
estimate	the MLE
gradient	the gradient at the estimated minimum of of the negative log-likelihood
hessian	the hessian at the estimated minimum of the negative log-likelihood
code	an integer indicating why the optimization process terminated
iterations	the number of iterations performed

For more details see nlm

References

Nikoloulopoulos, A.K. (2015a) A mixed effect model for bivariate meta-analysis of diagnostic test accuracy studies using a copula representation of the random effects distribution, *Statistics in Medicine*, 34:3842–3865.

See Also

rCopulaREMADA

Examples

```
nq=15
gl=gauss.quad.prob(nq,"uniform")
mgrid<- meshgrid(gl$n,gl$n)

data(LAG)
attach(LAG)
c270est.b=CopulaREMADA.beta(TP,FN,FP,TN,gl,mgrid,qcondcln270,tau2par.cln270)
detach(LAG)

data(MRI)
attach(MRI)
c270est.n=CopulaREMADA.norm(TP,FN,FP,TN,gl,mgrid,qcondcln270,tau2par.cln270)
detach(MRI)

data(CT)
attach(CT)
est.n=countermonotonicCopulaREMADA.norm(TP,FN,FP,TN,gl,mgrid)
est.b=countermonotonicCopulaREMADA.beta(TP,FN,FP,TN,gl,mgrid)
detach(CT)
```

CT *The computing tomography data*

Description

Data on 17 studies of computed tomography (CT) for the diagnosis of lymph node metastasis in women with cervical cancer, one of three imaging techniques in the meta-analysis in Scheidler et al. (1997). Diagnosis of metastatic disease by CT relies on nodal enlargement.

Usage

```
data(CT)
```

Format

A data frame with 17 observations on the following 4 variables.

TP the number of true positives

FN the number of false negatives

FP the number of false positives

TN the number of true negatives

References

Scheidler, J., H. Hricak, K. K. Yu, L. Subak, and M. R. Segal. (1997) Radiological evaluation of lymph node metastases in patients with cervical cancer: A meta-analysis. *Journal of the American Medical Association* 278: 1096–1101.

`cvinesim` *Simulation from a trivariate C-vine copula*

Description

Simulation from a trivariate C-vine copula

Usage

```
cvinesim(N,param,qcondcop12,qcondcop13,qcondcop23,
                  tau2par12,tau2par13,tau2par23)
```

Arguments

`N`	sample size
`param`	Kendall's tau values for margins (1,2), (1,3), (23|1)
`qcondcop12`	function for conditional copula cdf at the (1,2) bivariate margin
`qcondcop13`	function for conditional copula cdf at the (1,3) bivariate margin
`qcondcop23`	function for conditional copula cdf at the (2,3|1) bivariate margin
`tau2par12`	function for maping Kendall's tau at the (1,2) bivariate margin to copula parameter
`tau2par13`	function for maping Kendall's tau at the (1,3) bivariate margin to copula parameter
`tau2par23`	function for maping Kendall's tau at the (2,3|1) bivariate margin to the conditional copula parameter

Details

Choices are 'cop' in rcop are bvn, frk, cln, cln90 (rotated by 90 degrees cln), cln180 (rotated by 180 degrees cln), cln270 (rotated by 270 degrees cln).

See help page for dcop for the abbreviations of the copula names.

Value

Nx3 matrix with values in (0,1)

References

Joe H (2011) Dependence comparisons of vine copulae with four or more variables. In: Kurowicka D, Joe H, editors. *Dependence Modeling: Handbook on Vine Copulae*. Singapore: World Scientific; 2011. p. 139–164

Joe H (2014) *Dependence Modeling with Copulas*. Chapman & Hall

Joe H (2014) *CopulaModel: Dependence Modeling with Copulas*. URL http://copula.stat.ubc.ca/

See Also

qcondcop dcop rcop

---

dcop *Bivariate copula densities*

Description

Bivariate copula densities for parametric families.

Usage

```
dbvn(u,v,cpar)
dfrk(u,v,cpar)
dcln(u,v,cpar)
dcln90(u,v,cpar)
dcln270(u,v,cpar)
```

Arguments

u	value in interval 0,1; could be a vector
v	value in interval 0,1; could be a vector
cpar	copula parameter: scalar.

Details

Choices are 'cop' in dcop are bvn, frk, cln, cln90 (rotated by 90 degrees cln), cln180 (rotated by 180 degrees cln), cln270 (rotated by 270 degrees cln).

