Package ‘VineCopula’

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Type Package

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License GPL (>= 2)

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Description


Details

Vine copulas are a flexible class of dependence models consisting of bivariate building blocks (see e.g., Aas et al., 2009). This package is primarily made for the statistical analysis of vine copula models. The package includes tools for parameter estimation, model selection, simulation, goodness-of-fit tests, and visualization. Tools for estimation, selection and exploratory data analysis of bivariate copula models are also provided.

The DESCRIPTION file:
Remark

The package VineCopula is a continuation of the package CDVine by U. Schepsmeier and E. C. Brechmann (see Brechmann and Schepsmeier (2013)). It includes all functions implemented in CDVine for the bivariate case (BiCop-functions).

References


as.copuladata

Description

The function as.copuladata coerces an object (data.frame, matrix, list) to a copuladata object.

Usage

as.copuladata(data)

Arguments

data Either a data.frame, a matrix or a list containing copula data (i.e. data with uniform margins on [0,1]). The list elements have to be vectors of identical length.
Author(s)
Tobias Erhardt

See Also
pobs(), pairs.copuladata()

Examples

data(daxreturns)
data <- as.matrix(daxreturns)
class(as.copuladata(data))
data <- as.data.frame(daxreturns)
class(as.copuladata(data))
data <- as.list(daxreturns)
names(data) <- names(daxreturns)
class(as.copuladata(data))

BetaMatrix

Matrix of Empirical Blomqvist’s Beta Values

Description
This function computes the empirical Blomqvist’s beta.

Usage
BetaMatrix(data)

Arguments
data An N x d data matrix.

Value
Matrix of the empirical Blomqvist’s betas.

Author(s)
Ulf Schepsmeier
BiCop

References

See Also
TauMatrix(), BiCopPar2Beta(), RVinePar2Beta()

Examples

```r
data(daxreturns)
data <- as.matrix(daxreturns)

# compute the empirical Blomqvist's betas
BetaMatrix(data)
```

Constructing BiCop-objects

Description
This function creates an object of class BiCop and checks for family/parameter consistency.

Usage

```
BiCop(family, par, par2 = 0, tau = NULL, check.pars = TRUE)
```

Arguments

- **family**: An integer defining the bivariate copula family:
  - 0 = independence copula
  - 1 = Gaussian copula
  - 2 = Student t copula (t-copula)
  - 3 = Clayton copula
  - 4 = Gumbel copula
  - 5 = Frank copula
  - 6 = Joe copula
  - 7 = BB1 copula
  - 8 = BB6 copula
  - 9 = BB7 copula
  - 10 = BB8 copula
  - 13 = rotated Clayton copula (180 degrees; survival Clayton’’)
  - 14 = rotated Gumbel copula (180 degrees; survival Gumbel’’)
```
16 = rotated Joe copula (180 degrees; survival Joe) \\
17 = rotated BB1 copula (180 degrees; survival BB1) \\
18 = rotated BB6 copula (180 degrees; survival BB6) \\
19 = rotated BB7 copula (180 degrees; survival BB7) \\
20 = rotated BB8 copula (180 degrees; “survival BB8”) \\
23 = rotated Clayton copula (90 degrees) \\
‘24’ = rotated Gumbel copula (90 degrees) \\
‘26’ = rotated Joe copula (90 degrees) \\
‘27’ = rotated BB1 copula (90 degrees) \\
‘28’ = rotated BB6 copula (90 degrees) \\
‘29’ = rotated BB7 copula (90 degrees) \\
‘30’ = rotated BB8 copula (90 degrees) \\
‘33’ = rotated Clayton copula (270 degrees) \\
‘34’ = rotated Gumbel copula (270 degrees) \\
‘36’ = rotated Joe copula (270 degrees) \\
‘37’ = rotated BB1 copula (270 degrees) \\
‘38’ = rotated BB6 copula (270 degrees) \\
‘39’ = rotated BB7 copula (270 degrees) \\
‘40’ = rotated BB8 copula (270 degrees) \\
‘104’ = Tawn type 1 copula \\
‘114’ = rotated Tawn type 1 copula (180 degrees) \\
‘124’ = rotated Tawn type 1 copula (90 degrees) \\
‘134’ = rotated Tawn type 1 copula (270 degrees) \\
‘204’ = Tawn type 2 copula \\
‘214’ = rotated Tawn type 2 copula (180 degrees) \\
‘224’ = rotated Tawn type 2 copula (90 degrees) \\
‘234’ = rotated Tawn type 2 copula (270 degrees)

par

Copula parameter.

par2

Second parameter for bivariate copulas with two parameters (t, BB1, BB6, BB7, BB8, Tawn type 1 and type 2; default is par2 = 0). par2 should be a positive integer for the Students’s t copula family = 2.

tau

numeric; value of Kendall’s tau; has to lie in the interval (-1, 1). Can only be used with one-parameter families and the t copula. If tau is provided, par will be ignored.

check.pars

logical; default is TRUE; if FALSE, checks for family/parameter-consistency are omitted (should only be used with care).

Value

An object of class BiCop(). It is a list containing information about the bivariate copula. Its components are:

family, par, par2

copula family number and parameter(s).

npars

number of parameters,

familyname

name of the copula family,
BiCopCDF

Distribution Function of a Bivariate Copula

Description

This function evaluates the cumulative distribution function (CDF) of a given parametric bivariate copula.
Usage

BiCopCDF(u1, u2, family, par, par2 = 0, obj = NULL, check.pars = TRUE)

Arguments

u1, u2 numeric vectors of equal length with values in [0, 1].
family integer; single number or vector of size length(u1); defines the bivariate copula family:
0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton’’)
14 = rotated Gumbel copula (180 degrees; survival Gumbel’’)
16 = rotated Joe copula (180 degrees; survival Joe’’)
17 = rotated BB1 copula (180 degrees; survival BB1’’)
18 = rotated BB6 copula (180 degrees; survival BB6’’)
19 = rotated BB7 copula (180 degrees; survival BB7’’)
20 = rotated BB8 copula (180 degrees; “survival BB8”)
23 = rotated Clayton copula (90 degrees)
24 = rotated Gumbel copula (90 degrees)
26 = rotated Joe copula (90 degrees)
27 = rotated BB1 copula (90 degrees)
28 = rotated BB6 copula (90 degrees)
29 = rotated BB7 copula (90 degrees)
30 = rotated BB8 copula (90 degrees)
33 = rotated Clayton copula (270 degrees)
34 = rotated Gumbel copula (270 degrees)
36 = rotated Joe copula (270 degrees)
37 = rotated BB1 copula (270 degrees)
38 = rotated BB6 copula (270 degrees)
39 = rotated BB7 copula (270 degrees)
40 = rotated BB8 copula (270 degrees)
104 = Tawn type 1 copula
114 = rotated Tawn type 1 copula (180 degrees)
124 = rotated Tawn type 1 copula (90 degrees)
134 = rotated Tawn type 1 copula (270 degrees)
204 = Tawn type 2 copula
214 = rotated Tawn type 2 copula (180 degrees)
224 = rotated Tawn type 2 copula (90 degrees)
234 = rotated Tawn type 2 copula (270 degrees)
par numeric; single number or vector of size length(u1); copula parameter.

par2 numeric; single number or vector of size length(u1); second parameter for bivariate copulas with two parameters (BB1, BB6, BB7, BB8, Tawn type 1 and type 2; default: par2 = 0).

obj BiCop object containing the family and parameter specification.

check.pars logical; default is TRUE; if FALSE, checks for family/parameter-consistency are omitted (should only be used with care).

Details

If the family and parameter specification is stored in a BiCop() object obj, the alternative version

BiCopCDF(u1, u2, obj)

can be used.

Value

A numeric vector of the bivariate copula distribution function

• of the copula family
• with parameter(s) par, par2
• evaluated at u1 and u2.

Note

The calculation of the cumulative distribution function (CDF) of the Student’s t copula (family = 2) is only approximate. For numerical reasons, the degree of freedom parameter (par2) is rounded to an integer before calculation of the CDF.

Author(s)

Eike Brechmann

See Also

BiCopPDF(), BiCopHfunc(), BiCopSim(), BiCop()

Examples

## simulate from a bivariate Clayton copula
set.seed(123)
cop <- BiCop(family = 3, par = 3.4)
simdata <- BiCopSim(300, cop)

## evaluate the distribution function of the bivariate Clayton copula
u1 <- simdata[,1]
BiCopCheck

BiCopCheck
Check for family/parameter consistency in bivariate copula models

Description
The function checks if a certain combination of copula family and parameters can be used within other functions of this package.

Usage
BiCopCheck(family, par, par2 = 0, ...)

Arguments
family An integer defining the bivariate copula family:
0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton”)
14 = rotated Gumbel copula (180 degrees; survival Gumbel”)
16 = rotated Joe copula (180 degrees; survival Joe”)
17 = rotated BB1 copula (180 degrees; survival BB1”)
18 = rotated BB6 copula (180 degrees; survival BB6”)
19 = rotated BB7 copula (180 degrees; survival BB7”)
20 = rotated BB8 copula (180 degrees; “survival BB8”)
23 = rotated Clayton copula (90 degrees)
24 = rotated Gumbel copula (90 degrees)
26 = rotated Joe copula (90 degrees)
27 = rotated BB1 copula (90 degrees)
28 = rotated BB6 copula (90 degrees)
'29' = rotated BB7 copula (90 degrees)
'30' = rotated BB8 copula (90 degrees)
'33' = rotated Clayton copula (270 degrees)
'34' = rotated Gumbel copula (270 degrees)
'36' = rotated Joe copula (270 degrees)
'37' = rotated BB1 copula (270 degrees)
'38' = rotated BB6 copula (270 degrees)
'39' = rotated BB7 copula (270 degrees)
'40' = rotated BB8 copula (270 degrees)
'104' = Tawn type 1 copula
'114' = rotated Tawn type 1 copula (180 degrees)
'124' = rotated Tawn type 1 copula (90 degrees)
'134' = rotated Tawn type 1 copula (270 degrees)
'204' = Tawn type 2 copula
'214' = rotated Tawn type 2 copula (180 degrees)
'224' = rotated Tawn type 2 copula (90 degrees)
'234' = rotated Tawn type 2 copula (270 degrees)

par

Copula parameter.

par2

Second parameter for bivariate copulas with two parameters (t, BB1, BB6, BB7, BB8, Tawn type 1 and type 2; default is par2 = 0).

Value

A logical indicating whether the family can be used with the parameter specification.

Author(s)

Thomas Nagler

Examples

```r
## check parameter of Clayton copula
BiCopCheck(3, 1) # works

## Not run: BiCopCheck(3, -1) # does not work (only positive parameter is allowed)
```

**BiCopChiPlot**

*Chi-plot for Bivariate Copula Data*

**Description**

This function creates a chi-plot of given bivariate copula data.
Usage

\texttt{BiCopChiPlot(u1, u2, PLOT = TRUE, mode = "NULL", ...)}

Arguments

\texttt{u1, u2} \hspace{1cm} \text{Data vectors of equal length with values in [0, 1].}

\texttt{PLOT} \hspace{1cm} \text{Logical; whether the results are plotted. If PLOT = FALSE, the values lambda, chi and control.bounds are returned (see below; default: PLOT = TRUE).}

\texttt{mode} \hspace{1cm} \text{Character; whether a general, lower or upper chi-plot is calculated. Possible values are mode = "NULL", "upper" and "lower". "NULL" = general chi-plot (default) "upper" = upper chi-plot "lower" = lower chi-plot}

\texttt{...} \hspace{1cm} \text{Additional plot arguments.}

Details

For observations \(u_{i,j}, i = 1, ..., N, j = 1, 2\), the chi-plot is based on the following two quantities: the chi-statistics

\[ \chi_i = \frac{\hat{F}_{1,2}(u_{i,1}, u_{i,2}) - \hat{F}_1(u_{i,1})\hat{F}_2(u_{i,2})}{\sqrt{\hat{F}_1(u_{i,1})(1 - \hat{F}_1(u_{i,1}))\hat{F}_2(u_{i,2})(1 - \hat{F}_2(u_{i,2}))}} \]

and the lambda-statistics

\[ \lambda_i = 4\text{sgn}\left(\hat{F}_1(u_{i,1}), \hat{F}_2(u_{i,2})\right) \cdot \max\left(\hat{F}_1(u_{i,1})^2, \hat{F}_2(u_{i,2})^2\right), \]

where \(\hat{F}_1, \hat{F}_2\) and \(\hat{F}_{1,2}\) are the empirical distribution functions of the uniform random variables \(U_1\) and \(U_2\) and of \((U_1, U_2)\), respectively. Further, \(\hat{F}_1 = \hat{F}_1 - 0.5\) and \(\hat{F}_2 = \hat{F}_2 - 0.5\).

These quantities only depend on the ranks of the data and are scaled to the interval [0, 1]. \(\lambda_i\) measures a distance of a data point \((u_{i,1}, u_{i,2})\) to the center of the bivariate data set, while \(\chi_i\) corresponds to a correlation coefficient between dichotomized values of \(U_1\) and \(U_2\). Under independence it holds that \(\chi_i \sim N(0, 1)\) and \(\lambda_i \sim \mathcal{U}[-1, 1]\) asymptotically, i.e., values of \(\chi_i\) close to zero indicate independence—corresponding to \(F_{1,2} = F_1F_2\).

When plotting these quantities, the pairs of \((\lambda_i, \chi_i)\) will tend to be located above zero for positively dependent margins and vice versa for negatively dependent margins. Control bounds around zero indicate whether there is significant dependence present.

If mode = "lower" or "upper", the above quantities are calculated only for those \(\hat{u}_{i,1}\)'s and \(\hat{u}_{i,2}\)'s which are smaller/larger than the respective means of \(u_1 = (u_{1,1}, ..., u_{N,1})\) and \(u_2 = (u_{1,2}, ..., u_{N,2})\).

Value

\texttt{lambda} \hspace{1cm} \text{Lambda-statistics (x-axis).}

\texttt{chi} \hspace{1cm} \text{Chi-statistics (y-axis).}

\texttt{control.bounds} \hspace{1cm} \text{A 2-dimensional vector of bounds \((1.54/\sqrt{n}, -1.54/\sqrt{n})\), where \(n\) is the length of \(u_1\) and where the chosen values correspond to an approximate significance level of 10%.}
Author(s)

Natalia Belgorodski, Ulf Schepsmeier

References


Genest, C. and A. C. Favre (2007). Everything you always wanted to know about copula modeling but were afraid to ask. Journal of Hydrologic Engineering, 12 (4), 347-368.

See Also

BiCopMetaContour(), BiCopKPlot(), BiCopLambda()

Examples

## chi-plots for bivariate Gaussian copula data

```r
# simulate copula data
fam <- 1
tau <- 0.5
par <- BiCopTau2Par(fam, tau)
cop <- BiCop(fam, par)
set.seed(123)
dat <- BiCopSim(500, cop)

# create chi-plots
op <- par(mfrow = c(1, 3))
BiCopChiPlot(dat[,1], dat[,2], xlim = c(-1,1), ylim = c(-1,1),
  main="General chi-plot")
BiCopChiPlot(dat[,1], dat[,2], mode = "lower", xlim = c(-1,1),
  ylim = c(-1,1), main = "Lower chi-plot")
BiCopChiPlot(dat[,1], dat[,2], mode = "upper", xlim = c(-1,1),
  ylim = c(-1,1), main = "Upper chi-plot")
par(op)
```

Description

The function starts a shiny app which visualizes copula data and allows to compare it with overlays of density contours or simulated data from different copula families with fitted parameters. Several specifications for the margins are available.
Usage

BiCopCompare(u1, u2, familyset = NA, rotations = TRUE)

Arguments

u1, u2
Data vectors of equal length with values in [0, 1].

familyset
Vector of bivariate copula families to select from. The vector has to include at least one bivariate copula family that allows for positive and one that allows for negative dependence. If familyset = NA (default), selection among all possible families is performed. If a vector of negative numbers is provided, selection among all but abs(familyset) families is performed. Coding of bivariate copula families:

0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton"
14 = rotated Gumbel copula (180 degrees; survival Gumbel")
16 = rotated Joe copula (180 degrees; survival Joe"
17 = rotated BB1 copula (180 degrees; survival BB1")
18 = rotated BB6 copula (180 degrees; survival BB6"
19 = rotated BB7 copula (180 degrees; survival BB7")
20 = rotated BB8 copula (180 degrees; "survival BB8")
23 = rotated Clayton copula (90 degrees)
24 = rotated Gumbel copula (90 degrees)
26 = rotated Joe copula (90 degrees)
27 = rotated BB1 copula (90 degrees)
28 = rotated BB6 copula (90 degrees)
29 = rotated BB7 copula (90 degrees)
30 = rotated BB8 copula (90 degrees)
33 = rotated Clayton copula (270 degrees)
34 = rotated Gumbel copula (270 degrees)
36 = rotated Joe copula (270 degrees)
37 = rotated BB1 copula (270 degrees)
38 = rotated BB6 copula (270 degrees)
39 = rotated BB7 copula (270 degrees)
40 = rotated BB8 copula (270 degrees)
104 = Tawn type 1 copula
114 = rotated Tawn type 1 copula (180 degrees)
124 = rotated Tawn type 1 copula (90 degrees)
134 = rotated Tawn type 1 copula (270 degrees)
rotations If TRUE, all rotations of the families in familyset are included (or subtracted).

Value

A BiCop() object containing the model selected by the user.

Author(s)

Matthias Killiches, Thomas Nagler

Examples

```r
# load data
data(daxreturns)

# find a suitable copula family for the first two stocks
## Not run: fit <- BiCopCompare(daxreturns[, 1], daxreturns[, 2])
```

Description

This function simulates from a parametric bivariate copula, where one of the variables is fixed. I.e., we simulate either from $C_{2|1}(u_2|u_1; \theta)$ or $C_{1|2}(u_1|u_2; \theta)$, which are both conditional distribution functions of one variable given another.

Usage

```r
BiCopCondSim(
  N,
  cond.val,
  cond.var,
  family,
  par,
  par2 = 0,
  obj = NULL,
  check.pars = TRUE
)
```
Arguments

N
Number of observations simulated.
conditional.val
numeric vector of length N containing the values to condition on.
conditional.var
either 1 or 2; the variable to condition on.
family
integer; single number or vector of size N; defines the bivariate copula family:
0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton) \\
14 = rotated Gumbel copula (180 degrees; survival Gumbel)
16 = rotated Joe copula (180 degrees; survival Joe) \\
17 = rotated BB1 copula (180 degrees; survival BB1)
18 = rotated BB6 copula (180 degrees; survival BB6) \\
19 = rotated BB7 copula (180 degrees; survival BB7)
20 = rotated BB8 copula (180 degrees; “survival BB8”)
23 = rotated Clayton copula (90 degrees)
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‘30’ = rotated BB8 copula (90 degrees)
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‘134’ = rotated Tawn type 1 copula (270 degrees)
‘204’ = Tawn type 2 copula
‘214’ = rotated Tawn type 2 copula (180 degrees)
‘224’ = rotated Tawn type 2 copula (90 degrees)
‘234’ = rotated Tawn type 2 copula (270 degrees)

par
numeric; single number or vector of size N; copula parameter.
par2 numeric; single number or vector of size \( N \); second parameter for bivariate copulas with two parameters (t, BB1, BB6, BB7, BB8, Tawn type 1 and type 2; default: \( \text{par2} = 0 \)). \( \text{par2} \) should be a positive integer for the Students’s \( t \) copula family = 2.

obj BiCop object containing the family and parameter specification.

check.pars logical; default is \( \text{TRUE} \); if \( \text{FALSE} \), checks for family/parameter-consistency are omitted (should only be used with care).

Details

If the family and parameter specification is stored in a BiCop() object \( \text{obj} \), the alternative version

\[
\text{BiCopCondSim}(N, \text{cond.val}, \text{cond.var}, \text{obj})
\]

can be used.

Value

A length \( N \) vector of simulated from conditional distributions related to bivariate copula with family and parameter(s) \( \text{par}, \text{par2} \).

Author(s)

Thomas Nagler

See Also

BiCopCDF(), BiCopPDF(), RVineSim()

Examples

# create bivariate t-copula
\( \text{obj} \leftarrow \text{BiCop(family} = 2, \text{par} = -0.7, \text{par2} = 4) \)

# simulate 500 observations of (U1, U2)
\( \text{sim} \leftarrow \text{BiCopSim(500, } \text{obj}) \)
\( \text{hist(sim[, 1])} \) # data have uniform distribution
\( \text{hist(sim[, 2])} \) # data have uniform distribution

# simulate 500 observations of (U2 | U1 = 0.7)
\( \text{sim1} \leftarrow \text{BiCopCondSim(500, } \text{cond.val} = 0.7, \text{cond.var} = 1, \text{obj}) \)
\( \text{hist(sim1)} \) # not uniform!

# simulate 500 observations of (U1 | U2 = 0.1)
\( \text{sim2} \leftarrow \text{BiCopCondSim(500, } \text{cond.val} = 0.1, \text{cond.var} = 2, \text{obj}) \)
\( \text{hist(sim2)} \) # not uniform!
BiCopDeriv

Description

This function evaluates the derivative of a given parametric bivariate copula density with respect to its parameter(s) or one of its arguments.

Usage

BiCopDeriv(
  u1,
  u2,
  family,
  par,
  par2 = 0,
  deriv = "par",
  log = FALSE,
  obj = NULL,
  check.pars = TRUE
)

Arguments

u1, u2 numeric vectors of equal length with values in [0, 1].
family integer; single number or vector of size length(u1); defines the bivariate copula family:
0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
13 = rotated Clayton copula (180 degrees; survival Clayton’
14 = rotated Gumbel copula (180 degrees; survival Gumbel’)
16 = rotated Joe copula (180 degrees; “survival Joe”)
23 = rotated Clayton copula (90 degrees)
24 = rotated Gumbel copula (90 degrees)
26 = rotated Joe copula (90 degrees)
33 = rotated Clayton copula (270 degrees)
34 = rotated Gumbel copula (270 degrees)
36 = rotated Joe copula (270 degrees)
par numeric; single number or vector of size length(u1); copula parameter.
**Description**

BiCopDeriv

- **par2**: integer; single number or vector of size `length(u1)`; second parameter for the t-Copula; default is `par2 = 0`, should be an positive integer for the Students’s t copula family = 2.
- **deriv**: Derivative argument
  - "par" = derivative with respect to the first parameter (default)
  - "par2" = derivative with respect to the second parameter (only available for the t-copula)
  - "u1" = derivative with respect to the first argument `u1`
  - "u2" = derivative with respect to the second argument `u2`
- **log**: Logical; if TRUE than the derivative of the log-likelihood is returned (default: `log = FALSE`; only available for the derivatives with respect to the parameter(s) (`deriv = "par"` or `deriv = "par2"`).
- **obj**: BiCop object containing the family and parameter specification.
- **check.pars**: logical; default is TRUE; if FALSE, checks for family/parameter-consistency are omitted (should only be used with care).

**Details**

If the family and parameter specification is stored in a BiCop() object `obj`, the alternative version

```r
BiCopDeriv(u1, u2, obj, deriv = "par", log = FALSE)
```

can be used.

**Value**

A numeric vector of the bivariate copula derivative

- of the copula family
- with parameter(s) `par`, `par2`
- with respect to `deriv`,
- evaluated at `u1` and `u2`.

**Author(s)**

Ulf Schepsmeier

**References**


**See Also**

RVineGrad(), RVineHessian(), BiCopDeriv2(), BiCopHfuncDeriv(), BiCop()
BiCopDeriv2

Examples

```r
## simulate from a bivariate Student-t copula
set.seed(123)
cop <- BiCop(family = 2, par = -0.7, par2 = 4)
simdata <- BiCopSim(100, cop)

## derivative of the bivariate t-copula with respect to the first parameter
u1 <- simdata[,1]
u2 <- simdata[,2]
BiCopDeriv(u1, u2, cop, deriv = "par")

## estimate a Student-t copula for the simulated data
cop <- BiCopEst(u1, u2, family = 2)
## and evaluate its derivative w.r.t. the second argument u2
BiCopDeriv(u1, u2, cop, deriv = "u2")
```

BiCopDeriv2

Second Derivatives of a Bivariate Copula Density

Description

This function evaluates the second derivative of a given parametric bivariate copula density with respect to its parameter(s) and/or its arguments.

Usage

```r
BiCopDeriv2(
  u1, u2,
  family,
  par,
  par2 = 0,
  deriv = "par",
  obj = NULL,
  check.pars = TRUE
)
```

Arguments

- `u1, u2` numeric vectors of equal length with values in [0, 1].
- `family` integer; single number or vector of size `length(u1)`; defines the bivariate copula family:
  - 0 = independence copula
  - 1 = Gaussian copula
  - 2 = Student t copula (t-copula)
  - 3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
13 = rotated Clayton copula (180 degrees; survival Clayton’”)
16 = rotated Joe copula (180 degrees; “survival Joe”)
23 = rotated Clayton copula (90 degrees)
‘24’ = rotated Gumbel copula (90 degrees)
‘26’ = rotated Joe copula (90 degrees)
‘33’ = rotated Clayton copula (270 degrees)
‘34’ = rotated Gumbel copula (270 degrees)
‘36’ = rotated Joe copula (270 degrees)

par
Copula parameter.
par2
integer; single number or vector of size \text{length}(u1); second parameter for the t-Copula; default is \text{par2} = 0, should be an positive integer for the Students’s t copula family = 2.
deriv
Derivative argument
"par" = second derivative with respect to the first parameter (default)
"par2" = second derivative with respect to the second parameter (only available for the t-copula)
"u1" = second derivative with respect to the first argument \text{u1}
"u2" = second derivative with respect to the second argument \text{u2}
"par1par2" = second derivative with respect to the first and second parameter (only available for the t-copula)
"par1u1" = second derivative with respect to the first parameter and the first argument
"par2u1" = second derivative with respect to the second parameter and the first argument (only available for the t-copula)
"par1u2" = second derivative with respect to the first parameter and the second argument
"par2u2" = second derivative with respect to the second parameter and the second argument (only available for the t-copula)

obj
BiCop object containing the family and parameter specification.
check.pars
logical; default is TRUE; if FALSE, checks for family/parameter-consistency are omitted (should only be used with care).

Details
If the family and parameter specification is stored in a \text{BiCop()} object \text{obj}, the alternative version

\text{BiCopDeriv2}(u1, u2, \text{obj}, \text{deriv} = "par")

can be used.
Value

A numeric vector of the second-order bivariate copula derivative

- of the copula family
- with parameter(s) par, par2
- with respect to deriv
- evaluated at u1 and u2.

Author(s)

Ulf Schepsmeier, Jakob Stoeber

References


See Also

RVineGrad(), RVineHessian(), BiCopDeriv(), BiCopHfuncDeriv(), BiCop()

Examples

```r
## simulate from a bivariate Student-t copula
set.seed(123)
cop <- BiCop(family = 2, par = -0.7, par2 = 4)
simdata <- BiCopSim(100, cop)

## second derivative of the Student-t copula w.r.t. the first parameter
u1 <- simdata[,1]
u2 <- simdata[,2]
BiCopDeriv2(u1, u2, cop, deriv = "par")