The copula names are abbreviations for:

bvn = bivariate normal or Gaussian

frk = Frank

cln = Clayton or Mardia-Takahasi-Cook-Johnson

Value

pdf value(s).

References

Joe H (1997) *Multivariate Models and Dependence Concepts*. Chapman & Hall

Joe H (2014) *Dependence Modeling with Copulas*. Chapman & Hall

Joe H (2014) *CopulaModel: Dependence Modeling with Copulas*. URL http://copula.stat.ubc.ca/

See Also

qcondcop rcop

`hybridCopulaREMADA` *Maximum likelihood estimation for hybrid copula mixed models for combining case-control and cohort studies in meta-analysis of diagnostic tests*

Description

The estimated parameters can be obtained by using a quasi-Newton method applied to the logarithm of the joint likelihood. This numerical method requires only the objective function, i.e., the logarithm of the joint likelihood, while the gradients are computed numerically and the Hessian matrix of the second order derivatives is updated in each iteration. The standard errors (SE) of the ML estimates can be also obtained via the gradients and the Hessian computed numerically during the maximization process.

Usage

```
hybridCopulaREMADA.norm(TP,FN,FP,TN,type,perm,gl,mgrid1,mgrid2,
                qcondcop12,qcondcop13,
                tau2par12,tau2par13,qcond,tau2par)
hybridCopulaREMADA.beta(TP,FN,FP,TN,type,perm,gl,mgrid1,mgrid2,
                qcondcop12,qcondcop13,
                tau2par12,tau2par13,qcond,tau2par)
```

Arguments

`TP`	the number of true positives
`FN`	the number of false negatives
`FP`	the number of false positives
`TN`	the number of true negatives
`type`	a scalar indicating the study type: 1: Cohort study; 2: Case-control study.

perm	a scalar indicating the selected permutation of indices: 1: Pilot variable is the number of TP. The bivariate margins are 12, 13, 23|1; 2: Pilot variable is the number of TN. The bivariate margins are 23, 12, 13|2; 3: Pilot variable is the TP+FN. The bivariate margins are 13, 23, 12|3; 1:TP, 2:TN, 3:TP+FN
gl	a list containing the components of Gauss-Legendre nodes gl$nodes and weights gl$weights
mgrid1	a list containing three-dimensional arrays. For more details see meshgrid
mgrid2	a list containing two matrices with the rows of the output matrix x are copies of the vector gl$nodes; columns of the output matrix y are copies of the vector gl$nodes. For more details see also meshgrid
qcondcop12	function for conditional copula cdf at the (1,2) bivariate margin of the vine
qcondcop13	function for conditional copula cdf at the (1,3) bivariate margin of the vine
tau2par12	function for maping Kendall's tau at the (1,2) bivariate margin of the vine to copula parameter
tau2par13	function for maping Kendall's tau at the (1,3) bivariate margin of the vine to copula parameter
qcond	function for the bivariate conditional copula cdf
tau2par	function for maping Kendall's tau to the bivariate copula parameter

Value

A list containing the following components:

minimum	the value of the estimated minimum of the negative log-likelihood
estimate	the MLE
gradient	the gradient at the estimated minimum of of the negative log-likelihood
hessian	the hessian at the estimated minimum of the negative log-likelihood
code	an integer indicating why the optimization process terminated
iterations	the number of iterations performed

For more details see nlm

References

Nikoloulopoulos, A.K. (2016) Hybrid copula mixed models for combining case-control and cohort studies in meta-analysis of diagnostic tests *ArXiv e-prints*, arXiv:1604.05456.

See Also

VineCopulaREMADA, CopulaREMADA

Examples

```
# simulate the data from N=25 cohort studies
N=25
p=c(0.8,0.7,0.4)
g=c(0.1,0.1,0.05)
taus=c(-0.5,-0.3,-0.0001)
qcondcop12=qcondcop23=qcondcop13=qcondcln90
tau2par12=tau2par23=tau2par13=tau2par.cln90
simdat1=rVineCopulaREMADA.beta(N,p,g,taus,qcondcop12,qcondcop13,qcondcop23,
             tau2par12,tau2par13,tau2par23)
# simulate data from the N=25 case-control studies
tau=0.5
p=p[-3]
g=g[-3]
simdat2=rCopulaREMADA.beta(N,p,g,tau,rcln,tau2par.cln)
# combine the data
TP=c(simdat1$TP,simdat2$TP)
TN=c(simdat1$TN,simdat2$TN)
FP=c(simdat1$FP,simdat2$FP)
FN=c(simdat1$FN,simdat2$FN)
type=rep(c(1,2),each=N)

# fit the hybrid copula mixed model
nq=21
gl=gauss.quad.prob(nq,"uniform")
mgrid1<- meshgrid(gl$n,gl$n,gl$n,nargout=3)
mgrid2<- meshgrid(gl$n,gl$n)

perm=1
qcond=qcondcln
tau2par=tau2par.cln
# est=hybridCopulaREMADA.beta(TP,FN,FP,TN,type,perm,gl,mgrid1,mgrid2,
# qcondcop12,qcondcop13,tau2par12,tau2par13,qcond,tau2par)
```

LAG *The lymphangiography data*

Description

Data on 17 studies of lymphangiography (LAG) for the diagnosis of lymph node metastasis in women with cervical cancer, one of three imaging techniques in the meta-analysis in Scheidler et al. (1997). Diagnosis of metastatic disease by LAG is based on the presence of nodal-filling defects.

Usage

```
data(LAG)
```

Format

A data frame with 17 observations on the following 4 variables.

TP the number of true positives

FN the number of false negatives

FP the number of false positives

TN the number of true negatives

References

Scheidler, J., H. Hricak, K. K. Yu, L. Subak, and M. R. Segal (1997) Radiological evaluation of lymph node metastases in patients with cervical cancer: A meta-analysis. *Journal of the American Medical Association* 278: 1096–1101.

`MRI` *The magnetic resonance imaging data*

Description

Data on 10 studies of magnetic resonance imaging (MRI) for the diagnosis of lymph node metastasis in women with cervical cancer, the last imaging technique in the meta-analysis in Scheidler et al. (1997). Diagnosis of metastatic disease by MRI relies on nodal enlargement.

Usage

```
data(MRI)
```

Format

A data frame with 10 observations on the following 4 variables.

TP the number of true positives

FN the number of false negatives

FP the number of false positives

TN the number of true negatives

References

Scheidler, J., H. Hricak, K. K. Yu, L. Subak, and M. R. Segal (1997) Radiological evaluation of lymph node metastases in patients with cervical cancer: A meta-analysis. *Journal of the American Medical Association* 278: 1096–1101.

OGT *The orale glucose tolerance data*

Description

Data on 10 studies of the oral glucose tolerance test for the diagnosis of diabetes mellitus in patients during acute coronary syndrome hospitalization in Ye et al. (2012).

Usage

```
data(OGT)
```

Format

A data frame with 10 observations on the following 4 variables.

TP the number of true positives

FN the number of false negatives

FP the number of false positives

TN the number of true negatives

References

Ye Y, Xie H, Zhao X, Zhang S. (2012) The oral glucose tolerance test for the diagnosis of diabetes mellitus in patients during acute coronary syndrome hospitaliza- tion: a meta-analysis of diagnostic test accuracy. *Car- diovascular Diabetology*, 11(5):155.

qcondcop *Bivariate copula conditional quantile functions*

Description

Bivariate copula conditional quantile functions

Usage

```
qcondbvn(p,u,cpar)
qcondfrk(p,u,cpar)
qcondcln(p,u,cpar)
qcondcln90(p,u,cpar)
qcondcln270(p,u,cpar)
```

Arguments

u	conditioning value in interval 0,1; could be a vector
p	quantile in interval 0,1; could be a vector
cpar	copula parameter: scalar.

Details

Choices appending 'cop' are bvn, frk, cln, cln90 (rotated by 90 degrees cln), cln180 (rotated by 180 degrees cln), cln270 (rotated by 270 degrees cln).

See help page for dcop for the abbreviations of the copula names.

Value

inverse conditional cdf value(s)

References

Joe H (1997) *Multivariate Models and Dependence Concepts*. Chapman & Hall

Joe H (2014) *Dependence Modeling with Copulas*. Chapman & Hall

Joe H (2014) *CopulaModel: Dependence Modeling with Copulas*. URL http://copula.stat.ubc.ca/

See Also

dcop rcop

---

rcop *Simulation from parametric bivariate copula families*

Description

Simulation from parametric bivariate copula families

Usage

```
rbvn(N,cpar)
rfrk(N,cpar)
rcln(N,cpar)
rcln90(N,cpar)
rcln270(N,cpar)
```

Arguments

N	sample size
cpar	copula parameter: scalar

Details

Choices are 'cop' in rcop are bvn, frk, cln, cln90 (rotated by 90 degrees cln), cln180 (rotated by 180 degrees cln), cln270 (rotated by 270 degrees cln).