## estimate a Student-t copula for the simulated data
cop <- BiCopEst(u1, u2, family = 2)
## and evaluate its second derivative w.r.t. the second argument u2
BiCopDeriv2(u1, u2, cop, deriv = "u2")
```
**BiCopEst**  
*Parameter Estimation for Bivariate Copula Data*

### Description
This function estimates the parameter(s) of a bivariate copula using either inversion of empirical Kendall’s tau (for one parameter copula families only) or maximum likelihood estimation for implemented copula families.

#### Usage

```r
BiCopEst(
  u1, u2,
  family,
  method = "mle",
  se = FALSE,
  max.df = 30,
  max.BB = list(BB1 = c(5, 6), BB6 = c(6, 6), BB7 = c(5, 6), BB8 = c(6, 1)),
  weights = NA
)
```

#### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>u1, u2</td>
<td>Data vectors of equal length with values in [0, 1].</td>
</tr>
<tr>
<td>family</td>
<td>An integer defining the bivariate copula family:</td>
</tr>
<tr>
<td></td>
<td>0 = independence copula</td>
</tr>
<tr>
<td></td>
<td>1 = Gaussian copula</td>
</tr>
<tr>
<td></td>
<td>2 = Student t copula (t-copula)</td>
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<tr>
<td></td>
<td>3 = Clayton copula</td>
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<tr>
<td></td>
<td>4 = Gumbel copula</td>
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<tr>
<td></td>
<td>5 = Frank copula</td>
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<tr>
<td></td>
<td>6 = Joe copula</td>
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<td></td>
<td>7 = BB1 copula</td>
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<td>8 = BB6 copula</td>
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<td>9 = BB7 copula</td>
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<tr>
<td></td>
<td>10 = BB8 copula</td>
</tr>
<tr>
<td></td>
<td>13 = rotated Clayton copula (180 degrees; survival Clayton'')</td>
</tr>
<tr>
<td></td>
<td>14 = rotated Gumbel copula (180 degrees; survival Gumbel&quot;)</td>
</tr>
<tr>
<td></td>
<td>15 = rotated Joe copula (180 degrees; survival Joe'')</td>
</tr>
<tr>
<td></td>
<td>16 = rotated BB1 copula (180 degrees; survival BB1&quot;)</td>
</tr>
<tr>
<td></td>
<td>17 = rotated BB6 copula (180 degrees; survival BB6'')</td>
</tr>
<tr>
<td></td>
<td>18 = rotated BB7 copula (180 degrees; survival BB7&quot;)</td>
</tr>
<tr>
<td></td>
<td>19 = rotated BB8 copula (180 degrees; &quot;survival BB8&quot;)</td>
</tr>
<tr>
<td></td>
<td>20 = rotated BB8 copula (180 degrees; &quot;survival BB8&quot;)</td>
</tr>
<tr>
<td></td>
<td>23 = rotated Clayton copula (90 degrees)</td>
</tr>
<tr>
<td></td>
<td>'24' = rotated Gumbel copula (90 degrees)</td>
</tr>
<tr>
<td></td>
<td>'26' = rotated Joe copula (90 degrees)</td>
</tr>
</tbody>
</table>
method indicates the estimation method: either maximum likelihood estimation (method = "mle"; default) or inversion of Kendall's tau (method = "itau"). For method = "itau" only one parameter families and the Student t copula can be used (family = 1,2,3,4,5,6,13,14,16,23,24,26,33,34 or 36). For the t-copula, par2 is found by a crude profile likelihood optimization over the interval (2, 10).

se Logical; whether standard error(s) of parameter estimates is/are estimated (default: se = FALSE).

max.df Numeric; upper bound for the estimation of the degrees of freedom parameter of the t-copula (default: max.df = 30).

max.BB List; upper bounds for the estimation of the two parameters (in absolute values) of the BB1, BB6, BB7 and BB8 copulas (default: max.BB = list(BB1=c(5,6),BB6=c(6,6),BB7=c(5,6),BB8=c(6,1))).

weights Numerical; weights for each observation (optional).

Details

If method = "itau", the function computes the empirical Kendall's tau of the given copula data and exploits the one-to-one relationship of copula parameter and Kendall's tau which is available for many one parameter bivariate copula families (see BiCopPar2Tau() and BiCopTau2Par()). The inversion of Kendall's tau is however not available for all bivariate copula families (see above). If a two parameter copula family is chosen and method = "itau", a warning message is returned and the MLE is calculated.

For method = "mle" copula parameters are estimated by maximum likelihood using starting values obtained by method = "itau". If no starting values are available by inversion of Kendall's tau, starting values have to be provided given expert knowledge and the boundaries max.df and max.BB respectively. Note: The MLE is performed via numerical maximization using the L_BFGS-B method.
For the Gaussian, the t- and the one-parametric Archimedean copulas we can use the gradients, but for the BB copulas we have to use finite differences for the L_BFGS-B method.

A warning message is returned if the estimate of the degrees of freedom parameter of the t-copula is larger than max.df. For high degrees of freedom the t-copula is almost indistinguishable from the Gaussian and it is advised to use the Gaussian copula in this case. As a rule of thumb max.df = 30 typically is a good choice. Moreover, standard errors of the degrees of freedom parameter estimate cannot be estimated in this case.

Value

An object of class BiCop(), augmented with the following entries:

- se, se2: standard errors for the parameter estimates (if se = TRUE,
- nobs: number of observations,
- logLik: log likelihood
- AIC: Aikake's Information Criterion,
- BIC: Bayesian's Information Criterion,
- emptau: empirical value of Kendall's tau,
- p.value.indeptest: p-value of the independence test.

Note

For a comprehensive summary of the fitted model, use summary(object); to see all its contents, use str(object).

Author(s)

Ulf Schepsmeier, Eike Brechmann, Jakob Stoeber, Carlos Almeida

References


See Also

BiCop(), BiCopPar2Tau(), BiCopTau2Par(), RVineSeqEst(), BiCopSelect()

Examples

```r
## Example 1: bivariate Gaussian copula
dat <- BiCopSim(500, 1, 0.7)
u1 <- dat[, 1]
v1 <- dat[, 2]

# estimate parameters of Gaussian copula by inversion of Kendall's tau
est1.tau <- BiCopEst(u1, v1, family = 1, method = "itau")
est1.tau # short overview
```
summary(est1.tau) # comprehensive overview
str(est1.tau) # see all contents of the object

# check if parameter actually coincides with inversion of Kendall's tau
tau1 <- cor(u1, v1, method = "kendall")
all.equal(BiCopTau2Par(1, tau1), est1.tau$par)

# maximum likelihood estimate for comparison
est1.mle <- BiCopEst(u1, v1, family = 1, method = "mle")
summary(est1.mle)

## Example 2: bivariate Clayton and survival Gumbel copulas
# simulate from a Clayton copula
dat <- BiCopSim(500, 3, 2.5)
u2 <- dat[, 1]
v2 <- dat[, 2]

# empirical Kendall's tau
tau2 <- cor(u2, v2, method = "kendall")

# inversion of empirical Kendall's tau for the Clayton copula
BiCopTau2Par(3, tau2)
BiCopEst(u2, v2, family = 3, method = "itau")

# inversion of empirical Kendall's tau for the survival Gumbel copula
BiCopTau2Par(14, tau2)
BiCopEst(u2, v2, family = 14, method = "itau")

# maximum likelihood estimates for comparison
BiCopEst(u2, v2, family = 3, method = "mle")
BiCopEst(u2, v2, family = 14, method = "mle")

BiCopEstList

List of Maximum Likelihood Estimates for Several Bivariate Copula Families

Description
This function allows to compare bivariate copula models across a number of families w.r.t. the fit statistics log-likelihood, AIC, and BIC. For each family, the parameters are estimated by maximum likelihood.

Usage
BiCopEstList(u1, u2, familyset = NA, weights = NA, rotations = TRUE, ...)

BiCopEstList
Arguments

$u_1, u_2$  Data vectors of equal length with values in $[0, 1]$.

familyset  Vector of bivariate copula families to select from. The vector has to include at least one bivariate copula family that allows for positive and one that allows for negative dependence. If `familyset = NA` (default), selection among all possible families is performed.

Coding of bivariate copula families:

0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton ‘Var’)
14 = rotated Gumbel copula (180 degrees; survival Gumbel”)
16 = rotated Joe copula (180 degrees; survival Joe ‘Var’)
17 = rotated BB1 copula (180 degrees; survival BB1”)
18 = rotated BB6 copula (180 degrees; survival BB6 ‘Var’)
19 = rotated BB7 copula (180 degrees; survival BB7”)
20 = rotated BB8 copula (180 degrees; “survival BB8”)
23 = rotated Clayton copula (90 degrees)
24 = rotated Gumbel copula (90 degrees)
26 = rotated Joe copula (90 degrees)
27 = rotated BB1 copula (90 degrees)
28 = rotated BB6 copula (90 degrees)
29 = rotated BB7 copula (90 degrees)
30 = rotated BB8 copula (90 degrees)
33 = rotated Clayton copula (270 degrees)
34 = rotated Gumbel copula (270 degrees)
36 = rotated Joe copula (270 degrees)
37 = rotated BB1 copula (270 degrees)
38 = rotated BB6 copula (270 degrees)
39 = rotated BB7 copula (270 degrees)
40 = rotated BB8 copula (270 degrees)
104 = Tawn type 1 copula
114 = rotated Tawn type 1 copula (180 degrees)
124 = rotated Tawn type 1 copula (90 degrees)
134 = rotated Tawn type 1 copula (270 degrees)
204 = Tawn type 2 copula
214 = rotated Tawn type 2 copula (180 degrees)
224 = rotated Tawn type 2 copula (90 degrees)
234 = rotated Tawn type 2 copula (270 degrees)
weights  Numerical; weights for each observation (optional).
rotations  If TRUE, all rotations of the families in familyset are included.
...  further arguments passed to BiCopEst().

**Details**

First all available copulas are fitted using maximum likelihood estimation. Then the criteria are computed for all available copula families (e.g., if u1 and u2 are negatively dependent, Clayton, Gumbel, Joe, BB1, BB6, BB7 and BB8 and their survival copulas are not considered) and the family with the minimum value is chosen. For observations $u_{i,j}$, $i = 1, ..., N$, $j = 1, 2$, the AIC of a bivariate copula family $c$ with parameter(s) $\theta$ is defined as

$$AIC := -2 \sum_{i=1}^{N} \ln[c(u_{i,1}, u_{i,2}|\theta)] + 2k,$$

where $k = 1$ for one parameter copulas and $k = 2$ for the two parameter t-, BB1, BB6, BB7 and BB8 copulas. Similarly, the BIC is given by

$$BIC := -2 \sum_{i=1}^{N} \ln[c(u_{i,1}, u_{i,2}|\theta)] + \ln(N)k.$$

Evidently, if the BIC is chosen, the penalty for two parameter families is stronger than when using the AIC.

**Value**

A list containing

- models  a list of BiCop() objects corresponding to the ‘familyset” (only families corresponding to the sign of the empirical Kendall’s tau are used),
- summary  a data frame containing the log-likelihoods, AICs, and BICs of all the fitted models.

**Author(s)**

Thomas Nagler

**References**


**See Also**

BiCop(), BiCopEst()
Examples

```r
## compare models
data(daxreturns)
comp <- BiCopEstList(daxreturns[, 1], daxreturns[, 4])
```

**BiCopGofTest**

*Goodness-of-Fit Test for Bivariate Copulas*

**Description**

This function performs a goodness-of-fit test for bivariate copulas, either based on White’s information matrix equality (White, 1982) as introduced by Huang and Prokhorov (2011) or based on Kendall’s process (Wang and Wells, 2000; Genest et al., 2006). It computes the test statistics and p-values.

**Usage**

```r
BiCopGofTest(
  u1,
  u2,
  family,
  par = 0,
  par2 = 0,
  method = "white",
  max.df = 30,
  B = 100,
  obj = NULL
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>u1, u2</td>
<td>Numeric vectors of equal length with values in [0, 1].</td>
</tr>
<tr>
<td>family</td>
<td>An integer defining the bivariate copula family:</td>
</tr>
<tr>
<td></td>
<td>0 = independence copula</td>
</tr>
<tr>
<td></td>
<td>1 = Gaussian copula</td>
</tr>
<tr>
<td></td>
<td>2 = Student t copula (t-copula) (only for method = &quot;white&quot;; see details)</td>
</tr>
<tr>
<td></td>
<td>3 = Clayton copula</td>
</tr>
<tr>
<td></td>
<td>4 = Gumbel copula</td>
</tr>
<tr>
<td></td>
<td>5 = Frank copula</td>
</tr>
<tr>
<td></td>
<td>6 = Joe copula</td>
</tr>
<tr>
<td></td>
<td>7 = BB1 copula (only for method = &quot;kendall&quot;)</td>
</tr>
<tr>
<td></td>
<td>8 = BB6 copula (only for method = &quot;kendall&quot;)</td>
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<tr>
<td></td>
<td>9 = BB7 copula (only for method = &quot;kendall&quot;)</td>
</tr>
<tr>
<td></td>
<td>10 = BB8 copula (only for method =&quot;kendall&quot;)</td>
</tr>
<tr>
<td></td>
<td>13 = rotated Clayton copula (180 degrees; survival Clayton')</td>
</tr>
<tr>
<td></td>
<td>14 = rotated Gumbel copula</td>
</tr>
<tr>
<td></td>
<td>15 = rotated Gumbel'</td>
</tr>
</tbody>
</table>
```
16 = rotated Joe copula (180 degrees; survival Joe’)
17 = rotated BB1 copula (180 degrees; survival BB1’); only for method = "kendall"
18 = rotated BB6 copula (180 degrees; survival BB6’); only for method = "kendall"
19 = rotated BB7 copula (180 degrees; survival BB7’); only for method = "kendall"
20 = rotated BB8 copula (180 degrees; survival BB8’); only for method = "kendall"

‘23’ = rotated Clayton copula (90 degrees)
‘24’ = rotated Gumbel copula (90 degrees)
‘26’ = rotated Joe copula (90 degrees)

‘27’ = rotated BB1 copula (90 degrees; only for method = "kendall")
‘28’ = rotated BB6 copula (90 degrees; only for method = "kendall")
‘29’ = rotated BB7 copula (90 degrees; only for method = "kendall")
‘30’ = rotated BB8 copula (90 degrees; only for method = "kendall")
‘33’ = rotated Clayton copula (270 degrees)
‘34’ = rotated Gumbel copula (270 degrees)
‘36’ = rotated Joe copula (270 degrees)

‘37’ = rotated BB1 copula (270 degrees; only for method = "kendall")
‘38’ = rotated BB6 copula (270 degrees; only for method = "kendall")
‘39’ = rotated BB7 copula (270 degrees; only for method = "kendall")
‘40’ = rotated BB8 copula (270 degrees; only for method = "kendall")

par  Copula parameter (optional).
par2 Second parameter for bivariate t-copula (optional); default: par2 = 0.

method A string indicating the goodness-of-fit method:
"white" = goodness-of-fit test based on White’s information matrix equality (default)
"kendall" = goodness-of-fit test based on Kendall’s process

max.df Numeric; upper bound for the estimation of the degrees of freedom parameter
of the t-copula (default: max.df = 30).

B Integer; number of bootstrap samples (default: B = 100). For B = 0 only the test
statistics are returned.
WARNING: If B is chosen too large, computations will take very long.

obj  BiCop object containing the family and parameter specification.

Details

method = "white":
This goodness-of-fit test uses the information matrix equality of White (1982) and was investigated
by Huang and Prokhorov (2011). The main contribution is that under correct model specification
the Fisher Information can be equivalently calculated as minus the expected Hessian matrix or as
the expected outer product of the score function. The null hypothesis is

\[ H_0 : H(\theta) + C(\theta) = 0 \]

against the alternative

\[ H_0 : H(\theta) + C(\theta) \neq 0, \]

where \( H(\theta) \) is the expected Hessian matrix and \( C(\theta) \) is the expected outer product of the score
function. For the calculation of the test statistic we use the consistent maximum likelihood estimator \( \hat{\theta} \) and the sample counter parts of \( H(\theta) \) and \( C(\theta) \). The correction of the covariance-matrix
in the test statistic for the uncertainty in the margins is skipped. The implemented tests assumes
that where is no uncertainty in the margins. The correction can be found in Huang and Prokhorov
(2011). It involves two-dimensional integrals.
WARNING: For the t-copula the test may be unstable. The results for the t-copula therefore have
to be treated carefully.

method = "kendall":
This copula goodness-of-fit test is based on Kendall’s process as proposed by Wang and Wells
(2000). For computation of p-values, the parametric bootstrap described by Genest et al. (2006) is
used. For rotated copulas the input arguments are transformed and the goodness-of-fit procedure
for the corresponding non-rotated copula is used.

Value
For method = "white":

p.value Asymptotic p-value.
statistic The observed test statistic.

For method = "kendall"

p.value.CvM Bootstrapped p-value of the goodness-of-fit test using the Cramer-von Mises
statistic (if B > 0).
statistic.CvM The observed Cramer-von Mises test statistic.

p.value.KS Bootstrapped p-value of the goodness-of-fit test using the Kolmogorov-Smirnov
statistic (if B > 0).
statistic.KS The observed Kolmogorov-Smirnov test statistic.

Author(s)
Ulf Schepsmeier, Wanling Huang, Jiying Luo, Eike Brechmann

References
33(7), 751-771.


Based on the Probability Integral Transformation. Scandinavian Journal of Statistics, 33(2), 337-
https://mediatum.ub.tum.de/?id=1079291.


See Also
BiCopDeriv2(), BiCopDeriv(), BiCopIndTest(), BiCopVuongClarke()
Examples

```r
# simulate from a bivariate Clayton copula
simdata <- BiCopSim(100, 3, 2)
u1 <- simdata[,1]
u2 <- simdata[,2]

# perform White's goodness-of-fit test for the true copula
BiCopGofTest(u1, u2, family = 3)

# perform White's goodness-of-fit test for the Frank copula
BiCopGofTest(u1, u2, family = 5)

# perform Kendall's goodness-of-fit test for the true copula
BiCopGofTest(u1, u2, family = 3, method = "kendall", B=50)

# perform Kendall's goodness-of-fit test for the Frank copula
BiCopGofTest(u1, u2, family = 5, method = "kendall", B=50)
```

---

**BiCopHfunc**

*Conditional Distribution Function of a Bivariate Copula*

Description

Evaluate the conditional distribution function (h-function) of a given parametric bivariate copula.

Usage

```r
BiCopHfunc(u1, u2, family, par, par2 = 0, obj = NULL, check.pars = TRUE)
```

```r
BiCopHfunc1(u1, u2, family, par, par2 = 0, obj = NULL, check.pars = TRUE)
```

```r
BiCopHfunc2(u1, u2, family, par, par2 = 0, obj = NULL, check.pars = TRUE)
```

Arguments

- `u1`, `u2`: numeric vectors of equal length with values in \([0, 1]\).
- `family`: integer; single number or vector of size `length(u1)`; defines the bivariate copula family:
  - 0 = independence copula
  - 1 = Gaussian copula
  - 2 = Student t copula (t-copula)
  - 3 = Clayton copula
  - 4 = Gumbel copula
  - 5 = Frank copula
  - 6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton')
16 = rotated Joe copula (180 degrees; survival Joe')
18 = rotated BB6 copula (180 degrees; survival BB6')
20 = rotated BB8 copula (180 degrees; survival BB8')
23 = rotated Clayton copula (90 degrees)
26 = rotated Joe copula (90 degrees)
28 = rotated BB6 copula (90 degrees)
30 = rotated BB8 copula (90 degrees)
33 = rotated Clayton copula (270 degrees)
34 = rotated Gumbel copula (270 degrees)
36 = rotated Joe copula (270 degrees)
38 = rotated BB6 copula (270 degrees)
39 = rotated BB7 copula (270 degrees)
40 = rotated BB8 copula (270 degrees)
104 = Tawn type 1 copula
114 = rotated Tawn type 1 copula (180 degrees)
124 = rotated Tawn type 1 copula (90 degrees)
134 = rotated Tawn type 1 copula (270 degrees)
204 = Tawn type 2 copula
214 = rotated Tawn type 2 copula (180 degrees)
224 = rotated Tawn type 2 copula (90 degrees)
234 = rotated Tawn type 2 copula (270 degrees)

par numeric; single number or vector of size length(u1); copula parameter.
par2 numeric; single number or vector of size length(u1); second parameter for bivariate copulas with two parameters (t, BB1, BB6, BB7, BB8, Tawn type 1 and type 2; default: par2 = 0). par2 should be a positive integer for the Student's t copula family = 2.
obj BiCop object containing the family and parameter specification.
check.pars logical; default is TRUE; if FALSE, checks for family/parameter-consistency are omitted (should only be used with care).

Details

The h-function is defined as the conditional distribution function of a bivariate copula, i.e.,

\[ h_1(u_2|u_1; \theta) := P(U_2 \leq u_2|U_1 = u_1) = \frac{\partial C(u_1, u_2; \theta)}{\partial u_1}, \]
\[
    h_2(u_1|u_2; \theta) := P(U_1 \leq u_1|U_2 = u_2) = \frac{\partial C(u_1,u_2; \theta)}{\partial u_2},
\]
where \((U_1,U_2) \sim C\), and \(C\) is a bivariate copula distribution function with parameter(s) \(\theta\). For more details see Aas et al. (2009).

If the family and parameter specification is stored in a \texttt{BiCop()} object \texttt{obj}, the alternative versions

\begin{verbatim}
BiCopHfunc(u1, u2, obj)
BiCopHfunc1(u1, u2, obj)
BiCopHfunc2(u1, u2, obj)
\end{verbatim}

can be used.

\textbf{Value}

\texttt{BiCopHfunc} returns a list with

\begin{verbatim}
  hfunc1 Numeric vector of the conditional distribution function (h-function) of the cop-
  ula family with parameter(s) \texttt{par}, \texttt{par2} evaluated at \texttt{u2} given \texttt{u1}, i.e.,
  h1\((u_2|u_1; \theta)\).
  hfunc2 Numeric vector of the conditional distribution function (h-function) of the cop-
  ula family with parameter(s) \texttt{par}, \texttt{par2} evaluated at \texttt{u1} given \texttt{u2}, i.e.,
  h2\((u_1|u_2; \theta)\).
\end{verbatim}

\texttt{BiCopHfunc1} is a faster version that only calculates \texttt{hfunc1}; \texttt{BiCopHfunc2} only calculates \texttt{hfunc2}.

\textbf{Author(s)}

Ulf Schepsmeier

\textbf{References}


\textbf{See Also}

\texttt{BiCopHinv()}, \texttt{BiCopPDF()}, \texttt{BiCopCDF()}, \texttt{RVineLogLik()}, \texttt{RVineSeqEst()}, \texttt{BiCop()}

\textbf{Examples}

\begin{verbatim}
data(daxreturns)

# h-functions of the Gaussian copula
cop <- BiCop(family = 1, par = 0.5)
h <- BiCopHfunc(daxreturns[, 2], daxreturns[, 1], cop)

# or using the fast versions
h1 <- BiCopHfunc1(daxreturns[, 2], daxreturns[, 1], cop)
h2 <- BiCopHfunc2(daxreturns[, 2], daxreturns[, 1], cop)
all.equal(h$hfunc1, h1)
all.equal(h$hfunc2, h2)
\end{verbatim}
BiCopHfuncDeriv

Derivatives of the h-Function of a Bivariate Copula

Description

This function evaluates the derivative of a given conditional parametric bivariate copula (h-function) with respect to its parameter(s) or one of its arguments.

Usage

BiCopHfuncDeriv(
  u1,
  u2,
  family,
  par,
  par2 = 0,
  deriv = "par",
  obj = NULL,
  check.pars = TRUE
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>u1, u2</td>
<td>numeric vectors of equal length with values in [0, 1].</td>
</tr>
</tbody>
</table>
| family   | integer; single number or vector of size length(u1); defines the bivariate copula family: \ 
 0 = independence copula 
 1 = Gaussian copula 
 2 = Student t copula (t-copula) 
 3 = Clayton copula 
 4 = Gumbel copula 
 5 = Frank copula 
 6 = Joe copula 
 13 = rotated Clayton copula (180 degrees; survival Clayton”) \cr ‘14’ = rotated Gumbel copula (180 degrees; survival Gumbel’) 
 16 = rotated Joe copula (180 degrees; “survival Joe”) 
 23 = rotated Clayton copula (90 degrees) 
 ‘24’ = rotated Gumbel copula (90 degrees) 
 ‘26’ = rotated Joe copula (90 degrees) 
 ‘33’ = rotated Clayton copula (270 degrees) 
 ‘34’ = rotated Gumbel copula (270 degrees) 
 ‘36’ = rotated Joe copula (270 degrees) |
| par      | numeric; single number or vector of size length(u1); copula parameter. |
| par2     | integer; single number or vector of size length(u1); second parameter for the t-Copula; default is par2 = 0, should be an positive integer for the Students’s t copula family = 2. |
deriv  Derivative argument
"par" = derivative with respect to the first parameter (default)
"par2" = derivative with respect to the second parameter (only available for the
t-copula)
"u2" = derivative with respect to the second argument u2

obj  BiCop object containing the family and parameter specification.
check.pars  logical; default is TRUE; if FALSE, checks for family/parameter-consistency are
omitted (should only be used with care).

Details
If the family and parameter specification is stored in a BiCop() object obj, the alternative version

BiCopHfuncDeriv(u1, u2, obj, deriv = "par")

can be used.

Value
A numeric vector of the conditional bivariate copula derivative
• of the copula family,
• with parameter(s) par, par2,
• with respect to deriv,
• evaluated at u1 and u2.

Author(s)
Ulf Schepsmeier

References
Statistical Papers, 55 (2), 525-542.

See Also
RVineGrad(), RVineHessian(), BiCopDeriv2(), BiCopDeriv2(), BiCopHfuncDeriv(), BiCop()

Examples
## simulate from a bivariate Student-t copula
set.seed(123)
cop <- BiCop(family = 2, par = -0.7, par2 = 4)
simdata <- BiCopSim(100, cop)
BiCopHfuncDeriv2

# derivative of the conditional Student-t copula
# with respect to the first parameter
u1 <- simdata[,1]
u2 <- simdata[,2]
BiCopHfuncDeriv(u1, u2, cop, deriv = "par")

# estimate a Student-t copula for the simulated data
cop <- BiCopEst(u1, u2, family = 2)
# and evaluate the derivative of the conditional copula
# w.r.t. the second argument u2
BiCopHfuncDeriv(u1, u2, cop, deriv = "u2")

---

BiCopHfuncDeriv2  Second Derivatives of the h-Function of a Bivariate Copula

**Description**

This function evaluates the second derivative of a given conditional parametric bivariate copula (h-function) with respect to its parameter(s) and/or its arguments.

**Usage**

```r
BiCopHfuncDeriv2(
  u1,
  u2,
  family,
  par,
  par2 = 0,
  deriv = "par",
  obj = NULL,
  check.pars = TRUE
)
```

**Arguments**

- `u1`, `u2` numeric vectors of equal length with values in $[0, 1]$.
- `family` integer; single number or vector of size `length(u1)`; defines the bivariate copula family:
  - 0 = independence copula
  - 1 = Gaussian copula
  - 2 = Student t copula (t-copula)
  - 3 = Clayton copula
  - 4 = Gumbel copula
  - 5 = Frank copula
  - 6 = Joe copula
13 = rotated Clayton copula (180 degrees; survival Clayton ‘) cr ‘14’ = rotated Gumbel copula
survival Gumbel’)
16 = rotated Joe copula (180 degrees; “survival Joe”)
23 = rotated Clayton copula (90 degrees)
’24’ = rotated Gumbel copula (90 degrees)
’26’ = rotated Joe copula (90 degrees)
’33’ = rotated Clayton copula (270 degrees)
’34’ = rotated Gumbel copula (270 degrees)
’36’ = rotated Joe copula (270 degrees)

par numeric; single number or vector of size length(u1); copula parameter.
par2 integer; single number or vector of size length(u1); second parameter for the
t-Copula; default is par2 = 0, should be an positive integer for the Students’s t
copula family = 2.
deriv Derivative argument
"par" = second derivative with respect to the first parameter (default)
"par2" = second derivative with respect to the second parameter (only available
for the t-copula)
"u2" = second derivative with respect to the second argument u2
"par1 par2" = second derivative with respect to the first and second parameter
(only available for the t-copula)
"par1 u2" = second derivative with respect to the first parameter and the second
argument
"par2 u2" = second derivative with respect to the second parameter and the sec-
ond argument (only available for the t-copula)
obj BiCop object containing the family and parameter specification.
check.pars logical; default is TRUE; if FALSE, checks for family/parameter-consistency are
omitted (should only be used with care).

Details
If the family and parameter specification is stored in a BiCop() object obj, the alternative version

BiCopHfuncDeriv2(u1, u2, obj, deriv = “par”)

can be used.

Value
A numeric vector of the second-order conditional bivariate copula derivative

• of the copula family
• with parameter(s) par, par2
• with respect to deriv
• evaluated at u1 and u2.
**BiCopHinv**

**Author(s)**

Ulf Schepsmeier, Jakob Stoeber

**References**


**See Also**

RVineGrad(), RVineHessian(), BiCopDeriv(), BiCopDeriv2(), BiCopHfuncDeriv(), BiCop()

**Examples**

```r
## simulate from a bivariate Student-t copula
set.seed(123)
cop <- BiCop(family = 2, par = -0.7, par2 = 4)
simdata <- BiCopSim(100, cop)

## second derivative of the conditional bivariate t-copula
## with respect to the first parameter
u1 <- simdata[,1]
u2 <- simdata[,2]
BiCopHfuncDeriv2(u1, u2, cop, deriv = "par")

## estimate a Student-t copula for the simulated data
cop <- BiCopEst(u1, u2, family = 2)
## and evaluate the derivative of the conditional copula
## w.r.t. the second argument u2
BiCopHfuncDeriv2(u1, u2, cop, deriv = "u2")
```

---

**BiCopHinv**  
*Inverse Conditional Distribution Function of a Bivariate Copula*

**Description**

Evaluate the inverse conditional distribution function (inverse h-function) of a given parametric bivariate copula.

**Usage**

```r
BiCopHinv(u1, u2, family, par, par2 = 0, obj = NULL, check.pars = TRUE)
BiCopHinv1(u1, u2, family, par, par2 = 0, obj = NULL, check.pars = TRUE)
BiCopHinv2(u1, u2, family, par, par2 = 0, obj = NULL, check.pars = TRUE)
```
Arguments

- **u1, u2**: numeric vectors of equal length with values in $[0, 1]$.
- **family**: integer; single number or vector of size length(u1); defines the bivariate copula family:
  - $0$ = independence copula
  - $1$ = Gaussian copula
  - $2$ = Student t copula (t-copula)
  - $3$ = Clayton copula
  - $4$ = Gumbel copula
  - $5$ = Frank copula
  - $6$ = Joe copula
  - $7$ = BB1 copula
  - $8$ = BB6 copula
  - $9$ = BB7 copula
  - $10$ = BB8 copula
  - $13$ = rotated Clayton copula (180 degrees; survival Clayton"")
  - $14$ = rotated Gumbel copula (180 degrees; survival Gumbel"")
  - $16$ = rotated Joe copula (180 degrees; survival Joe"")
  - $17$ = rotated BB1 copula (180 degrees; survival BB1"")
  - $18$ = rotated BB6 copula (180 degrees; survival BB6"")
  - $19$ = rotated BB7 copula (180 degrees; survival BB7"")
  - $20$ = rotated BB8 copula (180 degrees; "survival BB8")
  - $23$ = rotated Clayton copula (90 degrees)
  - $24$ = rotated Gumbel copula (90 degrees)
  - $26$ = rotated Joe copula (90 degrees)
  - $27$ = rotated BB1 copula (90 degrees)
  - $28$ = rotated BB6 copula (90 degrees)
  - $29$ = rotated BB7 copula (90 degrees)
  - $30$ = rotated BB8 copula (90 degrees)
  - $33$ = rotated Clayton copula (270 degrees)
  - $34$ = rotated Gumbel copula (270 degrees)
  - $36$ = rotated Joe copula (270 degrees)
  - $37$ = rotated BB1 copula (270 degrees)
  - $38$ = rotated BB6 copula (270 degrees)
  - $39$ = rotated BB7 copula (270 degrees)
  - $40$ = rotated BB8 copula (270 degrees)
  - $104$ = Tawn type 1 copula
  - $114$ = rotated Tawn type 1 copula (180 degrees)
  - $124$ = rotated Tawn type 1 copula (90 degrees)
  - $134$ = rotated Tawn type 1 copula (270 degrees)
  - $204$ = Tawn type 2 copula
  - $214$ = rotated Tawn type 2 copula (180 degrees)
  - $224$ = rotated Tawn type 2 copula (90 degrees)
  - $234$ = rotated Tawn type 2 copula (270 degrees)

- **par**: numeric; single number or vector of size length(u1); copula parameter.
- **par2**: numeric; single number or vector of size length(u1); second parameter for
bivariate copulas with two parameters (t, BB1, BB6, BB7, BB8, Tawn type 1 and type 2; default: \( \text{par2} = 0 \)). \( \text{par2} \) should be an positive integer for the Students’ t copula family = 2.

**obj** BiCop object containing the family and parameter specification.

**check.pars** logical; default is `TRUE`; if `FALSE`, checks for family/parameter-consistency are omitted (should only be used with care).

### Details

The \( h \)-function is defined as the conditional distribution function of a bivariate copula, i.e.,

\[
\begin{align*}
\h_1(u_2|u_1; \theta) &:= P(U_2 \leq u_2|U_1 = u_1) = \frac{\partial C(u_1, u_2; \theta)}{\partial u_1}, \\
\h_2(u_1|u_2; \theta) &:= P(U_1 \leq u_1|U_2 = u_2) = \frac{\partial C(u_1, u_2; \theta)}{\partial u_2},
\end{align*}
\]

where \((U_1, U_2) \sim C\), and \( C \) is a bivariate copula distribution function with parameter(s) \( \theta \). For more details see Aas et al. (2009).

If the family and parameter specification is stored in a `BiCop()` object `obj`, the alternative version

\[
\text{BiCopHinv}(u_1, u_2, \text{obj}), \\
\text{BiCopHinv1}(u_1, u_2, \text{obj}), \\
\text{BiCopHinv2}(u_1, u_2, \text{obj})
\]

can be used.

### Value

`BiCopHinv` returns a list with

- `hinv1` Numeric vector of the inverse conditional distribution function (inverse \( h \)-function) of the copula family with parameter(s) \( \text{par} \), \( \text{par2} \) evaluated at \( u_2 \) given \( u_1 \), i.e., \( h^{-1}_1(u_2|u_1; \theta) \).

- `hinv2` Numeric vector of the inverse conditional distribution function (inverse \( h \)-function) of the copula family with parameter(s) \( \text{par} \), \( \text{par2} \) evaluated at \( u_1 \) given \( u_2 \), i.e., \( h^{-1}_2(u_1|u_2; \theta) \).

`BiCopHinv1` is a faster version that only calculates `hinv1`; `BiCopHinv2` only calculates `hinv2`.

### Author(s)

Ulf Schepsmeier, Thomas Nagler

### References

See Also

BiCopHfunc(), BiCopPDF(), BiCopCDF(), RVineLogLik(), RVineSeqEst(), BiCop()

Examples

# inverse h-functions of the Gaussian copula
cop <- BiCop(1, 0.5)
hi <- BiCopHinv(0.1, 0.2, cop)

# or using the fast versions
hi1 <- BiCopHinv1(0.1, 0.2, cop)
hi2 <- BiCopHinv2(0.1, 0.2, cop)
all.equal(hi$hinv1, hi1)
all.equal(hi$hinv2, hi2)

# check if it is actually the inverse
cop <- BiCop(3, 3)
all.equal(0.2, BiCopHfunc1(0.1, BiCopHinv1(0.1, 0.2, cop), cop))
all.equal(0.1, BiCopHfunc2(BiCopHinv2(0.1, 0.2, cop), 0.2, cop))

BiCopIndTest

Description

This function returns the p-value of a bivariate asymptotic independence test based on Kendall’s τ.

Usage

BiCopIndTest(u1, u2)

Arguments

u1, u2 Data vectors of equal length with values in [0, 1].

Details

The test exploits the asymptotic normality of the test statistic

\[ \text{statistic} := T = \sqrt{\frac{9N(N-1)}{2(2N+5)}} \times |\hat{\tau}|, \]

where \( N \) is the number of observations (length of \( u1 \)) and \( \hat{\tau} \) the empirical Kendall’s tau of the data vectors \( u1 \) and \( u2 \). The p-value of the null hypothesis of bivariate independence hence is asymptotically

\[ p.\text{value} = 2 \times (1 - \Phi(T)), \]

where \( \Phi \) is the standard normal distribution function.
Value

- statistic: Test statistic of the independence test.
- p.value: P-value of the independence test.

Author(s)

Jeffrey Dissmann

References

Genest, C. and A. C. Favre (2007). Everything you always wanted to know about copula modeling but were afraid to ask. Journal of Hydrologic Engineering, 12 (4), 347-368.

See Also

- `BiCopGofTest()`, `BiCopPar2Tau()`, `BiCopTau2Par()`, `BiCopSelect()`,
- `RVineCopSelect()`, `RVineStructureSelect()`

Examples

```r
## Example 1: Gaussian copula with large dependence parameter
cop <- BiCop(1, 0.7)
dat <- BiCopSim(500, cop)

# perform the asymptotic independence test
BiCopIndTest(dat[, 1], dat[, 2])

## Example 2: Gaussian copula with small dependence parameter
cop <- BiCop(1, 0.01)
dat <- BiCopSim(500, cop)

# perform the asymptotic independence test
BiCopIndTest(dat[, 1], dat[, 2])
```

---

**BiCopKDE**  

*Kernel estimate of a Bivariate Copula Density*

**Description**

A kernel density estimate of the copula density is visualized. The function provides the same options as `plot.BiCop()`. Further arguments can be passed to `kdecopula::kdecop()` to modify the estimate. The `kdecopula::kdecopula-package()` must be installed to use this function.

**Usage**

```r
BiCopKDE(u1, u2, type = "contour", margins, size, kde.pars = list(), ...)
```
Arguments

- **u1, u2**: numeric vectors of equal length with values in \([0, 1]\).
- **type**: plot type; either "contour" or "surface" (partial matching is activated) for a contour or perspective/surface plot respectively.
- **margins**: only relevant for types "contour" and "surface"; options are: "unif" for the original copula density, "norm" for the transformed density with standard normal margins, "exp" with standard exponential margins, and "flexp" with flipped exponential margins. Default is "norm" for type = "contour", and "unif" for type = "surface". "norm" for the transformed density with standard normal margins (partial matching is activated). Default is "norm" for type = "contour", and "unif" for type = "surface".
- **size**: integer; the plot is based on values on a size x size grid; default is 100 for type = "contour", and 25 for type = "surface".
- **kde.pars**: list of arguments passed to `kdecopula::kdecop()`.
- **...**: optional arguments passed to `contour()` or `wireframe()`.

Details

For further details on estimation see `kdecopula::kdecop()`.

Author(s)

Thomas Nagler

Examples

```r
# simulate data from Joe copula
cop <- BiCop(3, tau = 0.3)
u <- BiCopSim(1000, cop)
contour(cop) # true contours

# kernel contours with standard normal margins
BiCopKDE(u[, 1], u[, 2])
BiCopKDE(u[, 1], u[, 2], kde.pars = list(mult = 0.5)) # undersmooth
BiCopKDE(u[, 1], u[, 2], kde.pars = list(mult = 2)) # oversmooth

# kernel density with uniform margins
BiCopKDE(u[, 1], u[, 2], type = "surface", zlim = c(0, 4))
plot(cop, zlim = c(0, 4)) # true density

# kernel contours are also used in pairs.copuladata
data(daxreturns)
data <- as.copuladata(daxreturns)
pairs(data[c(4, 5, 14, 15)])
```
Description

This function creates a Kendall’s plot (K-plot) of given bivariate copula data.

Usage

BiCopKPlot(u1, u2, PLOT = TRUE, ...)

Arguments

u1, u2  Data vectors of equal length with values in [0, 1].
PLOT  Logical; whether the results are plotted. If PLOT = FALSE, the values W.in and Hi.sort are returned (see below; default: PLOT = TRUE).
...  Additional plot arguments.

Details

For observations $u_{ij}$, $i = 1, ..., N$, $j = 1, 2$, the K-plot considers two quantities: First, the ordered values of the empirical bivariate distribution function $H_i := \hat{F}_{U_1,U_2}(u_{i,1}, u_{i,2})$ and, second, $W_{i:N}$, which are the expected values of the order statistics from a random sample of size $N$ of the random variable $W = C(U_1, U_2)$ under the null hypothesis of independence between $U_1$ and $U_2$. $W_{i:N}$ can be calculated as follows

$$W_{i:n} = N \binom{N-1}{i-1} \int_0^1 \omega k_0(\omega)(K_0(\omega))^{i-1}(1 - K_0(\omega))^{N-i} d\omega,$$

where

$$K_0(\omega) = \omega - \omega \log(\omega),$$

and $k_0(\cdot)$ is the corresponding density.

K-plots can be seen as the bivariate copula equivalent to QQ-plots. If the points of a K-plot lie approximately on the diagonal $y = x$, then $U_1$ and $U_2$ are approximately independent. Any deviation from the diagonal line points towards dependence. In case of positive dependence, the points of the K-plot should be located above the diagonal line, and vice versa for negative dependence. The larger the deviation from the diagonal, the stronger is the degree of dependency. There is a perfect positive dependence if points $(W_{i:N}, H_i)$ lie on the curve $K_0(\omega)$ located above the main diagonal. If points $(W_{i:N}, H_i)$ however lie on the x-axis, this indicates a perfect negative dependence between $U_1$ and $U_2$.

Value

W.in  W-statistics (x-axis).
Hi.sort  H-statistics (y-axis).
BiCopLambda

Author(s)
Natalia Belgorodski, Ulf Schepsmeier

References
Genest, C. and A. C. Favre (2007). Everything you always wanted to know about copula modeling but were afraid to ask. Journal of Hydrologic Engineering, 12 (4), 347-368.

See Also
BiCopMetaContour(), BiCopChiPlot(), BiCopLambda(), BiCopGofTest()

Examples

## Gaussian and Clayton copulas
n <- 500
tau <- 0.5

# simulate from Gaussian copula
fam <- 1
par <- BiCopTau2Par(fam, tau)
cop1 <- BiCop(fam, par)
set.seed(123)
dat1 <- BiCopSim(n, cop1)

# simulate from Clayton copula
fam <- 3
par <- BiCopTau2Par(fam, tau)
cop2 <- BiCop(fam, par)
set.seed(123)
dat2 <- BiCopSim(n, cop2)

# create K-plots
op <- par(mfrow = c(1, 2))
BiCopKPlot(dat1[,1], dat1[,2], main = "Gaussian copula")
BiCopKPlot(dat2[,1], dat2[,2], main = "Clayton copula")
par(op)

BiCopLambda

Lambda-Function (Plot) for Bivariate Copula Data

Description
This function plots/returns the lambda-function of given bivariate copula data.
BiCopLambda

Usage

BiCopLambda(
  u1 = NULL,
  u2 = NULL,
  family = "emp",
  par = 0,
  par2 = 0,
  PLOT = TRUE,
  obj = NULL,
  ...
)

Arguments

- **u1, u2**: Data vectors of equal length with values in \([0, 1]\) (default: \(u1\) and \(u2 = NULL\)).
- **family**: An integer defining the bivariate copula family or indicating the empirical lambda-function:
  - "emp" = empirical lambda-function (default)
  - 1 = Gaussian copula; the theoretical lambda-function is simulated (no closed formula available)
  - 2 = Student-t copula; the theoretical lambda-function is simulated (no closed formula available)
  - 3 = Clayton copula
  - 4 = Gumbel copula
  - 5 = Frank copula
  - 6 = Joe copula
  - 7 = BB1 copula
  - 8 = BB6 copula
  - 9 = BB7 copula
  - 10 = BB8 copula
- **par**: Copula parameter; if the empirical lambda-function is chosen, \(par = NULL\) or 0 (default).
- **par2**: Second copula parameter for t-, BB1, BB6, BB7 and BB8 copulas (default: \(par2 = 0\)).
- **PLOT**: Logical; whether the results are plotted. If \(PLOT = FALSE\), the values empLambda and/or theoLambda are returned (see below; default: \(PLOT = TRUE\)).
- **obj**: BiCop object containing the family and parameter specification.
- **...**: Additional plot arguments.

Details

If the family and parameter specification is stored in a BiCop() object obj, the alternative versions

BiCopLambda(obj, PLOT = TRUE, ...)

and
BiCopLambda((u1, u2, obj, PLOT = TRUE, ...)

can be used.

Value

empLambda If the empirical lambda-function is chosen and PLOT = FALSE, a vector of the empirical lambda's is returned.
theoLambda If the theoretical lambda-function is chosen and PLOT = FALSE, a vector of the theoretical lambda's is returned.

Note

The λ-function is characteristic for each bivariate copula family and defined by Kendall’s distribution function $K$:

$$
\lambda(v, \theta) := v - K(v, \theta)
$$

with

$$
K(v, \theta) := P(C_{\theta}(U_1, U_2) \leq v), \ v \in [0, 1].
$$

For Archimedean copulas one has the following closed form expression in terms of the generator function $\varphi$ of the copula $C_{\theta}$:

$$
\lambda(v, \theta) = \frac{\varphi(v)}{\varphi'(v)},
$$

where $\varphi'$ is the derivative of $\varphi$. For more details see Genest and Rivest (1993) or Schepsmeier (2010).

For the bivariate Gaussian and Student-t copula no closed form expression for the theoretical λ-function exists. Therefore it is simulated based on samples of size 1000. For all other implemented copula families there are closed form expressions available.

The plot of the theoretical λ-function also shows the limits of the λ-function corresponding to Kendall’s tau $= 0$ and Kendall’s tau $= 1$ ($\lambda = 0$).

For rotated bivariate copulas one has to transform the input arguments $u_1$ and/or $u_2$. In particular, for copulas rotated by 90 degrees $u_1$ has to be set to $1-u_1$, for 270 degrees $u_2$ to $1-u_2$ and for survival copulas $u_1$ and $u_2$ to $1-u_1$ and $1-u_2$, respectively. Then λ-functions for the corresponding non-rotated copula families can be considered.

Author(s)

Ulf Schepsmeier

References


BiCopMetaContour

See Also

BiCopMetaContour(), BiCopKPlot(), BiCopChiPlot(), BiCop()

Examples

# simulate from Clayton copula
cop <- BiCop(3, tau = 0.5)
dat <- BiCopSim(1000, cop)

# create lambda-function plots
op <- par(mfrow = c(1, 3))
BiCopLambda(dat[, 1], dat[, 2]) # empirical lambda-function
BiCopLambda(cop) # theoretical lambda-function
BiCopLambda(dat[, 1], dat[, 2], cop) # both
par(op)

BiCopMetaContour

Contour Plot of Bivariate Meta Distribution

Description

Note: This function is deprecated and only available for backwards compatibility. See contour.BiCop() for contour plots of parametric copulas, and BiCopKDE() for kernel estimates.

Usage

BiCopMetaContour(
  u1 = NULL,
  u2 = NULL,
  bw = 1,
  size = 100,
  levels = c(0.01, 0.05, 0.1, 0.15, 0.2),
  family = "emp",
  par = 0,
  par2 = 0,
  PLOT = TRUE,
  margins = "norm",
  margins.par = 0,
  xlim = NA,
  obj = NULL,
  ...
)
Arguments

- \texttt{u1, u2} \quad \text{Data vectors of equal length with values in } [0, 1] \text{ (default: } u1 \text{ and } u2 = \text{NULL}).
- \texttt{bw} \quad \text{Bandwidth (smoothing factor; default: } bw = 1).\text{)
- \texttt{size} \quad \text{Number of grid points; default: } size = 100.\text{)
- \texttt{levels} \quad \text{Vector of contour levels. For Gaussian, Student-t or exponential margins the default value (levels = c(0.01, 0.05, 0.1, 0.15, 0.2)) typically is a good choice. For uniform margins we recommend levels = c(0.1, 0.3, 0.5, 0.7, 0.9, 1.1, 1.3, 1.5) and for Gamma margins levels = c(0.005, 0.01, 0.03, 0.05, 0.07, 0.09).} \text{)
- \texttt{family} \quad \text{An integer defining the bivariate copula family or indicating an empirical contour plot:}
  \begin{itemize}
  \item "emp" = empirical contour plot (default; margins can be specified by \texttt{margins})
  \item 0 = independence copula
  \item 1 = Gaussian copula
  \item 2 = Student t copula (t-copula)
  \item 3 = Clayton copula
  \item 4 = Gumbel copula
  \item 5 = Frank copula
  \item 6 = Joe copula
  \item 7 = BB1 copula
  \item 8 = BB6 copula
  \item 9 = BB7 copula
  \item 10 = BB8 copula
  \item 13 = rotated Clayton copula (180 degrees; survival Clayton" \text{“)} \text{ cr } `14` = rotated Gumbel copula (180 degrees; survival Gumbel")
  \item 16 = rotated Joe copula (180 degrees; survival Joe" \text{“)} \text{ cr } `17` = rotated BB1 copula (180 degrees; survival BB1")
  \item 18 = rotated BB6 copula (180 degrees; survival BB6" \text{“)} \text{ cr } `19` = rotated BB7 copula (180 degrees; survival BB7")
  \item 20 = rotated BB8 copula (180 degrees; "survival BB8")
  \item 23 = rotated Clayton copula (90 degrees)
  \item ’24’ = rotated Gumbel copula (90 degrees)
  \item ’26’ = rotated Joe copula (90 degrees)
  \item ’27’ = rotated BB1 copula (90 degrees)
  \item ’28’ = rotated BB6 copula (90 degrees)
  \item ’29’ = rotated BB7 copula (90 degrees)
  \item ’30’ = rotated BB8 copula (90 degrees)
  \item ’33’ = rotated Clayton copula (270 degrees)
  \item ’34’ = rotated Gumbel copula (270 degrees)
  \item ’36’ = rotated Joe copula (270 degrees)
  \item ’37’ = rotated BB1 copula (270 degrees)
  \item ’38’ = rotated BB6 copula (270 degrees)
  \item ’39’ = rotated BB7 copula (270 degrees)
  \item ’40’ = rotated BB8 copula (270 degrees)
  \item ’104’ = Tawn type 1 copula
  \item ’114’ = rotated Tawn type 1 copula (180 degrees)
'124' = rotated Tawn type 1 copula (90 degrees)
'134' = rotated Tawn type 1 copula (270 degrees)
'204' = Tawn type 2 copula
'214' = rotated Tawn type 2 copula (180 degrees)
'224' = rotated Tawn type 2 copula (90 degrees)
'234' = rotated Tawn type 2 copula (270 degrees)

par  Copula parameter; if empirical contour plot, par = NULL or 0 (default).
par2 Second copula parameter for t-, BB1, BB6, BB7, BB8, Tawn type 1 and type 2
       copulas (default: par2 = 0).
PLOT Logical; whether the results are plotted. If PLOT = FALSE, the values x, y and z
       are returned (see below; default: PLOT = TRUE).
margins Character; margins for the bivariate copula contour plot. Possible margins are:
       "norm" = standard normal margins (default)
       "t" = Student t margins with degrees of freedom as specified by margins.par
       "gamma" = Gamma margins with shape and scale as specified by margins.par
       "exp" = Exponential margins with rate as specified by margins.par
       "unif" = uniform margins
margins.par Parameter(s) of the distribution of the margins if necessary (default: margins.par
       = 0), i.e.,
       • a positive real number for the degrees of freedom of Student t margins (see
dt()).
       • a 2-dimensional vector of positive real numbers for the shape and scale
       parameters of Gamma margins (see dgamma()).
       • a positive real number for the rate parameter of exponential margins (see
dexp()).
xylim A 2-dimensional vector of the x- and y-limits. By default (xylim = NA) standard
       limits for the selected margins are used.
obj  BiCop object containing the family and parameter specification.
... Additional plot arguments.

Value

x A vector of length size with the x-values of the kernel density estimator with
    Gaussian kernel if the empirical contour plot is chosen and a sequence of values
    in xlim if the theoretical contour plot is chosen.

y A vector of length size with the y-values of the kernel density estimator with
    Gaussian kernel if the empirical contour plot is chosen and a sequence of values
    in xlim if the theoretical contour plot is chosen.

z A matrix of dimension size with the values of the density of the meta distribu-
    tion with chosen margins (see margins and margins.par) evaluated at the grid
    points given by x and y.

Note

The combination family = 0 (independence copula) and margins = "unif" (uniform margins) is
not possible because all z-values are equal.
Author(s)

Ulf Schepsmeier, Alexander Bauer

See Also

`BiCopChiPlot()`, `BiCopKPlot()`, `BiCopLambda()`

Examples

```r
## meta Clayton distribution with Gaussian margins
cop <- BiCop(family = 1, tau = 0.5)
BiCopMetaContour(obj = cop, main = "Clayton - normal margins")
# better:
contour(cop, main = "Clayton - normal margins")

## empirical contour plot with standard normal margins
dat <- BiCopSim(1000, cop)
BiCopMetaContour(dat[, 1], dat[, 2], bw = 2, family = "emp",
                main = "empirical - normal margins")
# better:
BiCopKDE(dat[, 1], dat[, 2],
          main = "empirical - normal margins")

## empirical contour plot with exponential margins
BiCopMetaContour(dat[, 1], dat[, 2], bw = 2,
                 main = "empirical - exponential margins",
                 margins = "exp", margins.par = 1)
# better:
BiCopKDE(dat[, 1], dat[, 2],
          main = "empirical - exponential margins",
          margins = "exp")
```

---

**BiCopName**

*Bivariate Copula Family Names*

Description

This function transforms the bivariate copula family number into its character expression and vice versa.

Usage