See help page for dcop for the abbreviations of the copula names.

Value

nx2 matrix with values in (0,1)

References

Joe H (1997) *Multivariate Models and Dependence Concepts*. Chapman & Hall

Joe H (2014) *Dependence Modeling with Copulas*. Chapman & Hall

Joe H (2014) *CopulaModel: Dependence Modeling with Copulas*. URL http://copula.stat.ubc.ca/

See Also

qcondcop dcop

---

rCopulaREMADA *Simulation from copula mixed models for diagnostic test accuaracy studies*

Description

To simulate the data we have used the following steps:

1. Simulate the study size n from a shifted gamma distribution with parameters $\alpha = 1.2, \beta = 0.01, lag = 30$ and round off to the nearest integer.

2. Simulate (u_1, u_2) from a parametric family of copulas 'cop'.

3. Convert to beta realizations or normal realizations.

4. Draw the number of diseased n_1 from a $B(n, 0.43)$ distribution.

5. Set $n_2 = n - n_1, y_j = n_j x_j$ and then round y_j for $j = 1, 2$.

Usage

```
rCopulaREMADA.norm(N,p,si,tau,rcop,tau2par)
rCopulaREMADA.beta(N,p,g,tau,rcop,tau2par)
```

Arguments

N	sample size
p	Pair (π_1, π_2) of sensitivity/specificity
si	Pair (σ_1, σ_2) of variability; normal margins
g	Pair (γ_1, γ_2) of variability; beta margins
tau	Kendall's tau value
rcop	function for copula generation
tau2par	function for mapping from Kendall's tau to copula parameter

Value

A list containing the following simulated components:

TP	the number of true positives
FN	the number of false negatives
FP	the number of false positives
TN	the number of true negatives

References

Nikoloulopoulos, A.K. (2015a) A mixed effect model for bivariate meta-analysis of diagnostic test accuracy studies using a copula representation of the random effects distribution, *Statistics in Medicine*, 34:3842–3865.

See Also

CopulaREMADA rcop

Examples

```
nq=15
gl=gauss.quad.prob(nq,"uniform")
mgrid<- meshgrid(gl$n,gl$n)

N=20
tau=-0.5
p=c(0.7,0.9)
g=c(0.2,0.1)
simDat=rCopulaREMADA.beta(N,p,g,tau,rcln270,tau2par.cln270)
TP=simDat$TP
TN=simDat$TN
FP=simDat$FP
FN=simDat$FN
c270est.b=CopulaREMADA.beta(TP,FN,FP,TN,gl,mgrid,qcondcln270,tau2par.cln270)

si=c(2,1)
tau=0.5
simDat=rCopulaREMADA.norm(N,p,si,tau,rcln,tau2par.cln)
```

```
TP=simDat$TP
TN=simDat$TN
FP=simDat$FP
FN=simDat$FN
cest.n=CopulaREMADA.norm(TP,FN,FP,TN,gl,mgrid,qcondcln,tau2par.cln)
```

`rVineCopulaREMADA` *Simulation from vine copula mixed models for diagnostic test accuaracy studies accounting for disease prevalence*

Description

To simulate the data we have used the following steps:

1. Simulate the study size n from a shifted gamma distribution with parameters $\alpha = 1.2, \beta = 0.01, lag = 30$ and round off to the nearest integer.

2. Simulate (u_1, u_2, u_3) from a trivariate C-vine copula. See also `cvinesim`.

3. Convert to beta realizations or normal realizations.

4. Set the number of diseased $n_1 = nx_1$.

5. Set $n_2 = n - n_1, y_j = n_j x_j$ and then round y_j for $j = 1, 2$.

Usage

```
rVineCopulaREMADA.beta(N,p,g,taus,qcondcop12,qcondcop13,qcondcop23,
             tau2par12,tau2par13,tau2par23)
rVineCopulaREMADA.norm(N,p,si,taus,qcondcop12,qcondcop13,qcondcop23,
             tau2par12,tau2par13,tau2par23)
```