```r
BiCopName(family, short = TRUE)
```

Arguments

- `family` - Bivariate copula family, either its number or its character expression (see table below).
<table>
<thead>
<tr>
<th>No.</th>
<th>Short name</th>
<th>Long name</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>&quot;I&quot;</td>
<td>&quot;Independence&quot;</td>
</tr>
<tr>
<td>1</td>
<td>&quot;N&quot;</td>
<td>&quot;Gaussian&quot;</td>
</tr>
<tr>
<td>2</td>
<td>&quot;t&quot;</td>
<td>&quot;t&quot;</td>
</tr>
<tr>
<td>3</td>
<td>&quot;C&quot;</td>
<td>&quot;Clayton&quot;</td>
</tr>
<tr>
<td>4</td>
<td>&quot;G&quot;</td>
<td>&quot;Gumbel&quot;</td>
</tr>
<tr>
<td>5</td>
<td>&quot;F&quot;</td>
<td>&quot;Frank&quot;</td>
</tr>
<tr>
<td>6</td>
<td>&quot;J&quot;</td>
<td>&quot;Joe&quot;</td>
</tr>
<tr>
<td>7</td>
<td>&quot;BB1&quot;</td>
<td>&quot;BB1&quot;</td>
</tr>
<tr>
<td>8</td>
<td>&quot;BB6&quot;</td>
<td>&quot;BB6&quot;</td>
</tr>
<tr>
<td>9</td>
<td>&quot;BB7&quot;</td>
<td>&quot;BB7&quot;</td>
</tr>
<tr>
<td>10</td>
<td>&quot;BB8&quot;</td>
<td>&quot;Frank-Joe&quot;</td>
</tr>
<tr>
<td>13</td>
<td>&quot;SC&quot;</td>
<td>&quot;Survival Clayton&quot;</td>
</tr>
<tr>
<td>14</td>
<td>&quot;SG&quot;</td>
<td>&quot;Survival Gumbel&quot;</td>
</tr>
<tr>
<td>16</td>
<td>&quot;SJ&quot;</td>
<td>&quot;Survival Joe&quot;</td>
</tr>
<tr>
<td>17</td>
<td>&quot;SBB1&quot;</td>
<td>&quot;Survival BB1&quot;</td>
</tr>
<tr>
<td>18</td>
<td>&quot;SBB6&quot;</td>
<td>&quot;Survival BB6&quot;</td>
</tr>
<tr>
<td>19</td>
<td>&quot;SBB7&quot;</td>
<td>&quot;Survival BB7&quot;</td>
</tr>
<tr>
<td>20</td>
<td>&quot;SBB8&quot;</td>
<td>&quot;Survival BB8&quot;</td>
</tr>
<tr>
<td>23</td>
<td>&quot;C90&quot;</td>
<td>&quot;Rotated Clayton 90 degrees&quot;</td>
</tr>
<tr>
<td>24</td>
<td>&quot;G90&quot;</td>
<td>&quot;Rotated Gumbel 90 degrees&quot;</td>
</tr>
<tr>
<td>26</td>
<td>&quot;J90&quot;</td>
<td>&quot;Rotated Joe 90 degrees&quot;</td>
</tr>
<tr>
<td>27</td>
<td>&quot;BB1_90&quot;</td>
<td>&quot;Rotated BB1 90 degrees&quot;</td>
</tr>
<tr>
<td>28</td>
<td>&quot;BB6_90&quot;</td>
<td>&quot;Rotated BB6 90 degrees&quot;</td>
</tr>
<tr>
<td>29</td>
<td>&quot;BB7_90&quot;</td>
<td>&quot;Rotated BB7 90 degrees&quot;</td>
</tr>
<tr>
<td>30</td>
<td>&quot;BB8_90&quot;</td>
<td>&quot;Rotated Frank-Joe 90 degrees&quot;</td>
</tr>
<tr>
<td>33</td>
<td>&quot;C270&quot;</td>
<td>&quot;Rotated Clayton 270 degrees&quot;</td>
</tr>
<tr>
<td>34</td>
<td>&quot;G270&quot;</td>
<td>&quot;Rotated Gumbel 270 degrees&quot;</td>
</tr>
<tr>
<td>36</td>
<td>&quot;J270&quot;</td>
<td>&quot;Rotated Joe 270 degrees&quot;</td>
</tr>
<tr>
<td>37</td>
<td>&quot;BB1_270&quot;</td>
<td>&quot;Rotated BB1 270 degrees&quot;</td>
</tr>
<tr>
<td>38</td>
<td>&quot;BB6_270&quot;</td>
<td>&quot;Rotated BB6 270 degrees&quot;</td>
</tr>
<tr>
<td>39</td>
<td>&quot;BB7_270&quot;</td>
<td>&quot;Rotated BB7 270 degrees&quot;</td>
</tr>
<tr>
<td>40</td>
<td>&quot;BB8_270&quot;</td>
<td>&quot;Rotated Frank-Joe 270 degrees&quot;</td>
</tr>
<tr>
<td>104</td>
<td>&quot;Tawn&quot;</td>
<td>&quot;Tawn type 1&quot;</td>
</tr>
<tr>
<td>114</td>
<td>&quot;Tawn180&quot;</td>
<td>&quot;Rotated Tawn type 1 180 degrees&quot;</td>
</tr>
<tr>
<td>124</td>
<td>&quot;Tawn90&quot;</td>
<td>&quot;Rotated Tawn type 1 90 degrees&quot;</td>
</tr>
<tr>
<td>134</td>
<td>&quot;Tawn270&quot;</td>
<td>&quot;Rotated Tawn type 1 270 degrees&quot;</td>
</tr>
<tr>
<td>204</td>
<td>&quot;Tawn2&quot;</td>
<td>&quot;Tawn type 2&quot;</td>
</tr>
<tr>
<td>214</td>
<td>&quot;Tawn2_180&quot;</td>
<td>&quot;Rotated Tawn type 2 180 degrees&quot;</td>
</tr>
<tr>
<td>224</td>
<td>&quot;Tawn2_90&quot;</td>
<td>&quot;Rotated Tawn type 2 90 degrees&quot;</td>
</tr>
<tr>
<td>234</td>
<td>&quot;Tawn2_270&quot;</td>
<td>&quot;Rotated Tawn type 2 270 degrees&quot;</td>
</tr>
</tbody>
</table>

**short** Logical; if the number of a bivariate copula family is used and short = TRUE (default), a short version of the corresponding character expression is returned, otherwise the long version.
BiCopPar2Beta

Blomqvist's Beta Value of a Bivariate Copula

Description

This function computes the theoretical Blomqvist's beta value of a bivariate copula for given parameter values.

Usage

BiCopPar2Beta(family, par, par2 = 0, obj = NULL, check.pars = TRUE)
Arguments

family           integer; single number or vector of size n; defines the bivariate copula family:
0 = independence copula
2 = Student t copula (t-copula)
1 = Gaussian copula
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton'
14 = rotated Gumbel copula (180 degrees; survival Gumbel'')
16 = rotated Joe copula (180 degrees; survival Joe'')
17 = rotated BB1 copula (180 degrees; survival BB1'')
18 = rotated BB6 copula (180 degrees; survival BB6'')
19 = rotated BB7 copula (180 degrees; survival BB7'')
20 = rotated BB8 copula (180 degrees; “survival BB8'’)
23 = rotated Clayton copula (90 degrees)
‘24’ = rotated Gumbel copula (90 degrees)
‘26’ = rotated Joe copula (90 degrees)
‘27’ = rotated BB1 copula (90 degrees)
‘28’ = rotated BB6 copula (90 degrees)
‘29’ = rotated BB7 copula (90 degrees)
‘30’ = rotated BB8 copula (90 degrees)
‘33’ = rotated Clayton copula (270 degrees)
‘34’ = rotated Gumbel copula (270 degrees)
‘36’ = rotated Joe copula (270 degrees)
‘37’ = rotated BB1 copula (270 degrees)
‘38’ = rotated BB6 copula (270 degrees)
‘39’ = rotated BB7 copula (270 degrees)
‘40’ = rotated BB8 copula (270 degrees)
‘104’ = Tawn type 1 copula
‘114’ = rotated Tawn type 1 copula (180 degrees)
‘124’ = rotated Tawn type 1 copula (90 degrees)
‘134’ = rotated Tawn type 1 copula (270 degrees)
‘204’ = Tawn type 2 copula
‘214’ = rotated Tawn type 2 copula (180 degrees)
‘224’ = rotated Tawn type 2 copula (90 degrees)
‘234’ = rotated Tawn type 2 copula (270 degrees)

Note that the Student’s t-copula is not allowed since the CDF of the t-copula is not implemented (see BiCopCDF()).

par           numeric; single number or vector of size n; copula parameter.
par2          numeric; single number or vector of size n; second parameter for the two parameter BB1, BB6, BB7, BB8, Tawn type 1 and type 2 copulas (default: par2 =
BiCopPar2Beta

obj BiCop object containing the family and parameter specification.
check.pars logical; default is TRUE; if FALSE, checks for family/parameter-consistency are omitted (should only be used with care).

Details

If the family and parameter specification is stored in a BiCop() object obj, the alternative version

BiCopPar2Beta(obj)

can be used.

Value

Theoretical value of Blomqvist’s beta corresponding to the bivariate copula family and parameter(s) par, par2.

Note

The number n can be chosen arbitrarily, but must agree across arguments.

Author(s)

Ulf Schepsmeier

References


Examples

## Example 1: Gaussian copula
BiCopPar2Beta(family = 1, par = 0.7)
BiCop(1, 0.7)$beta  # alternative

## Example 2: Clayton copula
BiCopPar2Beta(family = 3, par = 2)

## Example 3: different copula families
BiCopPar2Beta(family = c(3,4,6), par = 2:4)
BiCopPar2TailDep

Tail Dependence Coefficients of a Bivariate Copula

Description

This function computes the theoretical tail dependence coefficients of a bivariate copula for given parameter values.

Usage

BiCopPar2TailDep(family, par, par2 = 0, obj = NULL, check.pars = TRUE)

Arguments

family integer; single number or vector of size n; defines the bivariate copula family:
0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton”)
14 = rotated Gumbel copula (180 degrees; survival Gumbel”)
16 = rotated Joe copula (180 degrees; survival Joe”)
17 = rotated BB1 copula (180 degrees; survival BB1”)
18 = rotated BB6 copula (180 degrees; survival BB6”)
19 = rotated BB7 copula (180 degrees; survival BB7”)
20 = rotated BB8 copula (180 degrees; “survival BB8”)
23 = rotated Clayton copula (90 degrees)
24 = rotated Gumbel copula (90 degrees)
26 = rotated Joe copula (90 degrees)
27 = rotated BB1 copula (90 degrees)
28 = rotated BB6 copula (90 degrees)
29 = rotated BB7 copula (90 degrees)
30 = rotated BB8 copula (90 degrees)
33 = rotated Clayton copula (270 degrees)
34 = rotated Gumbel copula (270 degrees)
36 = rotated Joe copula (270 degrees)
37 = rotated BB1 copula (270 degrees)
38 = rotated BB6 copula (270 degrees)
39 = rotated BB7 copula (270 degrees)
40 = rotated BB8 copula (270 degrees)
'104' = Tawn type 1 copula
'114' = rotated Tawn type 1 copula (180 degrees)
'124' = rotated Tawn type 1 copula (90 degrees)
'134' = rotated Tawn type 1 copula (270 degrees)
'204' = Tawn type 2 copula
'214' = rotated Tawn type 2 copula (180 degrees)
'224' = rotated Tawn type 2 copula (90 degrees)
'234' = rotated Tawn type 2 copula (270 degrees)

par numeric; single number or vector of size \( n \); copula parameter.

par2 numeric; single number or vector of size \( n \); second parameter for bivariate copulas with two parameters (t, BB1, BB6, BB7, BB8, Tawn type 1 and type 2; default: \( \text{par2} = 0 \)). \( \text{par2} \) should be a positive integer for the Students’s t copula family = 2.

obj BiCop object containing the family and parameter specification.

check.pars logical; default is TRUE; if FALSE, checks for family/parameter-consistency are omitted (should only be used with care).

Details

If the family and parameter specification is stored in a BiCop object \( \text{obj} \), the alternative version

\[
\text{BiCopPar2TailDep(} \text{obj} \text{)}
\]

can be used.

Value

\( \lambda_L \) Lower tail dependence coefficient for the given bivariate copula family and parameter(s) \( \text{par}, \text{par2} \):

\[
\lambda_L = \lim_{u \to 0} \frac{C(u, u)}{u}
\]

\( \lambda_U \) Upper tail dependence coefficient for the given bivariate copula family and parameter(s) \( \text{par}, \text{par2} \):

\[
\lambda_U = \lim_{u \to 1} \frac{1 - 2u + C(u, u)}{1 - u}
\]

Lower and upper tail dependence coefficients for bivariate copula families and parameters (\( \theta \) for one parameter families and the first parameter of the t-copula with \( \nu \) degrees of freedom, \( \theta \) and \( \delta \) for the two parameter BB1, BB6, BB7 and BB8 copulas) are given in the following table.

<table>
<thead>
<tr>
<th>No.</th>
<th>Lower tail dependence</th>
<th>Upper tail dependence</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>2</td>
<td>( 2t_{\nu + 1} \left( -\sqrt{\nu + 1} \sqrt{\frac{1-\theta}{1+\theta}} \right) )</td>
<td>( 2t_{\nu + 1} \left( -\sqrt{\nu + 1} \sqrt{\frac{1-\theta}{1+\theta}} \right) )</td>
</tr>
<tr>
<td>3</td>
<td>( 2^{-1/\theta} )</td>
<td>-</td>
</tr>
</tbody>
</table>


\[
\begin{align*}
4 & \quad - & 2 - 2^{1/\theta} \\
5 & \quad - & - \\
6 & \quad - & 2 - 2^{1/\theta} \\
7 & \quad 2^{-1/(\theta \delta)} & 2 - 2^{1/\delta} \\
8 & \quad - & 2 - 2^{1/\theta} \\
9 & \quad 2^{-1/\delta} & 2 - 2^{1/\theta} \\
10 & \quad - & 2 - 2^{1/\theta} \text{ if } \delta = 1 \text{ otherwise } 0 \\
13 & \quad - & 2^{-1/\theta} \\
14 & \quad 2 - 2^{1/\theta} & - \\
16 & \quad 2 - 2^{1/\theta} & - \\
17 & \quad 2 - 2^{1/\delta} & 2^{-1/(\theta \delta)} \\
18 & \quad 2 - 2^{1/(\theta \delta)} & - \\
19 & \quad 2 - 2^{1/\theta} & 2^{-1/\delta} \\
20 & \quad 2 - 2^{1/\theta} \text{ if } \delta = 1 \text{ otherwise } 0 & - \\
23, 33 & \quad - & - \\
24, 34 & \quad - & - \\
26, 36 & \quad - & - \\
27, 37 & \quad - & - \\
28, 38 & \quad - & - \\
29, 39 & \quad - & - \\
30, 40 & \quad - & - \\
104, 204 & \quad - & \delta + 1 - (\delta^\theta + 1)^{1/\theta} \\
114, 214 & \quad 1 + \delta - (\delta^\theta + 1)^{1/\theta} & - \\
124, 224 & \quad - & - \\
134, 234 & \quad - & - 
\end{align*}
\]

**Note**

The number \( n \) can be chosen arbitrarily, but must agree across arguments.

**Author(s)**

Eike Brechmann

**References**


**See Also**

`BiCopPar2TailDep()`

**Examples**

```r
## Example 1: Gaussian copula
BiCopPar2TailDep(1, 0.7)
BiCop(1, 0.7)$taildep
# alternative
```
## Example 2: Student-t copula
BiCopPar2TailDep(2, c(0.6, 0.7, 0.8), 4)

## Example 3: different copula families
BiCopPar2TailDep(c(3, 4, 6), 2)

---

### BiCopPar2Tau

*Kendall’s Tau Value of a Bivariate Copula*

#### Description
This function computes the theoretical Kendall’s tau value of a bivariate copula for given parameter values.

#### Usage
BiCopPar2Tau(family, par, par2 = 0, obj = NULL, check.pars = TRUE)

#### Arguments
- **family**: integer; single number or vector of size m; defines the bivariate copula family:
  - 0 = independence copula
  - 1 = Gaussian copula
  - 2 = Student t copula (t-copula)
  - 3 = Clayton copula
  - 4 = Gumbel copula
  - 5 = Frank copula
  - 6 = Joe copula
  - 7 = BB1 copula
  - 8 = BB6 copula
  - 9 = BB7 copula
  - 10 = BB8 copula
  - 13 = rotated Clayton copula (180 degrees; survival Clayton"
  - 14 = rotated Gumbel copula (180 degrees; survival Gumbel"
  - 16 = rotated Joe copula (180 degrees; survival Joe"
  - 17 = rotated BB1 copula (180 degrees; survival BB1"
  - 18 = rotated BB6 copula (180 degrees; survival BB6"
  - 19 = rotated BB7 copula (180 degrees; survival BB7"
  - 20 = rotated BB8 copula (180 degrees; “survival BB8"
  - 23 = rotated Clayton copula (90 degrees)
  - 24 = rotated Gumbel copula (90 degrees)
  - 26 = rotated Joe copula (90 degrees)
  - 27 = rotated BB1 copula (90 degrees)
  - 28 = rotated BB6 copula (90 degrees)
  - 29 = rotated BB7 copula (90 degrees)
  - 30 = rotated BB8 copula (90 degrees)
  - 33 = rotated Clayton copula (270 degrees)
'34' = rotated Gumbel copula (270 degrees)
'36' = rotated Joe copula (270 degrees)
'37' = rotated BB1 copula (270 degrees)
'38' = rotated BB6 copula (270 degrees)
'39' = rotated BB7 copula (270 degrees)
'40' = rotated BB8 copula (270 degrees)
'104' = Tawn type 1 copula
'114' = rotated Tawn type 1 copula (180 degrees)
'124' = rotated Tawn type 1 copula (90 degrees)
'134' = rotated Tawn type 1 copula (270 degrees)
'204' = Tawn type 2 copula
'214' = rotated Tawn type 2 copula (180 degrees)
'224' = rotated Tawn type 2 copula (90 degrees)
'234' = rotated Tawn type 2 copula (270 degrees)

par numeric; single number or vector of size n; copula parameter.
par2 numeric; single number or vector of size n; second parameter for bivariate copulas with two parameters (t, BB1, BB6, BB7, BB8, Tawn type 1 and type 2; default: par2 = 0). Note that the degrees of freedom parameter of the t-copula does not need to be set, because the theoretical Kendall’s tau value of the t-copula is independent of this choice.
obj BiCop object containing the family and parameter specification.
check.pars logical; default is TRUE; if FALSE, checks for family/parameter-consistency are omitted (should only be used with care).

Details
If the family and parameter specification is stored in a BiCop() object obj, the alternative version

BiCopPar2Tau(obj)

can be used.

Value
Theoretical value of Kendall’s tau (vector) corresponding to the bivariate copula family and parameter vector $(\theta, \delta) = (\text{par}, \text{par2})$.

<table>
<thead>
<tr>
<th>No. (family)</th>
<th>Kendall’s tau (tau)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1, 2</td>
<td>$\frac{4}{3} \arcsin(\theta)$</td>
</tr>
<tr>
<td>3, 13</td>
<td>$\frac{\theta}{\theta+2}$</td>
</tr>
<tr>
<td>4, 14</td>
<td>$1 - \frac{\theta}{\theta}$</td>
</tr>
<tr>
<td>5</td>
<td>$1 - \frac{4}{3} \theta + 4 \frac{D_1(\theta)}{\theta}$</td>
</tr>
<tr>
<td></td>
<td>with $D_1(\theta) = \int_0^\theta \frac{x^{-\theta}}{\exp(x)-1} dx$ (Debye function)</td>
</tr>
<tr>
<td>6, 16</td>
<td>$1 + \frac{4}{\theta^2} \int_0^1 x \log(x)(1-x)^{2(1-\theta)/\theta} dx$</td>
</tr>
<tr>
<td>7, 17</td>
<td>$1 - \frac{1}{\theta(\theta+2)}$</td>
</tr>
</tbody>
</table>
8, 18 \[ 1 + 4 \int_0^1 \log(-(1-t)^\theta + 1) \int (1 - t - (1-t)^{-\theta} + (1-t)^{-\theta} t)/(\delta \theta) dt \]
9, 19 \[ 1 + 4 \int_0^1 ((1 - (1-t)^\theta - \delta - 1)/(\theta \delta (1-t)^{\theta-1} (1-t)^{\delta-1}) \]
10, 20 \[ 1 + 4 \int_0^1 (1 - t \delta)^{\theta - 1} ((1 - \delta)^{\theta} - 1)) \]
23, 33 \[ \int_0^1 x \log(x) (1-x)^{-2(1+\theta)/\theta} dx \]
24, 34 \[ -1 - \frac{1}{\theta} \]
26, 36 \[ -1 - \frac{3}{2} \int_0^1 x \log(x) (1-x)^{-2(1+\theta)/\theta} dx \]
27, 37 \[ -1 - \frac{1}{\theta(2-\theta)} \]
28, 38 \[ -1 - 4 \int_0^1 \log(-(1-t)^\theta + 1) \int (1 - t - (1-t)^\theta + (1-t)^\theta t)/(\delta \theta) dt \]
29, 39 \[ -1 - 4 \int_0^1 (1 - (1-t)^\theta - \theta - 1)/(\theta \delta (1-t)^{\theta-1} (1-t)^{\delta-1}) \]
30, 40 \[ -1 - 4 \int_0^1 \log (((1 + t \delta)^{\theta} - 1)/((1 + \delta)^{\theta} - 1)) \]
104, 114 \[ \int_0^1 t(1-t) A'(t)/A(t) dt \]
204, 214 \[ \int_0^1 t(1-t) A''(t)/A(t) dt \]
124, 134 \[ - \int_0^1 t(1-t) A''(t)/A(t) dt \]
224, 234 \[ - \int_0^1 t(1-t) A''(t)/A(t) dt \]

**Note**

The number n can be chosen arbitrarily, but must agree across arguments.

**Author(s)**

Ulf Schepsmeier, Tobias Erhardt

**References**


**See Also**

BiCopTau2Par(), BiCop()

**Examples**

```r
# Example 1: Gaussian copula
tau0 <- 0.5
rho <- BiCopTau2Par(family = 1, tau = tau0)
# transform back
tau <- BiCopPar2Tau(family = 1, par = rho)
```
BiCopPDF

Density of a Bivariate Copula

Description

This function evaluates the probability density function (PDF) of a given parametric bivariate copula.

Usage

BiCopPDF(u1, u2, family, par, par2 = 0, obj = NULL, check.pars = TRUE)

Arguments

u1, u2 numeric vectors of equal length with values in [0, 1].
family integer; single number or vector of size length(u1); defines the bivariate copula family:
0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula

## Example 2:
vpar <- seq(from = 1.1, to = 10, length.out = 100)
tauC <- BiCopPar2Tau(family = 3, par = vpar)
tauG <- BiCopPar2Tau(family = 4, par = vpar)
tauF <- BiCopPar2Tau(family = 5, par = vpar)
tauJ <- BiCopPar2Tau(family = 6, par = vpar)
plot(tauC ~ vpar, type = "l", ylim = c(0,1))
lines(tauG ~ vpar, col = 2)
lines(tauF ~ vpar, col = 3)
lines(tauJ ~ vpar, col = 4)

## Example 3: different copula families
theta <- BiCopTau2Par(family = c(3,4,6), tau = c(0.4, 0.5, 0.6))
BiCopPar2Tau(family = c(3,4,6), par = theta)
13 = rotated Clayton copula (180 degrees; survival Clayton"

14 = rotated Gumbel copula (180 degrees; survival Gumbel"

16 = rotated Joe copula (180 degrees; survival Joe"

17 = rotated BB1 copula (180 degrees; survival BB1"

18 = rotated BB6 copula (180 degrees; survival BB6"

19 = rotated BB7 copula (180 degrees; survival BB7"

20 = rotated BB8 copula (180 degrees; survival BB8"

23 = rotated Clayton copula (90 degrees)

24 = rotated Gumbel copula (90 degrees)

26 = rotated Joe copula (90 degrees)

27 = rotated BB1 copula (90 degrees)

28 = rotated BB6 copula (90 degrees)

29 = rotated BB7 copula (90 degrees)

30 = rotated BB8 copula (90 degrees)

33 = rotated Clayton copula (270 degrees)

34 = rotated Gumbel copula (270 degrees)

36 = rotated Joe copula (270 degrees)

37 = rotated BB1 copula (270 degrees)

38 = rotated BB6 copula (270 degrees)

39 = rotated BB7 copula (270 degrees)

40 = rotated BB8 copula (270 degrees)

104 = Tawn type 1 copula

114 = rotated Tawn type 1 copula (180 degrees)

124 = rotated Tawn type 1 copula (90 degrees)

134 = rotated Tawn type 1 copula (270 degrees)

204 = Tawn type 2 copula

214 = rotated Tawn type 2 copula (180 degrees)

224 = rotated Tawn type 2 copula (90 degrees)

234 = rotated Tawn type 2 copula (270 degrees)

par numeric; single number or vector of size length(u1); copula parameter.

par2 numeric; single number or vector of size length(u1); second parameter for

bivariate copulas with two parameters (t, BB1, BB6, BB7, BB8, Tawn type

1 and type 2; default: par2 = 0). par2 should be an positive integer for the

Students’s t copula family = 2.

obj BiCop object containing the family and parameter specification.

check.pars logical; default is TRUE; if FALSE, checks for family/parameter-consistency are

omitted (should only be used with care).

Details

If the family and parameter specification is stored in a BiCop() object obj, the alternative version

BiCopPDF(u1, u2, obj)

can be used.
BiCopSelect

Value

A numeric vector of the bivariate copula density

- of the copula family
- with parameter(s) par, par2
- evaluated at u1 and u2.

Author(s)

Eike Brechmann

See Also

BiCopCDF(), BiCopHfunc(), BiCopSim(), BiCop()

Examples

```r
## simulate from a bivariate Student-t copula
cop <- BiCop(family = 2, par = -0.7, par2 = 4)
simdata <- BiCopSim(100, cop)

## evaluate the density of the bivariate t-copula
u1 <- simdata[,1]
u2 <- simdata[,2]
BiCopPDF(u1, u2, cop)

## select a bivariate copula for the simulated data
fit <- BiCopSelect(u1, u2)
summary(fit)
## and evaluate its PDF
round(BiCopPDF(u1, u2, fit), 3)
```

Description

This function selects an appropriate bivariate copula family for given bivariate copula data using one of a range of methods. The corresponding parameter estimates are obtained by maximum likelihood estimation.
Usage

BiCopSelect(
  u1,
  u2,
  familyset = NA,
  selectioncrit = "AIC",
  indeptest = FALSE,
  level = 0.05,
  weights = NA,
  rotations = TRUE,
  se = FALSE,
  presel = TRUE,
  method = "mle"
)

Arguments

u1, u2 Data vectors of equal length with values in [0, 1].

familyset Vector of bivariate copula families to select from. The vector has to include at least one bivariate copula family that allows for positive and one that allows for negative dependence. If familyset = NA (default), selection among all possible families is performed. If a vector of negative numbers is provided, selection among all but abs(familyset) families is performed. Coding of bivariate copula families:

0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton”)
14 = rotated Gumbel copula (180 degrees; survival Gumbel”)
16 = rotated Joe copula (180 degrees; survival Joe”)
17 = rotated BB1 copula (180 degrees; survival BB1”)
18 = rotated BB6 copula (180 degrees; survival BB6”)
19 = rotated BB7 copula (180 degrees; survival BB7”)
20 = rotated BB8 copula (180 degrees; ”survival BB8”)
23 = rotated Clayton copula (90 degrees)
‘24’ = rotated Gumbel copula (90 degrees)
‘26’ = rotated Joe copula (90 degrees)
‘27’ = rotated BB1 copula (90 degrees)
‘28’ = rotated BB6 copula (90 degrees)
‘29’ = rotated BB7 copula (90 degrees)
'30' = rotated BB8 copula (90 degrees)
'33' = rotated Clayton copula (270 degrees)
'34' = rotated Gumbel copula (270 degrees)
'36' = rotated Joe copula (270 degrees)
'37' = rotated BB1 copula (270 degrees)
'38' = rotated BB6 copula (270 degrees)
'39' = rotated BB7 copula (270 degrees)
'40' = rotated BB8 copula (270 degrees)
'104' = Tawn type 1 copula
'114' = rotated Tawn type 1 copula (180 degrees)
'124' = rotated Tawn type 1 copula (90 degrees)
'134' = rotated Tawn type 1 copula (270 degrees)
'204' = Tawn type 2 copula
'214' = rotated Tawn type 2 copula (180 degrees)
'224' = rotated Tawn type 2 copula (90 degrees)
'234' = rotated Tawn type 2 copula (270 degrees)

`selectioncrit` Character indicating the criterion for bivariate copula selection. Possible choices: `selectioncrit = "AIC"` (default), "BIC", or "logLik".

`indeptest` Logical; whether a hypothesis test for the independence of \( u_1 \) and \( u_2 \) is performed before bivariate copula selection (default: `indeptest = FALSE`; see `BiCopIndTest()`). The independence copula is chosen if the null hypothesis of independence cannot be rejected.

`level` Numeric; significance level of the independence test (default: `level = 0.05`).

`weights` Numerical; weights for each observation (optional).

`rotations` If `TRUE`, all rotations of the families in `familyset` are included (or subtracted).

`se` Logical; whether standard error(s) of parameter estimates is/are estimated (default: `se = FALSE`).

`presel` Logical; whether to exclude families before fitting based on symmetry properties of the data. Makes the selection about 30% faster (on average), but may yield slightly worse results in few special cases.

`method` indicates the estimation method: either maximum likelihood estimation (`method = "mle"`; default) or inversion of Kendall's tau (`method = "itau"`). For `method = "itau"` only one parameter families and the Student t copula can be used (family = 1, 2, 3, 4, 5, 6, 13, 14, 16, 23, 24, 26, 33, 34 or 36). For the t-copula, \( \text{par2} \) is found by a crude profile likelihood optimization over the interval (2, 10).

**Details**

Copulas can be selected according to the Akaike and Bayesian Information Criteria (AIC and BIC, respectively). First all available copulas are fitted using maximum likelihood estimation. Then the criteria are computed for all available copula families (e.g., if \( u_1 \) and \( u_2 \) are negatively dependent, Clayton, Gumbel, Joe, BB1, BB6, BB7 and BB8 and their survival copulas are not considered) and the family with the minimum value is chosen. For observations \( u_{i,j}, \ i = 1, \ldots, N, \ j = 1, 2, \) the
AIC of a bivariate copula family \( c \) with parameter(s) \( \theta \) is defined as

\[
AIC := -2 \sum_{i=1}^{N} \ln[c(u_{i,1}, u_{i,2}|\theta)] + 2k,
\]

where \( k = 1 \) for one parameter copulas and \( k = 2 \) for the two parameter t-, BB1, BB6, BB7 and BB8 copulas. Similarly, the BIC is given by

\[
BIC := -2 \sum_{i=1}^{N} \ln[c(u_{i,1}, u_{i,2}|\theta)] + \ln(N)k.
\]

Evidently, if the BIC is chosen, the penalty for two parameter families is stronger than when using the AIC.

Additionally a test for independence can be performed beforehand.

**Value**

An object of class `BiCop()`, augmented with the following entries:

- `se`, `se2` standard errors for the parameter estimates (if `se = TRUE`,
- `nobs` number of observations,
- `logLik` log likelihood
- `AIC` Aikake's Informaton Criterion,
- `BIC` Bayesian's Informaton Criterion,
- `emptau` empirical value of Kendall’s tau,
- `p.value.indeptest` p-value of the independence test.

**Note**

For a comprehensive summary of the fitted model, use `summary(object)`; to see all its contents, use `str(object)`.

The parameters of the Student t and BB copulas are restricted (see defaults in `BiCopEst()` to avoid being close to their limiting cases.

**Author(s)**

Eike Brechmann, Jeffrey Dissmann, Thomas Nagler

**References**


See Also

BiCop(), BiCopEst(), RVineStructureSelect(), RVineCopSelect(), BiCopIndTest().

Examples

```r
## Example 1: Gaussian copula with large dependence parameter
par <- 0.7
fam <- 1
dat1 <- BiCopSim(500, fam, par)
# select the bivariate copula family and estimate the parameter(s)
cop1 <- BiCopSelect(dat1[, 1], dat1[, 2], familyset = 1:10,
                     indeptest = FALSE, level = 0.05)
cop1 # short overview
summary(cop1) # comprehensive overview
str(cop1) # see all contents of the object

## Example 2: Gaussian copula with small dependence parameter
par <- 0.01
fam <- 1
dat2 <- BiCopSim(500, fam, par)
# select the bivariate copula family and estimate the parameter(s)
cop2 <- BiCopSelect(dat2[, 1], dat2[, 2], familyset = 0:10,
                     indeptest = TRUE, level = 0.05)
summary(cop2)

## Example 3: empirical data
data(daxreturns)
cop3 <- BiCopSelect(daxreturns[, 1], daxreturns[, 4], familyset = 0:10)
summary(cop3)
```

BiCopSim

Simulation from a Bivariate Copula

Description

This function simulates from a given parametric bivariate copula.

Usage

BiCopSim(N, family, par, par2 = 0, obj = NULL, check.pars = TRUE)
Arguments

N
Number of bivariate observations simulated.

family
integer; single number or vector of size N; defines the bivariate copula family:
0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton
14 = rotated Gumbel copula (180 degrees; survival Gumbel)
16 = rotated Joe copula (180 degrees; survival Joe)
17 = rotated BB1 copula (180 degrees; survival BB1)
18 = rotated BB6 copula (180 degrees; survival BB6)
20 = rotated BB8 copula (180 degrees; survival BB8)
23 = rotated Clayton copula (90 degrees)
24 = rotated Gumbel copula (90 degrees)
26 = rotated Joe copula (90 degrees)
27 = rotated BB1 copula (90 degrees)
28 = rotated BB6 copula (90 degrees)
29 = rotated BB7 copula (90 degrees)
30 = rotated BB8 copula (90 degrees)
33 = rotated Clayton copula (270 degrees)
34 = rotated Gumbel copula (270 degrees)
36 = rotated Joe copula (270 degrees)
37 = rotated BB1 copula (270 degrees)
38 = rotated BB6 copula (270 degrees)
39 = rotated BB7 copula (270 degrees)
40 = rotated BB8 copula (270 degrees)
104 = Tawn type 1 copula
114 = rotated Tawn type 1 copula (180 degrees)
124 = rotated Tawn type 1 copula (90 degrees)
134 = rotated Tawn type 1 copula (270 degrees)
204 = Tawn type 2 copula
214 = rotated Tawn type 2 copula (180 degrees)
224 = rotated Tawn type 2 copula (90 degrees)
234 = rotated Tawn type 2 copula (270 degrees)

par
numeric; single number or vector of size N; copula parameter.

par2
numeric; single number or vector of size N; second parameter for bivariate copulas with two parameters (t, BB1, BB6, BB7, BB8, Tawn type 1 and type 2;
**BiCopTau2Par**

Parameter of a Bivariate Copula for a given Kendall’s Tau Value

---

**Description**

This function computes the parameter of a (one parameter) bivariate copula for a given value of Kendall’s tau.

**Usage**

```
BiCopTau2Par(family, tau, check.taus = TRUE)
```
Arguments

family integer; single number or vector of size \( n \); defines the bivariate copula family:
0 = independence copula
1 = Gaussian copula
2 = Student t copula (Here only the first parameter can be computed)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
13 = rotated Clayton copula (180 degrees; survival Clayton “Var/Var"
14 = rotated Gumbel copula (180 degrees; “survival Gumbel”)
16 = rotated Joe copula (180 degrees; “survival Joe”)
23 = rotated Clayton copula (90 degrees)
‘24 = rotated Gumbel copula (90 degrees)
‘26 = rotated Joe copula (90 degrees)
‘33 = rotated Clayton copula (270 degrees)
‘34 = rotated Gumbel copula (270 degrees)
‘36 = rotated Joe copula (270 degrees)
Note that (with exception of the t-copula) two parameter bivariate copula families cannot be used.

\( \tau \) numeric; single number or vector of size \( n \); Kendall’s tau value (vector with elements in \([−1,1]\)).

check.taus logical; default is TRUE; if FALSE, checks for family/\( \tau \)-consistency are omitted (should only be used with care).

Value

Parameter (vector) corresponding to the bivariate copula family and the value(s) of Kendall’s tau (\( \tau \)).

<table>
<thead>
<tr>
<th>No. (family)</th>
<th>Parameter (par)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1, 2</td>
<td>( \sin(\tau \pi) )</td>
</tr>
<tr>
<td>3, 13</td>
<td>( 2 \frac{\tau}{1-\tau} )</td>
</tr>
<tr>
<td>4, 14</td>
<td>( \frac{1}{1-\tau} )</td>
</tr>
<tr>
<td>5</td>
<td>no closed form expression (numerical inversion)</td>
</tr>
<tr>
<td>6, 16</td>
<td>no closed form expression (numerical inversion)</td>
</tr>
<tr>
<td>23, 33</td>
<td>( 2 \frac{\tau}{1+\tau} )</td>
</tr>
<tr>
<td>24, 34</td>
<td>( -\frac{1}{1+\tau} )</td>
</tr>
<tr>
<td>26, 36</td>
<td>no closed form expression (numerical inversion)</td>
</tr>
</tbody>
</table>

Note

The number \( n \) can be chosen arbitrarily, but must agree across arguments.

Author(s)

Jakob Stoeber, Eike Brechmann, Tobias Erhardt
BiCopVuongClarke

References


See Also

BiCopPar2Tau()

Examples

## Example 1: Gaussian copula
tau0 <- 0.5
rho <- BiCopTau2Par(family = 1, tau = tau0)
BiCop(1, tau = tau0)$par  # alternative

## Example 2:
vtau <- seq(from = 0.1, to = 0.8, length.out = 100)
thetaC <- BiCopTau2Par(family = 3, tau = vtau)
thetaG <- BiCopTau2Par(family = 4, tau = vtau)
thetaF <- BiCopTau2Par(family = 5, tau = vtau)
thetaJ <- BiCopTau2Par(family = 6, tau = vtau)
plot(thetaC ~ vtau, type = "l", ylim = range(thetaF))
lines(thetaG ~ vtau, col = 2)
lines(thetaF ~ vtau, col = 3)
lines(thetaJ ~ vtau, col = 4)

## Example 3: different copula families
theta <- BiCopTau2Par(family = c(3,4,6), tau = c(0.4, 0.5, 0.6))
BiCopPar2Tau(family = c(3,4,6), par = theta)

---

BiCopVuongClarke  Scoring Goodness-of-Fit Test based on Vuong And Clarke Tests for Bivariate Copula Data

Description

Based on the Vuong and Clarke tests this function computes a goodness-of-fit score for each bivariate copula family under consideration. For each possible pair of copula families the Vuong and the Clarke tests decides which of the two families fits the given data best and assigns a score—pro or contra a copula family—according to this decision.
Usage

BiCopVuongClarke(
    u1, u2,
    familyset = NA, 
    correction = FALSE, 
    level = 0.05, 
    rotations = TRUE
)

Arguments

u1, u2  Data vectors of equal length with values in [0, 1].

familyset  An integer vector of bivariate copula families under consideration, i.e., which are compared in the goodness-of-fit test. If familyset = NA (default), all possible families are compared. Possible families are:
0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton′′) \cr 14 = rotated Gumbel copula (180 degrees; survival Gumbel”)
16 = rotated Joe copula (180 degrees; survival Joe′′) \cr 17 = rotated BB1 copula (180 degrees; survival BB1”)
18 = rotated BB6 copula (180 degrees; survival BB6′′) \cr 19 = rotated BB7 copula (180 degrees; survival BB7”)
20 = rotated BB8 copula (180 degrees; ”survival BB8”)
23 = rotated Clayton copula (90 degrees)
24 = rotated Gumbel copula (90 degrees)
26 = rotated Joe copula (90 degrees)
27 = rotated BB1 copula (90 degrees)
28 = rotated BB6 copula (90 degrees)
29 = rotated BB7 copula (90 degrees)
30 = rotated BB8 copula (90 degrees)
33 = rotated Clayton copula (270 degrees)
34 = rotated Gumbel copula (270 degrees)
36 = rotated Joe copula (270 degrees)
37 = rotated BB1 copula (270 degrees)
38 = rotated BB6 copula (270 degrees)
39 = rotated BB7 copula (270 degrees)
40 = rotated BB8 copula (270 degrees)
'104' = Tawn type 1 copula
'114' = rotated Tawn type 1 copula (180 degrees)
'124' = rotated Tawn type 1 copula (90 degrees)
'134' = rotated Tawn type 1 copula (270 degrees)
'204' = Tawn type 2 copula
'214' = rotated Tawn type 2 copula (180 degrees)
'224' = rotated Tawn type 2 copula (90 degrees)
'234' = rotated Tawn type 2 copula (270 degrees)

correction
Correction for the number of parameters. Possible choices: correction = FALSE
(no correction; default), "Akaike" and "Schwarz".

level
Numerical; significance level of the tests (default: level = 0.05).

rotations
If TRUE, all rotations of the families in familyset are included (or subtracted).

Details
The Vuong as well as the Clarke test compare two models against each other and based on their
null hypothesis, allow for a statistically significant decision among the two models (see the docu-
mnetations of RVineVuongTest() and RVineClarkeTest() for descriptions of the two tests). In
the goodness-of-fit test proposed by Belgorodski (2010) this is used for bivariate copula selection.
It compares a model 0 to all other possible models under consideration. If model 0 is favored over
another model, a score of "+1" is assigned and similarly a score of "-1" if the other model is de-
termined to be superior. No score is assigned, if the respective test cannot discriminate between
two models. Both tests can be corrected for the numbers of parameters used in the copulas. Ei-
ther no correction (correction = FALSE), the Akaike correction (correction = "Akaike") or the
parsimonious Schwarz correction (correction = "Schwarz") can be used.

The models compared here are bivariate parametric copulas and we would like to determine which
family fits the data better than the other families. E.g., if we would like to test the hypothesis that the
bivariate Gaussian copula fits the data best, then we compare the Gaussian copula against all other
copulas under consideration. In doing so, we investigate the null hypothesis "The Gaussian copula
fits the data better than all other copulas under consideration", which corresponds to $k-1$ times the
hypothesis "The Gaussian copula $C_j$ fits the data better than copula $C_i$" for all $i = 1, \ldots, k, i \neq j$,
where $k$ is the number of bivariate copula families under consideration (length of familyset). This
procedure is done not only for one family but for all families under consideration, i.e., two scores,
one based on the Vuong and one based on the Clarke test, are returned for each bivariate copula
family. If used as a goodness-of-fit procedure, the family with the highest score should be selected.

For more and detailed information about the goodness-of-fit test see Belgorodski (2010).

Value
A matrix with Vuong test scores in the first and Clarke test scores in the second row. Column names
correspond to bivariate copula families (see above).

Author(s)
Ulf Schepsmeier, Eike Brechmann, Natalia Belgorodski
References


See Also

BiCopGofTest(), RVineVuongTest(), RVineClarkeTest(), BiCopSelect()

Examples

# simulate from a t-copula
dat <- BiCopSim(500, 2, 0.7, 5)

# apply the test for families 1-6
BiCopVuongClarke(dat[,1], dat[,2], familyset = 1:6)

C2RVine

Transform C-Vine to R-Vine Structure

Description

This function transforms a C-vine structure from the package CDVine to the corresponding R-vine structure.

Usage

C2RVine(order, family, par, par2 = rep(0, length(family)))

Arguments

order A d-dimensional vector specifying the order of the root nodes in the C-vine.
family A d*(d-1)/2 vector of pair-copula families with values
0 = independence copula
1 = Gaussian copula
2 = Student t copula (t-copula)
3 = Clayton copula
4 = Gumbel copula
5 = Frank copula
6 = Joe copula
7 = BB1 copula
8 = BB6 copula
9 = BB7 copula
10 = BB8 copula
13 = rotated Clayton copula (180 degrees; survival Clayton’’)
14 = rotated Gumbel copula (180 degrees; survival Gumbel’’)
16 = rotated Joe copula (180 degrees; survival Joe’’)
17 = rotated BB1 copula (180 degrees; survival BB1’’)
18 = rotated BB6 copula (180 degrees; survival BB6’’)
19 = rotated BB7 copula (180 degrees; survival BB7’’)
20 = rotated BB8 copula (180 degrees; “survival BB8’’)
23 = rotated Clayton copula (90 degrees)
‘24’ = rotated Gumbel copula (90 degrees)
‘26’ = rotated Joe copula (90 degrees)
‘27’ = rotated BB1 copula (90 degrees)
‘28’ = rotated BB6 copula (90 degrees)
‘29’ = rotated BB7 copula (90 degrees)
‘30’ = rotated BB8 copula (90 degrees)
‘33’ = rotated Clayton copula (270 degrees)
‘34’ = rotated Gumbel copula (270 degrees)
‘36’ = rotated Joe copula (270 degrees)
‘37’ = rotated BB1 copula (270 degrees)
‘38’ = rotated BB6 copula (270 degrees)
‘39’ = rotated BB7 copula (270 degrees)
‘40’ = rotated BB8 copula (270 degrees)
‘104’ = Tawn type 1 copula
‘114’ = rotated Tawn type 1 copula (180 degrees)
‘124’ = rotated Tawn type 1 copula (90 degrees)
‘134’ = rotated Tawn type 1 copula (270 degrees)
‘204’ = Tawn type 2 copula
‘214’ = rotated Tawn type 2 copula (180 degrees)
‘224’ = rotated Tawn type 2 copula (90 degrees)
‘234’ = rotated Tawn type 2 copula (270 degrees)

par
A d*(d-1)/2 vector of pair-copula parameters.

par2
A d*(d-1)/2 vector of second pair-copula parameters (optional; default: par2 = rep(0, length(family))), necessary for the t-, BB1, BB6, BB7, BB8, Tawn type 1 and type 2 copulas.

Value
An RVineMatrix() object.

Author(s)
Ulf Schepsmeier, Eike Brechmann
See Also

RVineMatrix(), D2RVine()

Examples

# set up C-vine copula model with mixed pair-copulas
d <- 4
dd <- d*(d-1)/2
order <- 1:d
family <- c(1, 2, 3, 4, 7, 3)
par <- c(0.5, 0.4, 2, 1.5, 1.2, 1.5)
par2 <- c(0, 5, 0, 0, 2, 0)

# transform to R-vine matrix notation
RVM <- C2RVine(order, family, par, par2)

Description

There are two plotting generics for RVineMatrix objects. plot.RVineMatrix plots one or all trees of a given R-vine copula model. Edges can be labeled with information about the corresponding pair-copula. contour.RVineMatrix produces a matrix of contour plots (using plot.BiCop()).

Usage

## S3 method for class 'RVineMatrix'
contour(x, tree = "ALL", xylim = NULL, cex.nums = 1, data = NULL, ...)

## S3 method for class 'RVineMatrix'
plot(x, tree = "ALL", type = 0, edge.labels = NULL, legend.pos = "bottomleft", interactive = FALSE, ...)

Arguments

x RVineMatrix object.
tree "ALL" or integer vector; specifies which trees are plotted.
xylim numeric vector of length 2; sets xlim and ylim for the contours
cex.nums numeric; expansion factor for font of the numbers.
data a data matrix for creating kernel density contours of each pair.

... Arguments passed to `network::plot.network()` or `plot.BiCop()` respectively.

type integer; specifies how to make use of variable names:
0 = variable names are ignored,
1 = variable names are used to annotate vertices,
2 = uses numbers in plot and adds a legend for variable names.

edge.labels character; either a vector of edge labels or one of the following:
"family" = pair-copula family abbreviation (see `BiCopName()`),
"par" = pair-copula parameters,
"tau" = pair-copula Kendall's tau (by conversion of parameters)
"family-par" = pair-copula family and parameters
"family-tau" = pair-copula family and Kendall's tau.

legend.pos the x argument for `graphics::legend()`.

interactive logical; if TRUE, the user is asked to adjust the positioning of vertices with his mouse.

Details

If you want the contour boxes to be perfect squares, the plot height should be $1.25/\text{length(tree)} \times (d - \text{min(tree)})$ times the plot width.

Author(s)

Thomas Nagler, Nicole Barthel

See Also

`RVineMatrix()`, `network::plot.network()`, `plot.BiCop()`, `BiCopName()`, `graphics::legend()`

Examples

```r
## build vine model
strucmat <- matrix(c(3, 1, 2, 2, 1, 0, 0, 1), 3, 3)
fammat <- matrix(c(0, 1, 6, 0, 0, 3, 0, 0, 0), 3, 3)
parmat <- matrix(c(0, 0.3, 3, 0, 0, 1, 0, 0, 0), 3, 3)
par2mat <- matrix(c(0, 0, 0, 0, 0, 0, 0, 0, 0), 3, 3)
RVM <- RVineMatrix(strucmat, fammat, parmat, par2mat)

# plot trees
## Not run: plot(RVM)

# show contour plots
contour(RVM)
```
**D2RVine**  
*Transform D-Vine to R-Vine Structure*

**Description**

This function transforms a D-vine structure from the package CDVine to the corresponding R-vine structure.

**Usage**

```r
D2RVine(order, family, par, par2 = rep(0, length(family)))
```

**Arguments**

- `order` A d-dimensional vector specifying the order of the nodes in the D-vine.
- `family` A d*(d-1)/2 vector of pair-copula families with values:
  - 0 = independence copula
  - 1 = Gaussian copula
  - 2 = Student t copula (t-copula)
  - 3 = Clayton copula
  - 4 = Gumbel copula
  - 5 = Frank copula
  - 6 = Joe copula
  - 7 = BB1 copula
  - 8 = BB6 copula
  - 9 = BB7 copula
  - 10 = BB8 copula
  - 13 = rotated Clayton copula (180 degrees; survival Clayton'')
  - 14 = rotated Gumbel copula (180 degrees; survival Gumbel”)
  - 16 = rotated Joe copula (180 degrees; survival Joe’’)
  - 17 = rotated BB1 copula (180 degrees; survival BB1”)
  - 18 = rotated BB6 copula (180 degrees; survival BB6’’)
  - 19 = rotated BB7 copula (180 degrees; survival BB7”)
  - 20 = rotated BB8 copula (180 degrees; “survival BB8”)
  - 23 = rotated Clayton copula (90 degrees)
  - 24 = rotated Gumbel copula (90 degrees)
  - 26 = rotated Joe copula (90 degrees)
  - 27 = rotated BB1 copula (90 degrees)
  - 28 = rotated BB6 copula (90 degrees)
  - 29 = rotated BB7 copula (90 degrees)
  - 30 = rotated BB8 copula (90 degrees)
  - 33 = rotated Clayton copula (270 degrees)
  - 34 = rotated Gumbel copula (270 degrees)
  - 36 = rotated Joe copula (270 degrees)
  - 37 = rotated BB1 copula (270 degrees)
  - 38 = rotated BB6 copula (270 degrees)
  - 39 = rotated BB7 copula (270 degrees)
```

- `par` A vector of copula parameters.
- `par2` A vector of copula parameters for rotated structures.
‘40’ = rotated BB8 copula (270 degrees)
‘104’ = Tawn type 1 copula
‘114’ = rotated Tawn type 1 copula (180 degrees)
‘124’ = rotated Tawn type 1 copula (90 degrees)
‘134’ = rotated Tawn type 1 copula (270 degrees)
‘204’ = Tawn type 2 copula
‘214’ = rotated Tawn type 2 copula (180 degrees)
‘224’ = rotated Tawn type 2 copula (90 degrees)
‘234’ = rotated Tawn type 2 copula (270 degrees)

par
A d*(d-1)/2 vector of pair-copula parameters.

par2
A d*(d-1)/2 vector of second pair-copula parameters (optional; default: par2 = rep(0, length(family))), necessary for the t-, BB1, BB6, BB7, BB8, Tawn type 1 and type 2 copulas.

Value
An RVineMatrix() object.

Author(s)
Ulf Schepsmeier

See Also
RVineMatrix(), C2RVine()

Examples

# set up D-vine copula model with mixed pair-copulas
d <- 4
dd <- d*(d-1)/2
order <- 1:d
family <- c(1, 2, 3, 4, 7, 3)
par <- c(0.5, 0.4, 2, 1.5, 1.2, 1.5)
par2 <- c(0, 5, 0, 0, 2, 0)

# transform to R-vine matrix notation
RVM <- D2RVine(order, family, par, par2)

---

**daxreturns**  
**Major German Stocks**

**Description**

This data set contains transformed standardized residuals of daily log returns of 15 major German stocks represented in the index DAX observed from January 2005 to August 2009. Each time series is filtered using a GARCH(1,1) model with Student t innovations.
Format

A data frame with 1158 observations on 15 variables. Column names correspond to ticker symbols of the stocks.

Source

Yahoo! Finance

See Also

RVineStructureSelect()

Examples

```r
# load the data set
data(daxreturns)

# compute the empirical Kendall's tau matrix
TauMatrix(daxreturns)
```

Description

This function provides pair plots for copula data. Using default setting it plots bivariate contour plots on the lower panel, scatter plots and correlations on the upper panel and histograms on the diagonal panel.

Usage

```r
## S3 method for class 'copuladata'
pairs(
x,  
labels = names(x),
...,  
lower.panel = lp.copuladata,  
upper.panel = up.copuladata,  
diag.panel = dp.copuladata,  
label.pos = 0.85,  
cex.labels = 1,  
gap = 0,  
method = "kendall",  
ccols = terrain.colors(11),  
margins = "norm"
)
```
pairs.copuladata

Arguments

x
   copuladata object.
labels
   variable names/labels.
...
   other graphical parameters (see graphics::par()) or options passed to BiCopKDE().
lower.panel
   panel function to be used on the lower diagonal panels (if not supplied, a default function is used)
upper.panel
   panel function to be used on the upper diagonal panels (if not supplied, a default function is used)
diag.panel
   panel function to be used on the diagonal panels (if not supplied, a default function is used)
label.pos
   y position of labels in the diagonal panel; default: label.pos = 0.85.
cex.labels
   magnification to be used for the labels of the diagonal panel; default: cex.labels = 1.
gap
   distance between subplots, in margin lines; default: gap = 0.
method
   a character string indicating which correlation coefficients are computed. One of "pearson", "kendall" (default), or "spearman"
ccols
   color to be used for the contour plots; default: ccols = terrain.colors(30).
margins
   character; margins for the contour plots. Options are: "unif" for the original copula density, "norm" for the transformed density with standard normal margins, "exp" with standard exponential margins, and "flexp" with flipped exponential margins.