Arguments

`N`	sample size
`p`	Vector (π_1, π_2, π_3) of sensitivity/specificity/prevalence
`si`	Vector $(\sigma_1, \sigma_2, \sigma_3)$ of variability; normal margins
`g`	Vector $(\gamma_1, \gamma_2, \gamma_3)$ of variability; beta margins
`taus`	Kendall's tau values
`qcondcop12`	function for conditional copula cdf at the (1,2) bivariate margin
`qcondcop13`	function for conditional copula cdf at the (1,3) bivariate margin
`qcondcop23`	function for conditional copula cdf at the (2,3|1) bivariate margin
`tau2par12`	function for maping Kendall's tau at the (1,2) bivariate margin to copula parameter
`tau2par13`	function for maping Kendall's tau at the (1,3) bivariate margin to copula parameter
`tau2par23`	function for maping Kendall's tau at the (2,3|1) bivariate margin to the conditional copula parameter

Value

A list containing the following simulated components:

TP	the number of true positives
FN	the number of false negatives
FP	the number of false positives
TN	the number of true negatives

References

Nikoloulopoulos, A.K. (2015b) A vine copula mixed effect model for trivariate meta-analysis of diagnostic test accuracy studies accounting for disease prevalence, *Statistical Methods in Medical Research*, DOI:10.1177/0962280215596769.

See Also

rCopulaREMADA rcop cvinesim

Examples

```
p=c(0.8,0.7,0.4)
g=c(0.1,0.1,0.05)
taus=c(-0.5,-0.3,-0.0001)
qcondcop12=qcondcop23=qcondcop13=qcondcln90
tau2par12=tau2par23=tau2par13=tau2par.cln90
rVineCopulaREMADA.beta(50,p,g,taus,qcondcop12,qcondcop13,qcondcop23,
             tau2par12,tau2par13,tau2par23)
```

SROC *Summary receiver operating characteristic curves for copula mixed effect models for bivariate meta-analysis of diagnostic test accuracy studies*

Description

Summary receiver operating characteristic (SROC) curves are demonstrated for the proposed models through quantile regression techniques and different characterizations of the estimated bivariate random effects distribution

Usage

```
SROC.norm(param,dcop,qcondcop,tau2par,TP,FN,FP,TN,points=TRUE,curves=TRUE)
SROC.beta(param,dcop,qcondcop,tau2par,TP,FN,FP,TN,points=TRUE,curves=TRUE)
SROC(param.beta,param.normal,TP,FN,FP,TN)
```

Arguments

param	A vector with the sensitivities, specifities, variabilities and Kendall's tau value (the latter only for SROC.norm and SROC.beta)
param.beta	A vector with the sensitivity, specifity and variabilities of the countermonotonic CopulaREMADA with beta margins
param.normal	A vector with the sensitivity, specifity and variabilities of the countermonotonic CopulaREMADA with normal margins
dcop	function for copula density
qcondcop	function for conditional copula cdf
tau2par	function for maping Kendall's tau to copula parameter
TP	the number of true positives
FN	the number of false negatives
FP	the number of false positives
TN	the number of true negatives
points	logical: print individual studies
curves	logical: print quantile regression curves

Value

Summary receiver operating characteristic curves

References

Nikoloulopoulos, A.K. (2015a) A mixed effect model for bivariate meta-analysis of diagnostic test accuracy studies using a copula representation of the random effects distribution, *Statistics in Medicine*, 34:3842–3865.

See Also

CopulaREMADA rCopulaREMADA

Examples

```
nq=15
gl=gauss.quad.prob(nq,"uniform")
mgrid<- meshgrid(gl$n,gl$n)

data(telomerase)
attach(telomerase)
est.n=countermonotonicCopulaREMADA.norm(TP,FN,FP,TN,gl,mgrid)
est.b=countermonotonicCopulaREMADA.beta(TP,FN,FP,TN,gl,mgrid)
SROC(est.b$e,est.n$e,TP,FN,FP,TN)
detach(telomerase)

data(LAG)
attach(LAG)
c180est.b=CopulaREMADA.beta(TP,FN,FP,TN,gl,mgrid,qcondcln180,tau2par.cln180)
```

```
SROC.beta(c180est.b$e,dcln180,qcondcln180,tau2par.cln180,TP,FN,FP,TN)
detach(LAG)

data(MRI)
attach(MRI)
c270est.n=CopulaREMADA.norm(TP,FN,FP,TN,gl,mgrid,qcondcln270,tau2par.cln270)
SROC.norm(c270est.n$e,dcln270,qcondcln270,tau2par.cln270,TP,FN,FP,TN)
detach(MRI)
```

`tau2par` *Mapping of Kendall's tau and copula parameter*

Description

Bivariate copulas: mapping of Kendall's tau and copula parameter.