Note

If the default panel functions are used

- col changes only the color of the points in the scatter plot (upper.panel)
- cex changes only the magnification of the points in the scatter plot (upper.panel)

Author(s)

Tobias Erhardt

See Also

  graphics::pairs(), as.copuladata(), BiCopKDE()

Examples

data(daxreturns)
data <- as.copuladata(daxreturns)
se1 <- c(4,5,14,15)
## pairs plot with default settings
pairs(data[sel])

## pairs plot with custom settings
nlevels <- 20
pairs(data[sel], cex = 2, pch = 1, col = "black",
      diag.panel = NULL, label.pos = 0.5,
      cex.labels = 2.5, gap = 1,
      method = "pearson", ccols = heat.colors(nlevels),
      margins = "flexp")

## pairs plot with own panel functions
up <- function(x, y) {
  # upper panel: empirical contour plot
  op <- par(usr = c(-3, 3, -3, 3), new = TRUE)
  BiCopKDE(x, y,
           levels = c(0.01, 0.05, 0.1, 0.15, 0.2),
           margins = "exp",
           axes = FALSE)
  on.exit(par(op))
}

lp <- function(x, y) {
  # lower panel: scatter plot (copula data) and correlation
  op <- par(usr = c(0, 1, 0, 1), new = TRUE)
  points(x, y, pch = 1, col = "black")
  r <- cor(x, y, method = "spearman") # Spearman's rho
  txt <- format(x = r, digits = 3, nsmall = 3)[1]
  text(x = 0.5, y = 0.5, labels = txt, cex = 1 + abs(r) * 2, col = "blue")
  on.exit(par(op))
}

dp <- function(x) {
  # diagonal panel: histograms (copula data)
  op <- par(usr = c(0, 1, 0, 1.5), new = TRUE)
  hist(x, freq = FALSE, add = TRUE, col = "brown", border = "black", main = "")
  abline(h = 1, col = "black", lty = 2)
  on.exit(par(op))
}

nlevels <- 20
pairs(data[sel],
      lower.panel = lp, upper.panel = up, diag.panel = dp, gap = 0.5)
Description

There are several options for plotting BiCop objects. The density of a bivariate copula density can be visualized as surface/perspective or contour plot. Optionally, the density can be coupled with standard normal margins (default for contour plots). Furthermore, a lambda-plot is available (cf., `BiCopLambda()`).

Usage

```r
## S3 method for class 'BiCop'
plot(x, type = "surface", margins, size, ...)

## S3 method for class 'BiCop'
contour(x, margins = "norm", size = 100L, ...)
```

Arguments

- `x` BiCop object.
- `type` plot type; either "surface", "contour", or "lambda" (partial matching is activated); the latter is only implemented for a few families (cf., `BiCopLambda()`).
- `margins` only relevant for types "contour" and "surface"; options are: "unif" for the original copula density, "norm" for the transformed density with standard normal margins, "exp" with standard exponential margins, and "fexp" with flipped exponential margins. Default is "norm" for type = "contour", and "unif" for type = "surface".
- `size` integer; only relevant for types "contour" and "surface"; the plot is based on values on a `size x size` grid; default is 100 for type = "contour", and 25 for type = "surface".
- `...` optional arguments passed to `contour()` or `wireframe()`.

Author(s)

Thomas Nagler

See Also

`BiCop()`, `contour()`, `wireframe()`

Examples

```r
## construct BiCop object for a Tawn copula
obj <- BiCop(family = 104, par = 2.5, par2 = 0.4)

## plots
plot(obj)  # surface plot of copula density
contour(obj)  # contour plot with standard normal margins
contour(obj, margins = "unif")  # contour plot of copula density
```
Pseudo-Observations

Description

Compute the pseudo-observations for the given data matrix.

Usage

pobs(
  x,  
  na.last = "keep", 
  ties.method = eval(formals(rank)$ties.method), 
  lower.tail = TRUE 
)

Arguments

x
  n × d-matrix of random variates to be converted to pseudo-observations.
na.last, ties.method
  are passed to rank(): see there.
lower.tail
  logical() which, if FALSE, returns the pseudo-observations when applying the empirical marginal survival functions.

Details

Given n realizations \( x_i = (x_{i1}, \ldots, x_{id})^T, i \in \{1, \ldots, n\} \) of a random vector \( X \), the pseudo-observations are defined via \( u_{ij} = r_{ij}/(n + 1) \) for \( i \in \{1, \ldots, n\} \) and \( j \in \{1, \ldots, d\} \), where \( r_{ij} \) denotes the rank of \( x_{ij} \) among all \( x_{kj}, k \in \{1, \ldots, n\} \). The pseudo-observations can thus also be computed by component-wise applying the empirical distribution functions to the data and scaling the result by \( n/(n + 1) \). This asymptotically negligible scaling factor is used to force the variates to fall inside the open unit hypercube, for example, to avoid problems with density evaluation at the boundaries. Note that pobs(, lower.tail=FALSE) simply returns 1-pobs().

Value

matrix of the same dimensions as x containing the pseudo-observations.

Note

This function is borrowed from the copula() package.

Author(s)

Marius Hofert
Examples

```r
## Simple definition of the function:
pobs

## simulate data from a multivariate normal distribution
library(mvtnorm)
set.seed(123)
Sigma <- matrix(c(2, 1, -0.2, 1, 1, 0.3, -0.2, 0.3, 0.5), 3, 3)
mu <- c(-3, 2, 1)
dat <- rmvnorm(500, sigma = Sigma)
pairs(dat) # plot observations

## compute pseudo-observations for copula inference
udat <- pobs(dat)
pairs(udat)
# estimate vine copula model
fit <- RVineStructureSelect(udat, familyset = c(1, 2))
```

---

**RVineAIC**  
*AIC and BIC of an R-Vine Copula Model*

**Description**

These functions calculate the Akaike and Bayesian Information criteria of a d-dimensional R-vine copula model for a given copula data set.

**Usage**

```r
RVineAIC(data, RVM, par = RVM$par, par2 = RVM$par2)
RVineBIC(data, RVM, par = RVM$par, par2 = RVM$par2)
```

**Arguments**

- `data`  
  An N x d data matrix (with uniform margins).

- `RVM`  
  An `RVineMatrix()` object including the structure and the pair-copula families and parameters.

- `par`  
  A d x d matrix with the pair-copula parameters (optional; default: `par = RVM$par`).

- `par2`  
  A d x d matrix with the second parameters of pair-copula families with two parameters (optional; default: `par2 = RVM$par2`).
Details

If $k$ denotes the number of parameters of an R-vine copula model with log-likelihood $l_{RVine}$ and parameter set $\theta$, then the Akaike Information Criterion (AIC) by Akaike (1973) is defined as

$$AIC := -2l_{RVine}(\theta|u) + 2k,$$

for observations $u = (u_1', ..., u_N')'$.

Similarly, the Bayesian Information Criterion (BIC) by Schwarz (1978) is given by

$$BIC := -2l_{RVine}(\theta|u) + \log(N)k.$$

Value

AIC, BIC are the computed AIC or BIC value, respectively.

pair.AIC, pair.BIC are the computed AIC or BIC value, respectively. Note: AIC = sum(pair.AIC) and similarly BIC = sum(pair.BIC).

Author(s)

Eike Brechmann

References


See Also

RVineLogLik(), RVineVuongTest(), RVineClarkeTest()

Examples

# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4,
           0, 2, 3, 4, 1,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)

# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4,
            0, 0, 3, 4, 1,
            0, 0, 0, 4, 1,
            0, 0, 0, 0, 3,
            0, 0, 0, 0, 0)
family <- matrix(family, 5, 5)

# define R-vine pair-copula parameter matrix
par <- c(0, 0.2, 0.9, 1.5, 3.9,
        0, 0, 1.1, 1.6, 0.9,
        0, 0, 1.9, 0.5,
        0, 0, 0, 4.8,
        0, 0, 0, 0, 0)
par <- matrix(par, 5, 5)

# define second R-vine pair-copula parameter matrix
par2 <- matrix(0, 5, 5)

# define RVineMatrix object
RVM <- RVineMatrix(Matrix = Matrix, family = family, par = par, par2 = par2,
                    names=c("V1", "V2", "V3", "V4", "V5"))

# simulate a sample of size 300 from the R-vine copula model
set.seed(123)
simdata <- RVineSim(300,RVM)

# compute AIC and BIC
RVineAIC(simdata, RVM)
RVineBIC(simdata, RVM)

RVineClarkeTest

Clarke Test Comparing Two R-Vine Copula Models

Description

This function performs a Clarke test between two d-dimensional R-vine copula models as specified by their RVineMatrix() objects.

Usage

RVineClarkeTest(data, RVM1, RVM2)

Arguments

data An N x d data matrix (with uniform margins).
RVM1, RVM2 RVineMatrix() objects of models 1 and 2.

Details

The test proposed by Clarke (2007) allows to compare non-nested models. For this let \( c_1 \) and \( c_2 \) be two competing vine copulas in terms of their densities and with estimated parameter sets \( \theta_1 \) and \( \theta_2 \). The null hypothesis of statistical indistinguishability of the two models is
\[ H_0 : P(m_i > 0) = 0.5 \forall i = 1, \ldots, N, \]

where \( m_i := \log \left[ \frac{c_1(u_i|\theta_1)}{c_2(u_i|\theta_2)} \right] \) for observations \( u_i, i = 1, \ldots, N. \)

Since under statistical equivalence of the two models the log likelihood ratios of the single observations are uniformly distributed around zero and in expectation 50% of the log likelihood ratios greater than zero, the test statistic

\[
\text{statistic} := B = \sum_{i=1}^{N} 1_{(0,\infty)}(m_i),
\]

where \( 1 \) is the indicator function, is distributed Binomial with parameters \( N \) and \( p = 0.5 \), and critical values can easily be obtained. Model 1 is interpreted as statistically equivalent to model 2 if \( B \) is not significantly different from the expected value \( Np = \frac{N}{2} \).

Like AIC and BIC, the Clarke test statistic may be corrected for the number of parameters used in the models. There are two possible corrections; the Akaike and the Schwarz corrections, which correspond to the penalty terms in the AIC and the BIC, respectively.

**Value**

- statistic, statistic.Akaike, statistic.Schwarz
  
  Test statistics without correction, with Akaike correction and with Schwarz correction.

- p.value, p.value.Akaike, p.value.Schwarz
  
  P-values of tests without correction, with Akaike correction and with Schwarz correction.

**Author(s)**

Jeffrey Dissmann, Eike Brechmann

**References**


**See Also**

RVineVuergTest(), RVineAIC(), RVineBIC()

**Examples**

```r
# vine structure selection time-consuming (~ 20 sec)

# load data set
data(daxreturns)

# select the R-vine structure, families and parameters
```
RVineCopSelect <- RVineStructureSelect(daxreturns[,1:5], c(1:6))
RVineCopSelect$Matrix
RVineCopSelect$par
RVineCopSelect$par2

# select the C-vine structure, families and parameters
CVM <- RVineStructureSelect(daxreturns[,1:5], c(1:6), type = "CVine")
CVM$Matrix
CVM$par
CVM$par2

# compare the two models based on the data
clarke <- RVineClarkeTest(daxreturns[,1:5], RVineCopSelect, CVM)
clarke$statistic
clarke$statistic.Schwarz
clarke$p.value
clarke$p.value.Schwarz

RVineCopSelect

Sequential Pair-Copula Selection and Estimation for R-Vine Copula Models

Description

This function fits a R-vine copula model to a d-dimensional copula data set. Pair-copula families are selected using BiCopSelect() and estimated sequentially.

Usage

RVineCopSelect(
  data,
  familyset = NA,
  Matrix,
  selectioncrit = "AIC",
  indeptest = FALSE,
  level = 0.05,
  trunclevel = NA,
  weights = NA,
  rotations = TRUE,
  se = FALSE,
  presel = TRUE,
  method = "mle",
  cores = 1
)
Arguments

data  N x d data matrix (with uniform margins).
familyset  integer vector of pair-copula families to select from. The vector has to include at least one pair-copula family that allows for positive and one that allows for negative dependence. Not listed copula families might be included to better handle limit cases. If familyset = NA (default), selection among all possible families is performed. If a vector of negative numbers is provided, selection among all but abs(familyset) is performed. Coding of pair copula families is the same as in BiCop().
Matrix  lower or upper triangular d x d matrix that defines the R-vine tree structure.
selectioncrit  Character indicating the criterion for pair-copula selection. Possible choices: selectioncrit = "AIC" (default), "BIC", or "logLik" (see BiCopSelect()).
indeptest  Logical; whether a hypothesis test for the independence of u1 and u2 is performed before bivariate copula selection (default: indeptest = FALSE; see BiCopIndTest()). The independence copula is chosen for a (conditional) pair if the null hypothesis of independence cannot be rejected.
level  numeric; significance level of the independence test (default: level = 0.05).
trunclevel  integer; level of truncation.
weights  Numerical; weights for each observation (optional).
rotations  logical; if TRUE, all rotations of the families in familyset are included.
se  Logical; whether standard errors are estimated (default: se = FALSE).
presel  Logical; whether to exclude families before fitting based on symmetry properties of the data. Makes the selection about 30\% (on average), but may yield slightly worse results in few special cases.
method  indicates the estimation method: either maximum likelihood estimation (method = "mle"; default) or inversion of Kendall's tau (method = "itau"). For method = "itau" only one parameter families and the Student t copula can be used (family = 1,2,3,4,5,6,13,14,16,23,24,26,33,34 or 36). For the t-copula, par2 is found by a crude profile likelihood optimization over the interval (2, 10].
cores  integer; if cores > 1, estimation will be parallelized within each tree (using foreach::foreach()). Note that parallelization causes substantial overhead and may be slower than single-threaded computation when dimension, sample size, or family set are small or method = "itau".

Details

R-vine copula models with unknown structure can be specified using RVineStructureSelect().

Value

An RVineMatrix() object with the selected families (RVM$family) as well as sequentially estimated parameters stored in RVM$par and RVM$par2. The object is augmented by the following information about the fit:
se, se2  standard errors for the parameter estimates (if se = TRUE; note that these are only approximate since they do not account for the sequential nature of the estimation,
nobs  number of observations,
logLik, pair.logLik  log likelihood (overall and pairwise)
AIC, pair.AIC  Akaike's Information Criterion (overall and pairwise),
BIC, pair.BIC  Bayesian's Information Criterion (overall and pairwise),
emptau  matrix of empirical values of Kendall's tau,
p.value.indeptest  matrix of p-values of the independence test.

Note
For a comprehensive summary of the vine copula model, use summary(object); to see all its contents, use str(object).

Author(s)
Eike Brechmann, Thomas Nagler

References

See Also
RVineMatrix(), BiCop(), BiCopSelect(), plot.RVineMatrix(), contour.RVineMatrix()

Examples

# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4, 0, 2, 3, 4, 1, 0, 0, 3, 4, 1, 0, 0, 0, 4, 1, 0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)
# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4, 0, 0, 3, 4, 1, 0, 0, 0, 4, 1, 0, 0, 0, 0, 1,
RVineCor2pcor

(Partial) Correlations for R-Vine Copula Models

Description

Correlations to partial correlations and vice versa for R-vines with independence, Gaussian and t-copulas.

Usage

RVineCor2pcor(RVM, corMat)

RVinePcor2cor(RVM)
Arguments

RVM

RVineMatrix() defining only the R-vine structure for Cor2pcor and providing as well the partial correlations for Pcor2cor.

corMat
correlation matrix

Value

RVM

RVineMatrix with transformed partial correlations (for Cor2pcor)

cor
correlation matrix (for Pcor2cor)

Note

The behavior of RVinePcor2ccor differs from older versions (<= 1.4). The RVM object is now normalized such that the order of the returned correlation matrix conforms with the correlation matrix of the data. If RVM$names are non-default, the initial ordering of the variables cannot be traced back and the matrix has to be interpreted as indicated by the row- and column names.

Examples

## create RVineMatrix-object for Gaussian vine
Matrix <- matrix(c(1, 3, 4, 2,
0, 3, 4, 2,
0, 0, 4, 2,
0, 0, 0, 2), 4, 4)
family <- matrix(c(0, 1, 1, 1,
0, 0, 1, 1,
0, 0, 0, 1,
0, 0, 0, 0), 4, 4)
par <- matrix(c(0, 0.2, 0, 0.6,
0, 0, 0.2, 0.6,
0, 0, 0, 0.6,
0, 0, 0, 0), 4, 4)
RVM <- RVineMatrix(Matrix, family, par)

## calculate correlation matrix corresponding to the R-Vine model
newcor <- RVinePcor2ccor(RVM)

## transform back to partial correlations
RVineCor2pcor(RVM, newcor)$par

## check if they are equal
all.equal(RVM$par, RVineCor2pcor(RVM, newcor)$par)
RVineGofTest

**Goodness-of-Fit Tests for R-Vine Copula Models**

### Description

This function performs a goodness-of-fit test for R-vine copula models. There are 15 different goodness-of-fit tests implemented, described in Schepsmeier (2013).

### Usage

```r
RVineGofTest(
  data, 
  RVM, 
  method = "White", 
  statistic = "CvM", 
  B = 200, 
  alpha = 2
)
```

### Arguments

- **data**: An N x d data matrix (with uniform margins).
- **RVM**: `RVineMatrix()` objects of the R-vine model under the null hypothesis.
  - Only the following copula families are allowed in `RVM$family` due to restrictions in `RVineGrad()` and `RVineHessian()`
    - 0 = independence copula
    - 1 = Gaussian copula
    - 2 = Student t copula (t-copula)
    - 3 = Clayton copula
    - 4 = Gumbel copula
    - 5 = Frank copula
    - 6 = Joe copula
    - 13 = rotated Clayton copula (180 degrees; survival Clayton’’)
    - 14 = rotated Gumbel copula (180 degrees; survival Gumbel”)
    - 16 = rotated Joe copula (180 degrees; “survival Joe”)  
    - 23 = rotated Clayton copula (90 degrees)  
    - ‘24’ = rotated Gumbel copula (90 degrees)  
    - ‘26’ = rotated Joe copula (90 degrees)  
    - ‘33’ = rotated Clayton copula (270 degrees)  
    - ‘34’ = rotated Gumbel copula (270 degrees)  
    - ‘36’ = rotated Joe copula (270 degrees)
- **method**: A string indicating the goodness-of-fit method:
  - "White" = goodness-of-fit test based on White’s information matrix equality (default)
  - "IR" = goodness-of-fit test based on the information ratio
- **statistic**: A string indicating the goodness-of-fit statistic:
  - "CvM" = Cramer-von Mises statistic
  - "CvW" = Cramer-von Mises statistic with weight
  - "K" = Kolmogorov statistic
  - "SW" = Swartz statistic
  - "AD" = Anderson-Darling statistic
  - "CD" = Cramer-Davies statistic
  - "W" = White statistic
- **B**: The number of bootstrap replications.
- **alpha**: The significance level.
"Breymann" = goodness-of-fit test based on the probability integral transform (PIT) and the aggregation to univariate data by Breymann et al. (2003).

"Berg" = goodness-of-fit test based on the probability integral transform (PIT) and the aggregation to univariate data by Berg and Bakken (2007).

"Berg2" = second goodness-of-fit test based on the probability integral transform (PIT) and the aggregation to univariate data by Berg and Bakken (2007).

"ECP" = goodness-of-fit test based on the empirical copula process (ECP)

"ECP2" = goodness-of-fit test based on the combination of probability integral transform (PIT) and empirical copula process (ECP) (Genest et al. 2009)

statistic A string indicating the goodness-of-fit test statistic type:
"CvM" = Cramer-von Mises test statistic (univariate for "Breymann", "Berg" and "Berg2", multivariate for "ECP" and "ECP2")
"KS" = Kolmogorov-Smirnov test statistic (univariate for "Breymann", "Berg" and "Berg2", multivariate for "ECP" and "ECP2")
"AD" = Anderson-Darling test statistic (only univariate for "Breymann", "Berg" and "Berg2")

B an integer for the number of bootstrap steps (default $B = 200$)
For $B = 0$ the asymptotic p-value is returned if available, otherwise only the test statistic is returned.
WARNING: If $B$ is chosen too large, computations will take very long.

alpha an integer of the set $2, 4, 6, \ldots$ for the "Berg2" goodness-of-fit test (default $alpha = 2$)

Details

method = "White":
This goodness-of-fit test uses the information matrix equality of White (1982) and was originally investigated by Huang and Prokhorov (2011) for copulas.
Schepsmeier (2012) enhanced their approach to the vine copula case.
The main contribution is that under correct model specification the Fisher Information can be equivalently calculated as minus the expected Hessian matrix or as the expected outer product of the score function. The null hypothesis is

$$H_0 : \mathbf{H}(\theta) + C(\theta) = 0$$

against the alternative

$$H_1 : \mathbf{H}(\theta) + C(\theta) \neq 0,$$

where $\mathbf{H}(\theta)$ is the expected Hessian matrix and $C(\theta)$ is the expected outer product of the score function.
For the calculation of the test statistic we use the consistent maximum likelihood estimator $\hat{\theta}$ and the sample counterparts of $\mathbf{H}(\theta)$ and $C(\theta)$.
The correction of the Covariance-Matrix in the test statistic for the uncertainty in the margins is skipped. The implemented test assumes that there is no uncertainty in the margins. The correction can be found in Huang and Prokhorov (2011) for bivariate copulas and in Schepsmeier (2013) for vine copulas. It involves multi-dimensional integrals.

method = "IR":
As the White test the information matrix ratio test is based on the expected Hessian matrix $\mathbf{H}(\theta)$
and the expected outer product of the score function $C(\theta)$.

$$H_0 : -H(\theta)^{-1}C(\theta) = I_p$$

against the alternative

$$H_1 : -H(\theta)^{-1}C(\theta) \neq I_p.$$ 

The test statistic can then be calculated as

$$IR_n := tr(\Phi(\theta))/p$$

with $\Phi(\theta) = -H(\theta)^{-1}C(\theta)$, $p$ is the number of parameters, i.e. the length of $\theta$, and $tr(A)$ is the trace of the matrix $A$.

For details see Schepsmeier (2013)

**method = "Breymann", method = "Berg" and method = "Berg2":**

These tests are based on the multivariate probability integral transform (PIT) applied inRVinePIT(). The multivariate data $y_i$ returned from the PIT are aggregated to univariate data by different aggregation functions $\Gamma(\cdot)$ in the sum

$$s_t = \sum_{i=1}^{d} \Gamma(y_{it}), t = 1, \ldots, n.$$  

In Breymann et al. (2003) the weight function is suggested as $\Gamma(\cdot) = \Phi^{-1}(\cdot)^2$, while in Berg and Bakken (2007) the weight function is either $\Gamma(\cdot) = |\cdot - 0.5|$ (method="Berg") or $\Gamma(\cdot) = (\cdot - 0.5)^\alpha, \alpha = 2, 4, 6, \ldots$ (method="Berg2"). Furthermore, the "Berg" and "Berg2" test are based on the order statistics of the PIT returns. See Berg and Bakken (2007) or Schepsmeier (2013) for details.

**method = "ECP" and method = "ECP2":**

Both tests are test for $H_0 : C \in C_0$ against $H_1 : C \notin C_0$ where $C$ denotes the (vine) copula distribution function and $C_0$ is a class of parametric (vine) copulas with $\Theta \subseteq \mathbb{R}^p$ being the parameter space of dimension $p$. They are based on the empirical copula process (ECP)

$$\hat{C}_n(u) - C_{\theta_n}(u),$$

with $u = (u_1, \ldots, u_d) \in [0, 1]^d$ and $\hat{C}_n(u) = \frac{1}{n+1} \sum_{t=1}^{n} \mathbf{1}_{\{U_{1t} \leq u_1, \ldots, U_{dt} \leq u_d\}}$. The ECP is utilized in a multivariate Cramer-von Mises (CvM) or multivariate Kolmogorov-Smirnov (KS) based test statistic. An extension of the ECP-test is the combination of the multivariate PIT approach with the ECP. The general idea is that the transformed data of a multivariate PIT should be "close" to the independence copula Genest et al. (2009). Thus a distance of CvM or KS type between them is considered. This approach is called ECP2. Again we refer to Schepsmeier (2013) for details.

**Value**

For method = "White":

- **White** test statistic
- **p.value** p-value, either asymptotic for $B = 0$ or bootstrapped for $B > 0$
For method = "IR":

IR test statistic (raw version as stated above)
p.value So far no p-value is returned nigher a asymptotic nor a bootstrapped one. How to calculated a bootstrapped p-value is explained in Schepsmeier (2013). Be aware, that the test statistics than have to be adjusted with the empirical variance.

For method = "Breymann", method = "Berg" and method = "Berg2":

CvM, KS, AD test statistic according to the choice of statistic
p.value p-value, either asymptotic for B = 0 or bootstrapped for B > 0. A asymptotic p-value is only available for the Anderson-Darling test statistic if the R-package ADGofTest is loaded. Furthermore, a asymptotic p-value can be calculated for the Kolmogorov-Smirnov test statistic. For the Cramer-von Mises no asymptotic p-value is available so far.

For method = "ECP" and method = "ECP2":

CvM, KS test statistic according to the choice of statistic
p.value bootstrapped p-value

Warning: The code for all the p-values are not yet approved since some of them are moved from R-code to C-code. If you need p-values the best way is to write your own algorithm as suggested in Schepsmeier (2013) to get bootstrapped p-values.

Author(s)

Ulf Schepsmeier

References


See Also

BiCopGofTest(), RVinePIT()}
Examples

```r
## time-consuming example

# load data set
data(daxreturns)

# select the R-vine structure, families and parameters
RVM <- RVineStructureSelect(daxreturns[,1:5], c(1:6))

# White test with asymptotic p-value
RVineGofTest(daxreturns[,1:5], RVM, B = 0)

# ECP2 test with Cramer-von-Mises test statistic and a bootstrap
# with 200 replications for the calculation of the p-value
RVineGofTest(daxreturns[,1:5], RVM, method = "ECP2",
statistic = "CvM", B = 200)
```

---

**RVineGrad**  
*Gradient of the Log-Likelihood of an R-Vine Copula Model*

Description

This function calculates the gradient of the log-likelihood of a d-dimensional R-vine copula model with respect to the copula parameter and evaluates it on a given copula data set.

Usage

```r
RVineGrad(
  data,  
  RVM,  
  par = RVM$par,  
  par2 = RVM$par2,  
  start.V = NA,  
  posParams = (RVM$family > 0)
)
```

Arguments

- **data**  
  An N x d data matrix (with uniform margins).