Usage

```
tau2par.bvn(tau)
tau2par.frk(tau)
tau2par.cln(tau)
tau2par.cln90(tau)
tau2par.cln180(tau)
tau2par.cln270(tau)
```

Arguments

`tau`	Kendall's tau for the copula

Details

For abbreviations of names of copula families (after the dot in function names), see dcop help page.

Value

copula parameter

References

Joe H (1997) *Multivariate Models and Dependence Concepts*. Chapman & Hall

Joe H (2014) *Dependence Modeling with Copulas*. Chapman & Hall

Joe H (2014) *CopulaModel: Dependence Modeling with Copulas*. URL http://copula.stat.ubc.ca/

See Also

dcop

telomerase *The telomerase data*

Description

In Glas et al. (2003) the telomerase marker for the diagnosis of bladder cancer is evaluated using 10 studies. The interest was to define if this non-invasive and cheap marker could replace the standard of cystoscopy or histopathology.

Usage

```
data(telomerase)
```

Format

A data frame with 10 observations on the following 4 variables.

TP the number of true positives

FN the number of false negatives

FP the number of false positives

TN the number of true negatives

References

Glas A.S., Roos D., Deutekom M., Zwinderman A.H., Bossuyt P.M., Kurth K.H. (2003) Tumor markers in the diagnosis of primary bladder cancer. A systematic review. *Journal of Urology* 169(6):1975–82.

vine.vuong *Vuong's test for the comparison of non-nested vine copula mixed models for diagnostic test accuaracy studies*

Description

Vuong (1989)'s test for the comparison of non-nested vine copula mixed models for diagnostic test accuaracy studies. It shows if a vine copula mixed model provides better fit than the standard GLMM. We compute the Vuong's test with Model 1 being the vine copula mixed model with BVN copula and normal margins, i.e., the standard GLMM.

Usage

```
vine.vuong.beta(qcondcop12,qcondcop13,qcondcop23,
tau2par12,tau2par13,tau2par23,param1,param2,TP,FN,FP,TN,perm,gl,mgrid)
vine.vuong.norm(qcondcop12,qcondcop13,qcondcop23,
tau2par12,tau2par13,tau2par23,param1,param2,TP,FN,FP,TN,perm,gl,mgrid)
tvine.vuong.beta(qcondcop12,qcondcop13,
tau2par12,tau2par13,param1,param2,TP,FN,FP,TN,perm,gl,mgrid)
tvine.vuong.norm(qcondcop12,qcondcop13,
tau2par12,tau2par13,param1,param2,TP,FN,FP,TN,perm,gl,mgrid)
tvine2.vuong.beta(qcondcop12,qcondcop13,
tau2par12,tau2par13,param1,param2,TP,FN,FP,TN,perm,gl,mgrid)
tvine2.vuong.norm(qcondcop12,qcondcop13,
tau2par12,tau2par13,param1,param2,TP,FN,FP,TN,perm,gl,mgrid)
```

Arguments

qcondcop12	function for conditional copula cdf at the (1,2) bivariate margin for Model 2
qcondcop13	function for conditional copula cdf at the (1,3) bivariate margin for Model 2
qcondcop23	function for conditional copula cdf at the (2,3|1) bivariate margin for Model 2
tau2par12	function for maping Kendall's tau at the (1,2) bivariate margin to copula parameter for Model 2
tau2par13	function for maping Kendall's tau at the (1,3) bivariate margin to copula parameter for Model 2
tau2par23	function for maping Kendall's tau at the (2,3|1) bivariate margin to the conditional copula parameter for Model 2
param1	parameters for the Model 1. i.e., the GLMM
param2	parameters for the Model 2
TP	the number of true positives
FN	the number of false negatives
FP	the number of false positives
TN	the number of true negatives
perm	a scalar indicating the selected permutation of indices: 1: Pilot variable is the number of TP. The bivariate margins are 12, 13, 23|1; 2: Pilot variable is the number of TN. The bivariate margins are 23, 12, 13|2; 3: Pilot variable is the TP+FN. The bivariate margins are 13, 23, 12|3; 1:TP, 2:TN, 3:TP+FN
gl	a list containing the components of Gauss-Legendre nodes `gl$nodes` and weights `gl$weights`
mgrid	a list containing three-dimensional arrays. For more details see meshgrid

Value

A list containing the following components:

z	the test statistic
p-value	the p-value

References

Nikoloulopoulos, A.K. (2015b) A vine copula mixed effect model for trivariate meta-analysis of diagnostic test accuracy studies accounting for disease prevalence, *Statistical Methods in Medical Research*, DOI:10.1177/0962280215596769.