- **RVM**  
  An `RVineMatrix()` object including the structure and the pair-copula families and parameters.  
  Only the following copula families are allowed in `RVM$family`  
  0 = independence copula  
  1 = Gaussian copula  
  2 = Student t copula (t-copula)  
  3 = Clayton copula
`4 = Gumbel copula`  
`5 = Frank copula`  
`6 = Joe copula`  
`13 = rotated Clayton copula (180 degrees; survival Clayton)`  
`14 = rotated Gumbel copula (180 degrees; survival Gumbel)``

`16 = rotated Joe copula (180 degrees; “survival Joe”)`  
`23 = rotated Clayton copula (90 degrees)`  
`24 = rotated Gumbel copula (90 degrees)`  
`26 = rotated Joe copula (90 degrees)`  
`33 = rotated Clayton copula (270 degrees)`  
`34 = rotated Gumbel copula (270 degrees)`  
`36 = rotated Joe copula (270 degrees)`

**par**
A d x d matrix with the pair-copula parameters (optional; default: `par = RVM$par`).

**par2**
A d x d matrix with the second parameters of pair-copula families with two parameters (optional; default: `par2 = RVM$par2`).

**start.V**
Transformations (h-functions and log-likelihoods of each pair-copula) of previous calculations (see output; default: `start.V = NA`).

**posParams**
A d x d matrix indicating which copula has to be considered in the gradient (default: `posParams = (RVM$family > 0)`).

**Details**
The ordering of the gradient is due to the ordering of the R-vine matrix. The gradient starts at the lower right corner of the R-vine matrix and goes column by column to the left and up, i.e. the first entry of the gradient is the last entry of the second last column of the `par`-matrix followed by the last entry of the third last column and the second last entry of this column. If there is a copula family with two parameters, i.e. the t-copula, the derivative with respect to the second parameter is at the end of the gradient vector in order of their occurrence.

**Value**
gradient The calculated gradient of the log-likelihood value of the R-vine copula model. (three matrices: `direct`, `indirect` and `value`).

**Note**
The gradient for R-vine copula models with two parameter Archimedean copulas, i.e. BB1, BB6, BB7, BB8 and their rotated versions can not yet be calculated. The derivatives of these bivariate copulas are more complicated.

**Author(s)**
Ulf Schepsmeier, Jakob Stoeber
References

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s00180-013-0423-8#.

See Also

BiCopDeriv(), BiCopDeriv2(), BiCopHfuncDeriv(), BiCopHfuncDeriv2(),
RVineMatrix(), RVineMLE(), RVineHessian()

Examples

# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4,
           0, 2, 3, 4, 1,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)

# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 3,
           0, 0, 0, 0, 0)
family <- matrix(family, 5, 5)

# define R-vine pair-copula parameter matrix
par <- c(0, 0.2, 0.9, 1.5, 3.9,
        0, 1.1, 1.6, 0.9,
        0, 0, 1.9, 0.5,
        0, 0, 0, 4.8,
        0, 0, 0, 0)
par <- matrix(par, 5, 5)

# define second R-vine pair-copula parameter matrix
par2 <- matrix(0, 5, 5)

# define RVineMatrix object
RVM <- RVineMatrix(Matrix = Matrix, family = family,
par = par, par2 = par2,
names = c("V1", "V2", "V3", "V4", "V5"))

# simulate a sample of size 300 from the R-vine copula model
set.seed(123)
simdata <- RVineSim(300, RVM)

# compute the gradient of the first row of the data
out2 <- RVineGrad(simdata[1,], RVM)
out2$gradient

---

**RVineHessian**

**Hessian Matrix of the Log-Likelihood of an R-Vine Copula Model**

**Description**

This function calculates the Hessian matrix of the log-likelihood of a d-dimensional R-vine copula model with respect to the copula parameter and evaluates it on a given copula data set.

**Usage**

RVineHessian(data, RVM)

**Arguments**

- **data**
  - An N x d data matrix (with uniform margins).

- **RVM**
  - An *RVineMatrix()* object including the structure, the pair-copula families, and the parameters.
  - Only the following copula families are allowed in *RVM*$family
    - 0 = independence copula
    - 1 = Gaussian copula
    - 2 = Student t copula (t-copula)
    - 3 = Clayton copula
    - 4 = Gumbel copula
    - 5 = Frank copula
    - 6 = Joe copula
    - 13 = rotated Clayton copula (180 degrees; survival Clayton'')
    - 14 = rotated Gumbel copula (180 degrees; survival Gumbel”)
    - 16 = rotated Joe copula (180 degrees; “survival Joe”)
    - 23 = rotated Clayton copula (90 degrees)
    - ‘24’ = rotated Gumbel copula (90 degrees)
    - ‘26’ = rotated Joe copula (90 degrees)
    - ‘33’ = rotated Clayton copula (270 degrees)
    - ‘34’ = rotated Gumbel copula (270 degrees)
    - ‘36’ = rotated Joe copula (270 degrees)
Value

hessian  The calculated Hessian matrix of the log-likelihood value of the R-vine copula model.
der  The product of the gradient vector with its transposed version.

Note

The Hessian matrix is not available for R-vine copula models with two parameter Archimedean copulas, i.e. BB1, BB6, BB7, BB8 and their rotated versions.

Author(s)

Ulf Schepsmeier, Jakob Stoeber

References


See Also

BiCopDeriv(), BiCopDeriv2(), BiCopHfuncDeriv(), BiCopHfuncDeriv2(), RVineMatrix(), RVineMLE(), RVineGrad()

Examples

# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4,
          0, 2, 3, 4, 1,
          0, 0, 3, 4, 1,
          0, 0, 0, 4, 1,
          0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)

# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4,
            0, 0, 3, 4, 1,
            0, 0, 0, 4, 1,
            0, 0, 0, 0, 3,
RVineLogLik

RVineLogLik

Log-Likelihood of an R-Vine Copula Model

Description

This function calculates the log-likelihood of a d-dimensional R-vine copula model for a given copula data set.

Usage

RVineLogLik(
  data,  # copula data set
  RVM,  # RVineMatrix object
  par = RVM$par,  # parameter matrix
  par2 = RVM$par2,  # second parameter matrix
  separate = FALSE,  # separate parameters
  verbose = TRUE,  # print progress
  check.pars = TRUE,  # check for valid parameters
  calculate.V = TRUE  # calculate the Hessian matrix
)
Arguments

- **data**
  An N x d data matrix (with uniform margins).

- **RVM**
  An `RVineMatrix()` object including the structure and the pair-copula families and parameters.

- **par**
  A d x d matrix with the pair-copula parameters (optional; default: `par = RVM$par`).

- **par2**
  A d x d matrix with the second parameters of pair-copula families with two parameters (optional; default: `par2 = RVM$par2`).

- **separate**
  Logical; whether log-likelihoods are returned point wisely (default: `separate = FALSE`).

- **verbose**
  In case something goes wrong, additional output will be plotted.

- **check.pars**
  Logical; default is `TRUE`; if `FALSE`, checks for family/parameter-consistency are omitted (should only be used with care).

- **calculate.V**
  Logical; whether V matrices should be calculated. Default is `TRUE`, but requires a lot of memory when dimension is large. Use `FALSE` for a memory efficient version.

Details

For observations \( \mathbf{u} = (\mathbf{u}_1', ..., \mathbf{u}_N')' \) the log-likelihood of a d-dimensional R-vine copula with \( d - 1 \) trees and corresponding edge sets \( E_1, ..., E_{d-1} \) is given by

\[
\loglik := l_{RVine}(\theta | \mathbf{u}) = \sum_{i=1}^{N} \sum_{\ell=1}^{d-1} \sum_{e \in E_\ell} \ln[c_{j(e),k(e)}|D(e)](F(u_{i,j(e)}|u_{i,D(e)}), F(u_{i,k(e)}|u_{i,D(e)})|\theta_{j(e),k(e)}|D(e))
\]

where \( \mathbf{u}_i = (u_{i,1}, ..., u_{i,d})' \in [0, 1]^d, \ i = 1, ..., N \). Further \( c_{j(e),k(e)}|D(e) \) denotes a bivariate copula density associated to an edge \( e \) and with parameter(s) \( \theta_{j(e),k(e)}|D(e) \). Conditional distribution functions such as \( F(u_{i,j(e)}|u_{i,D(e)}) \) are obtained recursively using the relationship

\[
h(u|v, \theta) := F(u|v) = dC_{uv_j|v_{-j}}(F(u|v_{-j}), F(v_j|v_{-j})) / dF(v_j|v_{-j}),
\]

where \( C_{uv_j|v_{-j}} \) is a bivariate copula distribution function with parameter(s) \( \theta \) and \( v_{-j} \) denotes a vector with the \( j \)-th component \( v_j \) removed. The notation of h-functions is introduced for convenience. For more details see Dissmann et al. (2013).

Value

- **loglik**
  The calculated log-likelihood value of the R-vine copula model.

- **V**
  The stored transformations (h-functions and log-likelihoods of each pair-copula) which may be used for posterior updates (three matrices: direct, indirect and value).

Author(s)

Ulf Schepsmeier, Jeffrey Dissmann, Jakob Stoeber
References


See Also

BiCopHfunc(), RVineMatrix(), RVineMLE(), RVineAIC(), RVineBIC()

Examples

# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4,
           0, 2, 3, 4, 1,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)

# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 3,
           0, 0, 0, 0, 0)
family <- matrix(family, 5, 5)

# define R-vine pair-copula parameter matrix
par <- c(0, 0.2, 0.9, 1.5, 3.9,
        0, 0, 1.1, 1.6, 0.9,
        0, 0, 0, 1.9, 0.5,
        0, 0, 0, 0, 4.8,
        0, 0, 0, 0, 0)
par <- matrix(par, 5, 5)

# define second R-vine pair-copula parameter matrix
par2 <- matrix(0, 5, 5)

# define RVineMatrix object
RVM <- RVineMatrix(Matrix = Matrix, family = family,
                    par = par, par2 = par2,
                    names = c("V1", "V2", "V3", "V4", "V5"))

# simulate a sample of size 300 from the R-vine copula model
set.seed(123)
simdata <- RVineSim(300, RVM)

# compute the log-likelihood
ll <- RVineLogLik(simdata, RVM, separate = FALSE)
ll$loglik
# compute the pointwise log-likelihoods
ll <- RVineLogLik(simdata, RVM, separate = TRUE)
ll$loglik

RVineMatrix

R-Vine Copula Model in Matrix Notation

Description

This function creates an RVineMatrix() object which encodes an R-vine copula model. It contains the matrix identifying the R-vine tree structure, the matrix identifying the copula families utilized and two matrices for corresponding parameter values.

Usage

RVineMatrix(
    Matrix,
    family = array(0, dim = dim(Matrix)),
    par = array(NA, dim = dim(Matrix)),
    par2 = array(NA, dim = dim(Matrix)),
    names = NULL,
    check.pars = TRUE
)

Arguments

Matrix

Lower (or upper) triangular d x d matrix that defines the R-vine tree structure.

family

Lower (or upper) triangular d x d matrix with zero diagonal entries that assigns the pair-copula families to each (conditional) pair defined by Matrix (default: family = array(0, dim = dim(Matrix))). The bivariate copula families are defined as follows:

0 = independence copula  
1 = Gaussian copula  
2 = Student t copula (t-copula)  
3 = Clayton copula  
4 = Gumbel copula  
5 = Frank copula  
6 = Joe copula  
7 = BB1 copula  
8 = BB6 copula  
9 = BB7 copula  
10 = BB8 copula  
13 = rotated Clayton copula (180 degrees; survival Clayton”)  
14 = rotated Gumbel copula (180 degrees; survival Gumbel”)  
16 = rotated Joe copula (180 degrees; survival Joe”)  
17 = rotated BB1 copula (180 degrees; survival BB1”)
18 = rotated BB6 copula (180 degrees; survival BB6’)
19 = rotated BB7 copula (180 degrees; survival BB7’)
20 = rotated BB8 copula (180 degrees; “survival BB8”)
23 = rotated Clayton copula (90 degrees)
’24’ = rotated Gumbel copula (90 degrees)
’26’ = rotated Joe copula (90 degrees)
’27’ = rotated BB1 copula (90 degrees)
’28’ = rotated BB6 copula (90 degrees)
’29’ = rotated BB7 copula (90 degrees)
’30’ = rotated BB8 copula (90 degrees)
’33’ = rotated Clayton copula (270 degrees)
’34’ = rotated Gumbel copula (270 degrees)
’36’ = rotated Joe copula (270 degrees)
’37’ = rotated BB1 copula (270 degrees)
’38’ = rotated BB6 copula (270 degrees)
’39’ = rotated BB7 copula (270 degrees)
’40’ = rotated BB8 copula (270 degrees)
’104’ = Tawn type 1 copula
’114’ = rotated Tawn type 1 copula (180 degrees)
’124’ = rotated Tawn type 1 copula (90 degrees)
’134’ = rotated Tawn type 1 copula (270 degrees)
’204’ = Tawn type 2 copula
’214’ = rotated Tawn type 2 copula (180 degrees)
’224’ = rotated Tawn type 2 copula (90 degrees)
’234’ = rotated Tawn type 2 copula (270 degrees)

par
Lower (or upper) triangular d x d matrix with zero diagonal entries that assigns
the (first) pair-copula parameter to each (conditional) pair defined by Matrix
(default: par = array(NA, dim = dim(Matrix))).

par2
Lower (or upper) triangular d x d matrix with zero diagonal entries that assigns
the second parameter for pair-copula families with two parameters to each (condi-
tional) pair defined by Matrix (default: par2 = array(NA, dim = dim(Matrix))).

names
A vector of names for the d variables; default: names = NULL.

check.pars
logical; default is TRUE; if FALSE, checks for family/parameter-consistency are
omitted (should only be used with care).

Value
An object of class RVineMatrix(), i.e., a list with the following components:

Matrix
R-vine tree structure matrix.

family
pair-copula family matrix with values as above.

par
pair-copula parameter matrix.

par2
second pair-copula parameter matrix with parameters necessary for pair-copula
families with two parameters.

names
variable names (defaults to V1, V2, ...).
RVineMatrix

MaxMat, CondDistr

additional matrices required internally for evaluating the density etc.,

type the type of the vine copula structure; possible types are:

• "C-vine": all trees consist of a star,
• "D-vine": all trees consist of a path,
• "R-vine": all structures that are neither a C- nor D-vine,

tau Kendall’s tau matrix,
taildep matrices of lower and upper tail dependence coefficients,
beta Blomqvist’s beta matrix.

Objects of this class are also returned by the RVineSeqEst(), RVineCopSelect(), and RVineStructureSelect() functions. In this case, further information about the fit is added.

Note

For a comprehensive summary of the vine copula model, use summary(object); to see all its contents, use str(object).

The RVineMatrix() function automatically checks if the given matrix is a valid R-vine matrix (see RVineMatrixCheck()).

Although the function allows upper triangular matrices as its input, it will always store them as lower triangular matrices.

Author(s)

Jeffrey Dissmann, Thomas Nagler

References


See Also

RVineMatrixCheck(), RVineSeqEst(), RVineCopSelect(), RVineStructureSelect(), RVineSim(), C2RVine(), D2RVine()

Examples

# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4,
           0, 2, 3, 4, 1,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)

# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4,
RVineMatrixCheck

RVineMatrixCheck

R-Vine Matrix Check

Description

The given matrix is tested to be a valid R-vine matrix.

Usage

RVineMatrixCheck(M)

Arguments

M A d x d vine matrix.
RVineMatrixCheck

Value

code 1 for OK;
-4 matrix is neither lower nor upper triangular;
-3 diagonal can not be put in order d:1;
-2 for not permutation of j:d in column d-j;
-1 if cannot find proper binary array from array in natural order.

Note

The matrix M do not have to be given in natural order or the diagonal in order d:1. The test checks if it can be done in order to be a valid R-vine matrix.
If a function in this package needs the natural order the RVineMatrix object is automatically "normalized".
The function RVineMatrix() automatically checks if the given R-vine matrix is valid.

Author(s)

Harry Joe

References


See Also

RVineMatrix()

Examples

A1 <- matrix(c(6, 0, 0, 0, 0, 0, 5, 5, 0, 0, 0, 0, 3, 4, 4, 0, 0, 0, 4, 3, 3, 3, 0, 0, 1, 1, 2, 2, 2, 0, 2, 2, 1, 1, 1, 1, 6, 6, byrow = TRUE)
b1 <- RVineMatrixCheck(A1)
print(b1)
# improper vine matrix, code=-1
A2 <- matrix(c(6, 0, 0, 0, 0, 0, 5, 5, 0, 0, 0, 0, 4, 4, 4, 0, 0, 0, 1, 3, 3, 3, 0, 0, 3, 1, 2, 2, 2, 0, 2, 2, 1, 1, 1, 1, 6, 6, byrow = TRUE)
b2 <- RVineMatrixCheck(A2)
print(b2)
# improper vine matrix, code=-2
A3 <- matrix(c(6, 0, 0, 0, 0, 0,
RVineMatrixNormalize

3, 5, 0, 0, 0, 0,
3, 4, 4, 0, 0, 0,
4, 3, 3, 0, 0, 0,
1, 1, 2, 2, 2, 0,
2, 2, 1, 1, 1, 1), 6, 6, byrow = TRUE)
b3 <- RVineMatrixCheck(A3)
print(b3)

RVineMatrixNormalize

Normalization of R-Vine Matrix

Description
An RVineMatrix() is permuted to achieve a natural ordering (i.e. diag(RVM$Matrix) == d:1)

Usage
RVineMatrixNormalize(RVM)

Arguments

RVM RVineMatrix() defining the R-vine structure

Value

RVM An RVineMatrix() in natural ordering with entries in RVM$names keeping track
of the reordering.

Examples

Matrix <- matrix(c(5, 2, 3, 1, 4,
                   0, 2, 3, 4, 1,
                   0, 0, 3, 4, 1,
                   0, 0, 0, 4, 1,
                   0, 0, 0, 0, 1), 5, 5)
family <- matrix(1,5,5)
par <- matrix(c(0, 0.2, 0.9, 0.5, 0.8,
               0, 0, 0.1, 0.6, 0.9,
               0, 0, 0, 0.7, 0.5,
               0, 0, 0, 0, 0.8,
               0, 0, 0, 0, 0), 5, 5)

# define RVineMatrix object
RVM <- RVineMatrix(Matrix, family, par)

# normalise the RVine
RVineMatrixNormalize(RVM)
RVineMatrixSample  Random sampling of R-Vine matrices

Description
Sample R-Vine matrices based on the algorithm of Joe et al. (2011).

Usage
RVineMatrixSample(d, size = 1, naturalOrder = FALSE)

Arguments
d  Dimension of the R-Vine matrices.
size  Number of matrices to sample.
naturalOrder  Should the matrices be in the natural order (default: naturalOrder = FALSE).

Value
A list of length size with each element containing one R-Vine matrix.

Note
For some reason, our implementation of Joe et al.’s algorithm always returns a star in the first tree. To fix this, we sample a vine matrix of dimension d + 1 and remove the first tree afterwards.

Author(s)
Thibault Vatter

References

See Also
RVineMatrix(), RVineMatrixCheck()

Examples
# Matrix and sample sizes
d <- 10
size <- 5

# Sample R-vine matrices
RVM <- RVineMatrixSample(d, size)
RVineMLE

Maximum Likelihood Estimation of an R-Vine Copula Model

Description

This function calculates the maximum likelihood estimate (MLE) of the R-vine copula model parameters using sequential estimates as initial values (if not provided).

Usage

RVineMLE(
  data,
  RVM,
  start = RVM$par,
  start2 = RVM$par2,
  maxit = 200,
  max.df = 30,
  max.BB = list(BB1 = c(5, 6), BB6 = c(6, 6), BB7 = c(5, 6), BB8 = c(6, 1)),
  grad = FALSE,
  hessian = FALSE,
  se = FALSE,
  ...
)

Arguments

data An N x d data matrix (with uniform margins).
RVM An RVineMatrix() object including the structure and the pair-copula families and parameters (if known).
start Lower triangular d x d matrix with zero diagonal entries with starting values for the pair-copula parameters (optional; otherwise they are calculated via RVineSeqEst(); default: start = RVM$par).
start2 Lower triangular d x d matrix with zero diagonal entries with starting values for the second parameters of pair-copula families with two parameters (optional; otherwise they are calculated via RVineSeqEst(); default: start2 = RVM$par2).
maxit The maximum number of iteration steps (optional; default: maxit = 200).
max.df Numeric; upper bound for the estimation of the degrees of freedom parameter of the t-copula (default: max.df = 30; for more details see BiCopEst()).
max.BB  List; upper bounds for the estimation of the two parameters (in absolute values) of the BB1, BB6, BB7 and BB8 copulas
(default: max.BB = list(BB1=c(5,6),BB6=c(6,6),BB7=c(5,6),BB8=c(6,1))).

grad  If RVM$family only contains one parameter copula families or the t-copula the analytical gradient can be used for maximization of the log-likelihood (see RVineGrad(); default: grad = FALSE).

hessian  Logical; whether the Hessian matrix of parameter estimates is estimated (default: hessian = FALSE). Note that this is not the Hessian Matrix calculated via RVineHessian() but via finite differences.

se  Logical; whether standard errors of parameter estimates are estimated on the basis of the Hessian matrix (see above; default: se = FALSE).

Value

**RVM**  RVineMatrix() object with the calculated parameters stored in RVM$par and RVM$par2. Additional information about the fit is added (e.g., log-likelihood, AIC, BIC).

**value**  Optimized log-likelihood value corresponding to the estimated pair-copula parameters.

**convergence**  An integer code indicating either successful convergence (convergence = 0) or an error:
1 = the iteration limit maxit has been reached
51 = a warning from the "L-BFGS-B" method; see component message for further details
52 = an error from the "L-BFGS-B" method; see component message for further details

**message**  A character string giving any additional information returned by optim(), or NULL.

**counts**  A two-element integer vector giving the number of calls to fn and gr respectively. This excludes those calls needed to compute the Hessian, if requested, and any calls to fn to compute a finite-difference approximation to the gradient.

**hessian**  If hessian = TRUE, the Hessian matrix is returned. Its calculation is on the basis of finite differences (output of optim).

Note

RVineMLE uses the L-BFGS-B method for optimization.
If the analytical gradient is used for maximization, computations may be up to 10 times faster than using finite differences.

Author(s)

Ulf Schepsmeier, Jeffrey Dissmann
References


See Also

RVineSeqEst(), RVineStructureSelect(), RVineMatrix(), RVineGrad(), RVineHessian()

Examples

# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4, 0, 2, 3, 4, 1, 0, 0, 3, 4, 1, 0, 0, 0, 4, 1, 0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)

# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4, 0, 0, 3, 4, 1, 0, 0, 0, 4, 1, 0, 0, 0, 3, 0, 0, 0, 0, 0)
family <- matrix(family, 5, 5)

# define R-vine pair-copula parameter matrix
par <- c(0, 0.2, 0.9, 1.5, 3.9, 0, 0, 1.1, 1.6, 0.9, 0, 0, 0, 1.9, 0.5, 0, 0, 0, 4.8, 0, 0, 0, 0, 0)
par <- matrix(par, 5, 5)

# define second R-vine pair-copula parameter matrix
par2 <- matrix(0, 5, 5)

# define RVineMatrix object
RVM <- RVineMatrix(Matrix = Matrix, family = family,
par = par, par2 = par2,
names = c("V1", "V2", "V3", "V4", "V5"))

# simulate a sample of size 300 from the R-vine copula model
set.seed(123)
simdata <- RVineSim(300, RVM)

# compute the MLE
mle <- RVineMLE(simdata, RVM, grad = TRUE, trace = 0)

# compare parameters
round(mle$RVM$par - RVM$par, 2)

---

RVinePar2Beta  Blomqvist’s Beta Values of an R-Vine Copula Model

Description

This function computes the values of Blomqvist’s beta corresponding to the parameters of an R-vine copula model.

Usage

RVinePar2Beta(RVM, check.pars = TRUE)

Arguments

RVM An RVineMatrix() object.
   Note that the Student’s t-copula is not allowed since the CDF of the t-copula is not implemented (see BiCopCDF() and BiCopPar2Beta()).
check.pars logical; default is TRUE; if FALSE, checks for family/parameter-consistency are omitted (should only be used with care).

Value

Matrix with the same structure as the family and parameter matrices of the RVineMatrix() object RVM where the entries are values of Blomqvist’s beta corresponding to the families and parameters of the R-vine copula model given by RVM.

Author(s)

Ulf Schepsmeier

See Also

RVineMatrix(), BiCopPar2Beta()

Examples

# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4,
            0, 2, 3, 4, 1,
            0, 0, 3, 4, 1,
            0, 0, 0, 4, 1,
            0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)
# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 3,
           0, 0, 0, 0, 0)
family <- matrix(family, 5, 5)

# define R-vine pair-copula parameter matrix
par <- c(0, 0.2, 0.9, 1.5, 3.9,
        0, 0.1, 1.6, 0.9,
        0, 0, 1.9, 0.5,
        0, 0, 0, 4.8,
        0, 0, 0, 0, 0)
par <- matrix(par, 5, 5)

# define second R-vine pair-copula parameter matrix
par2 <- matrix(0, 5, 5)

# define RVineMatrix object
RVM <- RVineMatrix(Matrix = Matrix, family = family,
par = par, par2 = par2,
names = c("V1", "V2", "V3", "V4", "V5"))

# compute the Blomqvist's beta values
BlomBeta <- RVinePar2Beta(RVM)

RVinePar2Tau

Kendall’s Tau Values of an R-Vine Copula Model

Description
This function computes the values of Kendall’s tau corresponding to the parameters of an R-vine copula model.

Usage
RVinePar2Tau(RVM, check.pars = TRUE)

Arguments

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>RVM</td>
<td>An RVineMatrix() object.</td>
</tr>
<tr>
<td>check.pars</td>
<td>logical; default is TRUE; if FALSE, checks for family/parameter-consistency are omitted (should only be used with care).</td>
</tr>
</tbody>
</table>
Value

Matrix with the same structure as the family and parameter matrices of the `RVineMatrix()` object `RVM` where the entries are values of Kendall’s tau corresponding to the families and parameters of the R-vine copula model given by `RVM`.

Author(s)

Jeffrey Dissmann

See Also

`RVineMatrix()`, `BiCopPar2Tau()`

Examples

```r
# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4,
           0, 2, 3, 4, 1,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)

# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4,
            0, 0, 3, 4, 1,
            0, 0, 0, 4, 1,
            0, 0, 0, 0, 3,
            0, 0, 0, 0, 0)
family <- matrix(family, 5, 5)

# define R-vine pair-copula parameter matrix
par <- c(0, 0.2, 0.9, 1.5, 3.9,
        0, 1.1, 1.6, 0.9,
        0, 0, 1.9, 0.5,
        0, 0, 0, 4.8,
        0, 0, 0, 0)
par <- matrix(par, 5, 5)

# define second R-vine pair-copula parameter matrix
par2 <- matrix(0, 5, 5)

# define RVineMatrix object
RVM <- RVineMatrix(Matrix = Matrix, family = family,
                    par = par, par2 = par2,
                    names = c("V1", "V2", "V3", "V4", "V5"))

# compute the Kendall's tau values
tau <- RVinePar2Tau(RVM)
```
Description
This function calculates the probability density function of a d-dimensional R-vine copula.

Usage
RVinePDF(newdata, RVM, verbose = TRUE)

Arguments
newdata  An N x d data matrix that specifies where the density shall be evaluated.
RVM      An RVineMatrix() object including the structure and the pair-copula families and parameters.
verbose  In case something goes wrong, additional output will be plotted.

Details
The density of a $d$-dimensional R-vine copula with $d-1$ trees and corresponding edge sets $E_1, \ldots, E_{d-1}$ is given by

$$
\prod_{\ell=1}^{d-1} \prod_{e \in E_{\ell}} c_{j(e),k(e)|D(e)}(F(u_{j(e)}|u_{D(e)}), F(u_{k(e)}|u_{D(e)})|\theta_{j(e),k(e)|D(e)}),
$$

where $u = (u_1, \ldots, u_d)' \in [0,1]^d$. Further $c_{j(e),k(e)|D(e)}$ denotes a bivariate copula density associated to an edge $e$ and with parameter(s) $\theta_{j(e),k(e)|D(e)}$. Conditional distribution functions such as $F(u_{j(e)}|u_{D(e)})$ are obtained recursively using the relationship

$$
h(u|v, \theta) := F(u|v) = dC_{uv_j|v_{-j}}(F(u|v_{-j}), F(u_j|v_{-j}))/dF(v_j|v_{-j}),
$$

where $C_{uv_j|v_{-j}}$ is a bivariate copula distribution function with parameter(s) $\theta$ and $v_{-j}$ denotes a vector with the $j$-th component $v_j$ removed. The notation of h-functions is introduced for convenience. For more details see Dissmann et al. (2013).

The function is actually just a wrapper to RVineLogLik().

Author(s)
Thomas Nagler

References
RVinePIT

See Also

BiCopHfunc(), RVineMatrix(), RVineMLE(), RVineAIC(), RVineBIC()

Examples

# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4,
          0, 2, 3, 4, 1,
          0, 0, 3, 4, 1,
          0, 0, 0, 4, 1,
          0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)

# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 3,
           0, 0, 0, 0, 0)
family <- matrix(family, 5, 5)

# define R-vine pair-copula parameter matrix
par <- c(0, 0.2, 0.9, 1.5, 3.9,
        0, 0, 1.1, 1.6, 0.9,
        0, 0, 1.9, 0.5,
        0, 0, 0, 4.8,
        0, 0, 0, 0)
par <- matrix(par, 5, 5)

# define second R-vine pair-copula parameter matrix
par2 <- matrix(0, 5, 5)

# define RVineMatrix object
RVM <- RVineMatrix(Matrix = Matrix, family = family,
                   par = par, par2 = par2,
                   names = c("V1", "V2", "V3", "V4", "V5"))

# compute the density at (0.1, 0.2, 0.3, 0.4, 0.5)
RVinePDF(c(0.1, 0.2, 0.3, 0.4, 0.5), RVM)

RVinePIT

Probability Integral Transformation for R-Vine Copula Models

Description

This function applies the probability integral transformation (PIT) for R-vine copula models to given copula data.
Usage

RVinePIT(data, RVM)

Arguments

data          An N x d data matrix (with uniform margins).
RVM           RVineMatrix() objects of the R-vine model.

Details

The multivariate probability integral transformation (PIT) of Rosenblatt (1952) transforms the copula data \( u = (u_1, \ldots, u_d) \) with a given multivariate copula \( C \) into independent data in \([0, 1]^d\), where \( d \) is the dimension of the data set.

Let \( u = (u_1, \ldots, u_d) \) denote copula data of dimension \( d \). Further let \( C \) be the joint cdf of \( u = (u_1, \ldots, u_d) \). Then Rosenblatt’s transformation of \( u \), denoted as \( y = (y_1, \ldots, y_d) \), is defined as

\[
y_1 := u_1, \quad y_2 := C(u_2|u_1), \ldots, y_d := C(u_d|u_1, \ldots, u_{d-1}),
\]

where \( C(u_k|u_1, \ldots, u_{k-1}) \) is the conditional copula of \( U_k \) given \( U_1 = u_1, \ldots, U_{k-1} = u_{k-1}, k = 2, \ldots, d \). The data vector \( y = (y_1, \ldots, y_d) \) is now i.i.d. with \( y_i \sim U[0, 1] \). The algorithm for the R-vine PIT is given in the appendix of Schepsmeier (2015).

Value

An N x d matrix of PIT data from the given R-vine copula model.

Author(s)

Ulf Schepsmeier

References


See Also

RVineGofTest()

Examples

# load data set
data(daxreturns)

# select the R-vine structure, families and parameters
RVM <- RVineStructureSelect(daxreturns[,1:3], c(1:6))
# PIT data
pit <- RVinePIT(daxreturns[,1:3], RVM)

par(mfrow = c(1,2))
plot(daxreturns[,1], daxreturns[,2]) # correlated data
plot(pit[,1], pit[,2]) # i.i.d. data

cor(pit, method = "kendall")

---

RVineSeqEst

Sequential Estimation of an R-Vine Copula Model

Description

This function sequentially estimates the pair-copula parameters of a d-dimensional R-vine copula model as specified by the corresponding RVineMatrix() object.

Usage

RVineSeqEst(
  data,
  RVM,
  method = "mle",
  se = FALSE,
  max.df = 30,
  max.BB = list(BB1 = c(5, 6), BB6 = c(6, 6), BB7 = c(5, 6), BB8 = c(6, 1)),
  progress = FALSE,
  weights = NA,
  cores = 1
)

Arguments

data An N x d data matrix (with uniform margins).
RVM An RVineMatrix() object including the structure, the pair-copula families and the pair-copula parameters (if they are known).
method indicates the estimation method: either maximum likelihood estimation (method = "mle"; default) or inversion of Kendall’s tau (method = "itau"). For method = "itau" only one parameter families and the Student t copula can be used (family = 1, 2, 3, 4, 5, 6, 13, 14, 16, 23, 24, 26, 33, 34 or 36). For the t-copula, par2 is found by a crude profile likelihood optimization over the interval (2, 10].
se Logical; whether standard errors are estimated (default: se = FALSE).
max.df Numeric; upper bound for the estimation of the degrees of freedom parameter of the t-copula (default: max.df = 30; for more details see BiCopEst()).
max.BB  List; upper bounds for the estimation of the two parameters (in absolute values) of the BB1, BB6, BB7 and BB8 copulas (default: max.BB = list(BB1=c(5,6),BB6=c(6,6),BB7=c(5,6),BB8=c(6,1))).

progress  Logical; whether the pairwise estimation progress is printed (default: progress = FALSE).

weights  Numerical; weights for each observation (optional).

cores  integer; if cores > 1, estimation will be parallelized within each tree (using foreach::foreach()). However, the overhead caused by parallelization is likely to make the function run slower unless sample size is really large and method = "itau".

Details
The pair-copula parameter estimation is performed tree-wise, i.e., for each R-vine tree the results from the previous tree(s) are used to calculate the new copula parameters using BiCopEst().

Value
An RVineMatrix() object with the sequentially estimated parameters stored in RVM$par and RVM$par2. The object is augmented by the following information about the fit:

se, se2  standard errors for the parameter estimates (if se = TRUE); note that these are only approximate since they do not account for the sequential nature of the estimation,
nobs  number of observations,
logLik, pair.logLik  log likelihood (overall and pairwise)
AIC, pair.AIC  Akaike’s Information Criterion (overall and pairwise),
BIC, pair.BIC  Bayesian’s Information Criterion (overall and pairwise),
emptau  matrix of empirical values of Kendall’s tau,
p.value.indeptest  matrix of p-values of the independence test.

Note
For a comprehensive summary of the fitted model, use summary(object); to see all its contents, use str(object).

Author(s)
Ulf Schepsmeier, Jeffrey Dissmann, Thomas Nagler

See Also
RVineMatrix(), BiCop(), BiCopEst(), plot.RVineMatrix(), contour.RVineMatrix()
# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 4, 1,
           0, 2, 3, 4, 1,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)

# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4,
            0, 0, 3, 4, 1,
            0, 0, 0, 4, 1,
            0, 0, 0, 0, 3,
            0, 0, 0, 0, 0)
family <- matrix(family, 5, 5)

# define R-vine pair-copula parameter matrix
par <- c(0, 0.2, 0.9, 1.5, 3.9,
        0, 0, 1.1, 1.6, 0.9,
        0, 0, 0, 1.9, 0.5,
        0, 0, 0, 0, 4.8,
        0, 0, 0, 0, 0)
par <- matrix(par, 5, 5)

# define second R-vine pair-copula parameter matrix
par2 <- matrix(0, 5, 5)

# define RVineMatrix object
RVM <- RVineMatrix(Matrix = Matrix, family = family,
                    par = par, par2 = par2,
                    names = c("V1", "V2", "V3", "V4", "V5"))

# simulate a sample of size 300 from the R-vine copula model
set.seed(123)
simdata <- RVineSim(300, RVM)

# sequential estimation
summary(RVineSeqEst(simdata, RVM, method = "itau", se = TRUE))
summary(RVineSeqEst(simdata, RVM, method = "mle", se = TRUE))
Usage

RVineSim(N, RVM, U = NULL)

Arguments

N  Number of d-dimensional observations to simulate.
RVM An RVineMatrix() object containing the information of the R-vine copula model. Optionally, a length-N list of RVineMatrix() objects sharing the same structure, but possibly different family/parameter can be supplied.
U  If not NULL(), an (N,d)-matrix of U[0,1] random variates to be transformed to the copula sample.

Value

An N x d matrix of data simulated from the given R-vine copula model.

Author(s)

Jeffrey Dissmann

References


See Also

RVineMatrix(), BiCopSim()

Examples

# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4,
            0, 2, 3, 4, 1,
            0, 0, 3, 4, 1,
            0, 0, 0, 4, 1,
            0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)

# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 3,
           0, 0, 0, 0, 0)
family <- matrix(family, 5, 5)

# define R-vine pair-copula parameter matrix
par <- c(0, 0.2, 0.9, 1.5, 3.9,
         0, 0, 1.1, 1.6, 0.9,
         0, 0, 0, 1.9, 0.5,
         0, 0, 0, 0, 4.8,
         0, 0, 0, 0, 0)
par <- matrix(par, 5, 5)

# define second R-vine pair-copula parameter matrix
par2 <- matrix(0, 5, 5)

# define RVineMatrix object
RVM <- RVineMatrix(Matrix = Matrix, family = family,
                    par = par, par2 = par2,
                    names = c("V1", "V2", "V3", "V4", "V5"))

# simulate a sample of size 300 from the R-vine copula model
set.seed(123)
simdata <- RVineSim(300, RVM)

---

**RVineStdError**

**Standard Errors of an R-Vine Copula Model**

**Description**

This function calculates the standard errors of a d-dimensional R-vine copula model given the Hessian matrix.

**Usage**

RVineStdError(hessian, RVM)

**Arguments**

- **hessian**: The Hessian matrix of the given R-vine.
- **RVM**: An **RVineMatrix()** object including the structure, the pair-copula families, and the parameters.

**Value**

- **se**: The calculated standard errors for the first parameter matrix. The entries are ordered with respect to the ordering of the RVM$par matrix.
- **se2**: The calculated standard errors for the second parameter matrix.

**Note**

The negative Hessian matrix should be positive semidefinite. Otherwise NAs will be returned in some entries and the non-NA entries may be wrong. If the negative Hessian matrix is negative definite, then one could try a near positive matrix. The package Matrix provides a function called nearPD to estimate a matrix which is positive definite and close to the given matrix.
Author(s)
Ulf Schepsmeier, Jakob Stoeber

References

See Also
BiCopDeriv(), BiCopDeriv2(), BiCopHfuncDeriv(), BiCopHfuncDeriv2(), RVineMatrix(), RVineHessian(), RVineGrad()

Examples

# define 5-dimensional R-vine tree structure matrix
Matrix <- c(5, 2, 3, 1, 4,
           0, 2, 3, 4, 1,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 1)
Matrix <- matrix(Matrix, 5, 5)

# define R-vine pair-copula family matrix
family <- c(0, 1, 3, 4, 4,
           0, 0, 3, 4, 1,
           0, 0, 0, 4, 1,
           0, 0, 0, 0, 3,
           0, 0, 0, 0, 0)
family <- matrix(family, 5, 5)

# define R-vine pair-copula parameter matrix
par <- c(0, 0.2, 0.9, 1.5, 3.9,
        0, 1.1, 1.6, 0.9,
        0, 0, 1.9, 0.5,
        0, 0, 0, 4.8,
        0, 0, 0, 0)
par <- matrix(par, 5, 5)

# define second R-vine pair-copula parameter matrix
```
par2 <- matrix(0, 5, 5)

# define RVineMatrix object
RVM <- RVineMatrix(Matrix = Matrix, family = family,
                   par = par, par2 = par2,
                   names = c("V1", "V2", "V3", "V4", "V5"))

# simulate a sample of size 300 from the R-vine copula model
set.seed(123)
simdata <- RVineSim(300, RVM)

# compute the Hessian matrix of the first row of the data
out2 <- RVineHessian(simdata, RVM)

# get the standard errors
RVineStdError(out2$hessian, RVM)
```

---

**RVineStructureSelect**  
*Sequential Specification of R- and C-Vine Copula Models*

**Description**

This function fits either an R- or a C-vine copula model to a d-dimensional copula data set. Tree structures are determined and appropriate pair-copula families are selected using `BiCopSelect()` and estimated sequentially (forward selection of trees).

**Usage**

```
RVineStructureSelect(data,  
familyset = NA,  
type = 0,  
selectioncrit = "AIC",  
indeptest = FALSE,  
level = 0.05,  
trunclevel = NA,  
progress = FALSE,  
weights = NA,  
treecrit = "tau",  
rotations = TRUE,  
se = FALSE,  
presel = TRUE,  
method = "mle",  
cores = 1  
)
```
Arguments

- **data**: An N x d data matrix (with uniform margins).
- **familyset**: An integer vector of pair-copula families to select from. The vector has to include at least one pair-copula family that allows for positive and one that allows for negative dependence. Not listed copula families might be included to better handle limit cases. If `familyset = NA` (default), selection among all possible families is performed. Coding of pair-copula families is the same as in `BiCop()`.
- **type**: Type of the vine model to be specified:
  - 0 or "RVine" = R-vine (default)
  - 1 or "CVine" = C-vine

C- and D-vine copula models with pre-specified order can be specified using `CDVineCopSelect` of the package CDVine. Similarly, R-vine copula models with pre-specified tree structure can be specified using `RVineCopSelect()`.
- **selectioncrit**: Character indicating the criterion for pair-copula selection. Possible choices: `selectioncrit = "AIC"` (default), "BIC", or "logLik" (see `BiCopSelect()`).
- **indeptest**: logical; whether a hypothesis test for the independence of \( u_1 \) and \( u_2 \) is performed before bivariate copula selection (default: `indeptest = FALSE`; see `BiCopIndTest()`). The independence copula is chosen for a (conditional) pair if the null hypothesis of independence cannot be rejected.
- **level**: numeric; significance level of the independence test (default: `level = 0.05`).
- **trunclevel**: integer; level of truncation.
- **progress**: logical; whether the tree-wise specification progress is printed (default: `progress = FALSE`).
- **weights**: numeric; weights for each observation (optional).
- **treecrit**: edge weight for Dissman’s structure selection algorithm, see Details.
- **rotations**: If TRUE, all rotations of the families in `familyset` are included.
- **se**: Logical; whether standard errors are estimated (default: `se = FALSE`).
- **presel**: Logical; whether to exclude families before fitting based on symmetry properties of the data. Makes the selection about 30\% (on average), but may yield slightly worse results in few special cases.
- **method**: indicates the estimation method: either maximum likelihood estimation (method = "mle"; default) or inversion of Kendall’s tau (method = "itau"). For method = "itau" only one parameter families and the Student t copula can be used (\( family = 1, 2, 3, 4, 5, 6, 13, 14, 16, 23, 24, 26, 33, 34 \) or 36). For the t-copula, \( \text{par2} \) is found by a crude profile likelihood optimization over the interval (2, 10].
- **cores**: integer; if `cores > 1`, estimation will be parallelized within each tree (using `foreach::foreach()`). Note that parallelization causes substantial overhead and may be slower than single-threaded computation when dimension, sample size, or family set are small or `method = "itau"`.

Details

R-vine trees are selected using maximum spanning trees w.r.t. some edge weights. The most commonly used edge weight is the absolute value of the empirical Kendall’s tau, say \( \hat{\tau}_{ij} \). Then,
the following optimization problem is solved for each tree:

$$\max \sum_{\text{edges } e_{ij} \in \text{spanning tree}} |\hat{\tau}_{ij}|,$$

where a spanning tree is a tree on all nodes. The setting of the first tree selection step is always a complete graph. For subsequent trees, the setting depends on the R-vine construction principles, in particular on the proximity condition.

Some commonly used edge weights are implemented:

- "tau" absolute value of empirical Kendall’s tau.
- "rho" absolute value of empirical Spearman’s rho.
- "AIC" Akaike information (multiplied by -1).
- "BIC" Bayesian information criterion (multiplied by -1).
- "cAIC" corrected Akaike information criterion (multiplied by -1).

If the data contain NAs, the edge weights in "tau" and "rho" are multiplied by the square root of the proportion of complete observations. This penalizes pairs where less observations are used.

The criteria "AIC", "BIC", and "cAIC" require estimation and model selection for all possible pairs. This is computationally expensive and much slower than "tau" or "rho". The user can also specify a custom function to calculate the edge weights. The function has to be of type `function(u1, u2, weights) ...` and must return a numeric value. The weights argument must exist, but does not have to be used. For example, "tau" (without using weights) can be implemented as follows:

```r
function(u1, u2, weights)
abs(cor(u1, u2, method = "kendall", use = "complete.obs"))
```

The root nodes of C-vine trees are determined similarly by identifying the node with strongest dependencies to all other nodes. That is we take the node with maximum column sum in the empirical Kendall’s tau matrix.

Note that a possible way to determine the order of the nodes in the D-vine is to identify a shortest Hamiltonian path in terms of weights $1 - |\hat{\tau}_{ij}|$. This can be established for example using the package TSP. Example code is shown below.

**Value**

An `RVineMatrix()` object with the selected structure (`RVM$Matrix`) and families (`RVM$family`) as well as sequentially estimated parameters stored in `RVM$par` and `RVM$par2`. The object is augmented by the following information about the fit:

- `se`, `se2` standard errors for the parameter estimates; note that these are only approximate since they do not account for the sequential nature of the estimation,
- `nobs` number of observations,
- `logLik`, `pair.logLik` log likelihood (overall and pairwise)
- `AIC`, `pair.AIC` Akaike’s Information Criterion (overall and pairwise),
- `BIC`, `pair.BIC` Bayesian’s Information Criterion (overall and pairwise),
emptau  matrix of empirical values of Kendall’s tau,
p.value.indeptest  matrix of p-values of the independence test.

Note
For a comprehensive summary of the vine copula model, use summary(object); to see all its contents, use str(object).

Author(s)
Jeffrey Dissmann, Eike Brechmann, Ulf Schepsmeier, Thomas Nagler

References

See Also
RVineMatrix(), BiCop(), RVineCopSelect(), plot.RVineMatrix(), contour.RVineMatrix()

Examples

# load data set
data(daxreturns)

# select the R-vine structure, families and parameters
# using only the first 4 variables and the first 250 observations
# we allow for the copula families: Gauss, t, Clayton, Gumbel, Frank and Joe
daxreturns <- daxreturns[1:250, 1:4]
RVM <- RVineStructureSelect(daxreturns, c(1:6), progress = TRUE)

## see the object's content or a summary
str(RVM)
summary(RVM)

## inspect the fitted model using plots
## Not run: plot(RVM)  # tree structure
countour(RVM)  # contour plots of all pair-copulas

## estimate a C-vine copula model with only Clayton, Gumbel and Frank copulas
CVM <- RVineStructureSelect(daxreturns, c(3,4,5), "CVine")

## determine the order of the nodes in a D-vine using the package TSP
library(TSP)
d <- dim(daxreturns)[2]
M <- 1 - abs(TauMatrix(daxreturns))
hamilton <- insert_dummy(TSP(M), label = "cut")
sol <- solve_TSP(hamilton, method = "repetitive_nn")
order <- cut_tour(sol, "cut")
DVM <- D2RVine(order, family = rep(0, d*(d-1)/2), par = rep(0, d*(d-1)/2))
RVineCopSelect(daxreturns, c(1:6), DVM$Matrix)

RVineTreePlot

**Visualization of R-Vine Tree Structure**

**Description**

Function is deprecated since VineCopula 2.0. Use `plot.RVineMatrix()` instead.

**Usage**

RVineTreePlot(
  x,
  tree = "ALL",
  type = 0,
  edge.labels = NULL,
  legend.pos = "bottomleft",
  interactive = FALSE,
  ...
)

**Arguments**

- **x**: RVineMatrix object.
- **tree**: "ALL" or integer vector; specifies which trees are plotted.
- **type**: integer; specifies how to make use of variable names:
  0 = variable names are ignored,
  1 = variable names are used to annotate vertices,
  2 = uses numbers in plot and adds a legend for variable names.
- **edge.labels**: character; either a vector of edge labels or one of the following:
  "family" = pair-copula family abbreviation (see `BiCopName()`),
  "par" = pair-copula parameters,
  "tau" = pair-copula Kendall’s tau (by conversion of parameters)
  "family-par" = pair-copula family and parameters
  "family-tau" = pair-copula family and Kendall’s tau.
- **legend.pos**: the x argument for `graphics::legend()`.
- **interactive**: logical; if TRUE, the user is asked to adjust the positioning of vertices with his mouse.
- **...**: Arguments passed to `network::plot.network()`.
RVineVuongTest

Author(s)
Thomas Nagler

See Also
plot.RVineMatrix()

RVineVuongTest

Vuong Test Comparing Two R-Vine Copula Models

Description
This function performs a Vuong test between two d-dimensional R-vine copula models as specified by their RVineMatrix() objects.

Usage
RVineVuongTest(data, RVM1, RVM2)

Arguments
- data: An N x d data matrix (with uniform margins).
- RVM1, RVM2: RVineMatrix() objects of models 1 and 2.

Details
The likelihood-ratio based test proposed by Vuong (1989) can be used for comparing non-nested models. For this let $c_1$ and $c_2$ be two competing vine copulas in terms of their densities and with estimated parameter sets $\hat{\theta}_1$ and $\hat{\theta}_2$. We then compute the standardized sum, $\nu$, of the log differences of their pointwise likelihoods

$$m_i := \log \left[ \frac{c_1(u_i|\hat{\theta}_1)}{c_2(u_i|\hat{\theta}_2)} \right]$$

for observations $u_i \in [0,1]$, $i = 1, ..., N$, i.e.,

$$\text{statistic} := \nu = \frac{1}{n} \sum_{i=1}^{N} m_i \sqrt{\sum_{i=1}^{N} (m_i - \bar{m})^2}$$

Vuong (1989) shows that $\nu$ is asymptotically standard normal. According to the null-hypothesis

$$H_0 : E[m_i] = 0 \forall i = 1, ..., N,$$

we hence prefer vine model 1 to vine model 2 at level $\alpha$ if

$$\nu > \Phi^{-1} \left( 1 - \frac{\alpha}{2} \right),$$

where $\Phi^{-1}$ denotes the inverse of the standard normal distribution function. If $\nu < -\Phi^{-1} \left( 1 - \frac{\alpha}{2} \right)$ we choose model 2. If, however, $|\nu| \leq \Phi^{-1} \left( 1 - \frac{\alpha}{2} \right)$, no decision among the models is possible.

Like AIC and BIC, the Vuong test statistic may be corrected for the number of parameters used in the models. There are two possible corrections; the Akaike and the Schwarz corrections, which correspond to the penalty terms in the AIC and the BIC, respectively.
Value

statistic, statistic.Akaike, statistic.Schwarz
Test statistics without correction, with Akaike correction and with Schwarz correction.

p.value, p.value.Akaike, p.value.Schwarz
P-values of tests without correction, with Akaike correction and with Schwarz correction.

Author(s)

Jeffrey Dissmann, Eike Brechmann

References


See Also

RVineClarkeTest(), RVineAIC(), RVineBIC()

Examples

# vine structure selection time-consuming (~ 20 sec)
# load data set
data(daxreturns)

# select the R-vine structure, families and parameters
RVM <- RVineStructureSelect(daxreturns[,1:5], c(1:6))

# select the C-vine structure, families and parameters
CVM <- RVineStructureSelect(daxreturns[,1:5], c(1:6), type = "CVine")

# compare the two models based on the data
vuong <- RVineVuongTest(daxreturns[,1:5], RVM, CVM)
vuong$statistic
evuong$statistic.Schwarz
evuong$p.value
evuong$p.value.Schwarz
Description

This function computes the empirical Kendall’s tau using the algorithm by Knight (1966).

Usage

`TauMatrix(data, weights = NA)`

Arguments

data: An N x d data matrix.
weights: Numerical; weights for each observation (optional).

Value

Matrix of the empirical Kendall’s taus.

Author(s)

Ulf Schepsmeier

References


See Also

`BiCopTau2Par()`, `BiCopPar2Tau()`, `BiCopEst()`

Examples

```r
data(daxreturns)
Data <- as.matrix(daxreturns)

# compute the empirical Kendall's taus
TauMatrix(Data)
```
Description

This functionality is deprecated in 'VineCopula'. Use the package 'VC2copula' instead.

Usage

copulaFromFamilyIndex(family, par, par2 = 0)
surClaytonCopula(param = c(1, 1))
r90ClaytonCopula(param = c(1, 1))
r270ClaytonCopula(param = c(1, 1))
surGumbelCopula(param = c(1, 1))
r90GumbelCopula(param = c(1, 1))
r270GumbelCopula(param = c(1, 1))
joeBiCopula(param = c(1, 1))
surJoeBiCopula(param = c(1, 1))
r90JoeBiCopula(param = c(1, 1))
r270JoeBiCopula(param = c(1, 1))
BB1Copula(param = c(1, 1))
surBB1Copula(param = c(1, 1))
r90BB1Copula(param = c(1, 1))
r270BB1Copula(param = c(1, 1))
BB6Copula(param = c(1, 1))
surBB6Copula(param = c(1, 1))
r90BB6Copula(param = c(1, 1))
r270BB6Copula(param = c(1, 1))
BB7Copula(param = c(1, 1))
surBB7Copula(param = c(1, 1))
r90BB7Copula(param = c(1, 1))
r270BB7Copula(param = c(1, 1))
BB8Copula(param = c(1, 1))
surBB8Copula(param = c(1, 1))
r90BB8Copula(param = c(1, 1))
r270BB8Copula(param = c(1, 1))
tawnT1Copula(param = c(1, 1))
surTawnT1Copula(param = c(1, 1))
r90TawnT1Copula(param = c(1, 1))
r270TawnT1Copula(param = c(1, 1))
tawnT2Copula(param = c(1, 1))
surTawnT2Copula(param = c(1, 1))
r90TawnT2Copula(param = c(1, 1))
r270TawnT2Copula(param = c(1, 1))
vineCopula(RVM, type = "CVine")

Arguments

- family 
- par 
- par2 
- param 
- RVM 
- type
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