Vuong Q.H. (1989) Likelihood ratio tests for model selection and non-nested hypotheses. *Econometrica* 57(2), 307–333.

See Also

CopulaREMADA

Examples

```
nq=15
gl=gauss.quad.prob(nq,"uniform")
mgrid=meshgrid(gl$n,gl$n,gl$n,nargout=3)

data(betaDG)
attach(betaDG)
#nest.n2=VineCopulaREMADA.norm(TP,FN,FP,TN,2,gl,mgrid,
#qcondbvn,qcondbvn,qcondbvn,
#tau2par.bvn,tau2par.bvn,tau2par.bvn)
nest.n2.est= #nest.n2$e
c(0.87186926,  0.13696066,  0.70614956,  0.69152133,
0.51780203,  0.70883558, -0.41354870,0.07701287, -0.12111253)
#c090est.b2=VineCopulaREMADA.beta(TP,FN,FP,TN,2,gl,mgrid,
#qcondcln90,qcondcln,qcondcln90,tau2par.cln90,tau2par.cln,tau2par.cln90)
c090est.b2.est= #c090est.b2$e
c(0.85528463,  0.14667571,  0.68321231,  0.04897466,
0.02776290,  0.08561436, -0.34639172, 0.04621924, -0.21627977)
c090vuong.b2=vine.vuong.beta(qcondcln90,qcondcln,qcondcln90,
tau2par.cln90,tau2par.cln,tau2par.cln90,
nest.n2.est,c090est.b2.est,TP,FN,FP,TN,2,gl,mgrid)
c090vuong.b2
detach(betaDG)
```

`VineCopulaREMADA` *Maximum likelihood estimation for (truncated) vine copula mixed models for diagnostic test accurracy studies accounting for disease prevalence*

Description

The estimated parameters can be obtained by using a quasi-Newton method applied to the logarithm of the joint likelihood. This numerical method requires only the objective function, i.e., the logarithm of the joint likelihood, while the gradients are computed numerically and the Hessian matrix of the second order derivatives is updated in each iteration. The standard errors (SE) of the ML estimates can be also obtained via the gradients and the Hessian computed numerically during the maximization process.

Usage

```
VineCopulaREMADA.norm(TP,FN,FP,TN,perm,gl,mgrid,
                              qcondcop12,qcondcop13,qcondcop23,
                              tau2par12,tau2par13,tau2par23)
VineCopulaREMADA.beta(TP,FN,FP,TN,perm,gl,mgrid,
                              qcondcop12,qcondcop13,qcondcop23,
                              tau2par12,tau2par13,tau2par23)
tVineCopulaREMADA.norm(TP,FN,FP,TN,perm,gl,mgrid,
                              qcondcop12,qcondcop13,
                              tau2par12,tau2par13)
tVineCopulaREMADA.beta(TP,FN,FP,TN,perm,gl,mgrid,
                              qcondcop12,qcondcop13,
                              tau2par12,tau2par13)
```

Arguments

TP	the number of true positives
FN	the number of false negatives
FP	the number of false positives
TN	the number of true negatives
perm	a scalar indicating the selected permutation of indices: 1: Pilot variable is the number of TP. The bivariate margins are 12, 13, 23|1; 2: Pilot variable is the number of TN. The bivariate margins are 23, 12, 13|2; 3: Pilot variable is the TP+FN. The bivariate margins are 13, 23, 12|3; 1:TP, 2:TN, 3:TP+FN
gl	a list containing the components of Gauss-Legendre nodes `gl$nodes` and weights `gl$weights`
mgrid	a list containing three-dimensional arrays. For more details see `meshgrid`
qcondcop12	function for conditional copula cdf at the (1,2) bivariate margin
qcondcop13	function for conditional copula cdf at the (1,3) bivariate margin
qcondcop23	function for conditional copula cdf at the (2,3|1) bivariate margin
tau2par12	function for maping Kendall's tau at the (1,2) bivariate margin to copula parameter
tau2par13	function for maping Kendall's tau at the (1,3) bivariate margin to copula parameter
tau2par23	function for maping Kendall's tau at the (2,3|1) bivariate margin to the conditional copula parameter

Value

A list containing the following components:

minimum	the value of the estimated minimum of the negative log-likelihood
estimate	the MLE

gradient	the gradient at the estimated minimum of of the negative log-likelihood
hessian	the hessian at the estimated minimum of the negative log-likelihood
code	an integer indicating why the optimization process terminated
iterations	the number of iterations performed

For more details see nlm

References

Nikoloulopoulos, A.K. (2015b) A vine copula mixed effect model for trivariate meta-analysis of diagnostic test accuracy studies accounting for disease prevalence, *Statistical Methods in Medical Research*, DOI:10.1177/0962280215596769.

See Also

rVineCopulaREMADA

Examples

```
nq=15
gl=gauss.quad.prob(nq,"uniform")
mgrid=meshgrid(gl$n,gl$n,gl$n,nargout=3)

data(OGT)
attach(OGT)
#out=tVineCopulaREMADA.norm(TP,FN,FP,TN,1,gl,mgrid,
#qcondbvn,qcondbvn,tau2par.bvn,tau2par.bvn)
detach(OGT)
```

---

vuong *Vuong's test for the comparison of non-nested copula mixed models for diagnostic test accuaracy studies*

Description

Vuong (1989)'s test for the comparison of non-nested copula mixed models for diagnostic test accuaracy studies. It shows if a copula mixed model provides better fit than the standard GLMM. We compute the Vuong's test with Model 1 being the copula mixed model with BVN copula and normal margins, i.e., the standard GLMM.

Usage

```
vuong.norm(qcond,tau2par,param1,param2,TP,FN,FP,TN,gl,mgrid)
vuong.beta(qcond,tau2par,param1,param2,TP,FN,FP,TN,gl,mgrid)
countermonotonicity.vuong(param1,param2,TP,FN,FP,TN,gl,mgrid)
```

Arguments

qcond	function for conditional copula cdf for Model 2
tau2par	function for maping Kendall's tau to copula parameter for Model 2
param1	parameters for the Model 1. i.e., the GLMM
param2	parameters for the Model 2
TP	the number of true positives
FN	the number of false negatives
FP	the number of false positives
TN	the number of true negatives
gl	a list containing the components of Gauss-Legendre nodes gl$nodes and weights gl$weights
mgrid	a list containing two matrices with the rows of the output matrix X are copies of the vector gl$nodes; columns of the output matrix Y are copies of the vector gl$nodes. For more details see meshgrid

Value

A list containing the following components:

z	the test statistic
p-value	the p-value

References

Nikoloulopoulos, A.K. (2015a) A mixed effect model for bivariate meta-analysis of diagnostic test accuracy studies using a copula representation of the random effects distribution, *Statistics in Medicine*, 34:3842–3865.

Vuong Q.H. (1989) Likelihood ratio tests for model selection and non-nested hypotheses. *Econometrica* 57(2), 307–333.

See Also

CopulaREMADA

Examples

```
nq=15
gl=gauss.quad.prob(nq,"uniform")
mgrid<- meshgrid(gl$n,gl$n)

data(MRI)
attach(MRI)
c270est.b=CopulaREMADA.beta(TP,FN,FP,TN,gl,mgrid,qcondcln270,tau2par.cln270)
nest.n=CopulaREMADA.norm(TP,FN,FP,TN,gl,mgrid,qcondbvn,tau2par.bvn)
c90est.n=CopulaREMADA.norm(TP,FN,FP,TN,gl,mgrid,qcondcln90,tau2par.cln90)
vuong.beta(qcondcln270,tau2par.cln270,nest.n$e,c270est.b$e,TP,FN,FP,TN,gl,mgrid)
```

```
vuong.norm(qcondcln90,tau2par.cln90,nest.n$e,c90est.n$e,TP,FN,FP,TN,gl,mgrid)
detach(MRI)

data(CT)
attach(CT)
est.n=countermonotonicCopulaREMADA.norm(TP,FN,FP,TN,gl,mgrid)
est.b=countermonotonicCopulaREMADA.beta(TP,FN,FP,TN,gl,mgrid)
countermonotonicity.vuong(est.n$e,est.b$e,TP,FN,FP,TN,gl,mgrid)
detach(CT)
```

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