Package ‘MMDCopula’

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BiCopConfIntMMD

Confidence intervals for the estimated parameter of a bivariate parametric copula using MMD estimation

Description

Confidence intervals for the estimated parameter of a bivariate parametric copula using MMD estimation

Usage

BiCopConfIntMMD(
  x1, x2, family, nResampling = 100,
  subsamplingSize = length(x1),
  corrSubSampling = TRUE,
  level = 0.95,
  ...
)

Arguments

  x1 vector of observations of the first coordinate.
  x2 vector of observations of the second coordinate.
  family parametric family of copulas. Supported families are:
    • 1: Gaussian copulas
    • 3: Clayton copulas
    • 4: Gumbel copulas
    • 5: Frank copulas
    • MO: Marshall-Olkin copulas
  nResampling number of resampling times.
  subsamplingSize size of the subsample. By default it is length(u1), i.e. this corresponds to the nonparametric boostrap.
  corrSubSampling this parameter is only used for subsampling-based confidence intervals. If TRUE, the confidence interval uses the corrected subsample empirical process.
  level the nominal confidence level.
  ... other parameters to be given to BiCopEstMMD or BiCopEst.MO.
Value

a list with the confidence intervals CI.Tau for Kendall’s tau and CI.Par for the corresponding parameter.

References


Examples

data = VineCopula::BiCopSim(N = 50, family = 1, par = 0.3)
result = BiCopConfIntMMD(x1 = data[,1], x2 = data[,2], family = 1, 
nResampling = 2, subsamplingSize = 10, niter = 10)

data_ = VineCopula::BiCopSim(N = 1000, family = 1, par = 0.3)
result_ = BiCopConfIntMMD(x1 = data_[,1], x2 = data_[,2], family = 1)
result_$CI.Tau
result_$CI.Par

BiCopEst.MO

Estimation of Marshall-Olkin copulas

Description

Estimation of Marshall-Olkin copulas

Usage

BiCopEst.MO(
  ul, 
  u2, 
  method, 
  par.start = 0.5, 
  kernel = "gaussian.Phi", 
  gamma = 0.95, 
  alpha = 1, 
  niter = 100, 
  C_eta = 1, 
  ndrawings = 10, 
  naveraging = 1 
)
Arguments

- **u1**: vector of observations of the first coordinate, in \([0, 1]\).
- **u2**: vector of observations of the second coordinate, in \([0, 1]\).
- **method**: a character giving the name of the estimation method, among:
  - **curve**: \(\alpha\) is estimated by inversion of the probability measure of the diagonal \(\{(u, v) : u = v\}\)
  - **itau**: \(\alpha\) is estimated by inversion of Kendall's tau
  - **MMD**: \(\alpha\) is estimated by MMD optimization
- **par.start**: starting parameter of the gradient descent. (only used for method = "MMD")
- **kernel**: the kernel used in the MMD distance (only used for method = "MMD"): it can be a function taking in parameter \((u1, u2, v1, v2, gamma, alpha)\) or a name giving the kernel to use in the list:
  - **gaussian**: Gaussian kernel \(k(x, y) = \exp(-\|\frac{x-y}{\gamma}\|_2^2)\)
  - **exp.12**: \(k(x, y) = \exp(-\|\frac{x-y}{\gamma}\|_2)\)
  - **exp.11**: \(k(x, y) = \exp(-\|\frac{x-y}{\gamma}\|_1)\)
  - **inv.12**: \(k(x, y) = 1/(1 + \|\frac{x-y}{\gamma}\|_2)^\alpha\)
  - **inv.11**: \(k(x, y) = 1/(1 + \|\frac{x-y}{\gamma}\|_1)^\alpha\)

Each of these names can receive the suffix ".Phi", such as "gaussian.Phi" to indicates that the kernel \(k(x, y)\) is replaced by \(k(\Phi^{-1}(x), \Phi^{-1}(y))\) where \(\Phi^{-1}\) denotes the quantile function of the standard Normal distribution.

- **gamma**: parameter \(\gamma\) to be used in the kernel. (only used for method = "MMD")
- **alpha**: parameter \(\alpha\) to be used in the kernel, if any. (only used for method = "MMD")
- **niter**: the stochastic gradient algorithm is composed of two phases: a first "burn-in" phase and a second "averaging" phase. If niter is of size 1, the same number of iterations is used for both phases of the stochastic gradient algorithm. If niter is of size 2, then niter[1] iterations are done for the burn-in phase and niter[2] for the averaging phase. (only used for method = "MMD")
- **C_eta**: a multiplicative constant controlling for the size of the gradient descent step. The step size is then computed as C_eta / sqrt(i_iter) where i_iter is the index of the current iteration of the stochastic gradient algorithm. (only used for method = "MMD")
- **ndrawings**: number of replicas of the stochastic estimate of the gradient drawn at each step. The gradient is computed using the average of these replicas. (only used for method = "MMD")
- **naveraging**: number of full run of the stochastic gradient algorithm that are averaged at the end to give the final estimated parameter. (only used for method = "MMD")

Value

the estimated parameter (alpha) of the Marshall-Olkin copula.
BiCopEstMMD

References

See Also
BiCopSim.MO for the estimation of Marshall-Olkin copulas. BiCopEstMMD for the estimation of other parametric copula families by MMD.

Examples
U <- BiCopSim.MO(n = 1000, alpha = 0.2)
estimatedPar <- BiCopEst.MO(u1 = U[,1], u2 = U[,2], method = "MMD", niter = 1, ndrawings = 1)
estimatedPar <- BiCopEst.MO(u1 = U[,1], u2 = U[,2], method = "MMD")

BiCopEstMMD

Estimation of parametric bivariate copulas using stochastic gradient descent on the MMD criteria

Description
This function uses computes the MMD-estimator of a bivariate copula family. This computation is done through a stochastic gradient algorithm, that is itself computed by the function BiCopGradMMD(). The main arguments are the two vectors of observations, and the copula family. The bidimensional copula families are indexed in the same way as in VineCopula::BiCop() (which computes the MLE estimator).

Usage
BiCopEstMMD(
  u1,
  u2,
  family,
  tau = NULL,
  par = NULL,
  par2 = NULL,
  kernel = "gaussian",
  gamma = 0.23,
  alpha = 1,
  niter = 100,
  C_eta = 1,
  epsilon = 1e-04,
  method = "QMCV",
  quasiRNG = "sobol",
  ndrawings = 10
)


Arguments

u1 vector of observations of the first coordinate, in \([0, 1]\).

u2 vector of observations of the second coordinate, in \([0, 1]\).

family the chosen family of copulas (see the documentation of the class VineCopula::BiCop() for the available families).

tau the copula family can be parametrized by the parameter \(\text{par}\) or by Kendall’s \(\tau\). Here, the user can choose the initial value of tau for the stochastic gradient algorithm. If NULL, a random value is chosen instead.

par if different from NULL, the parameter \(\tau\) is ignored, and the initial parameter must be given here. The initial Kendall’s \(\tau\) is then computed thanks to VineCopula::BiCopPar2Tau().

par2 initial value for the second parameter, if any. (Works only for Student copula).

kernel the kernel used in the MMD distance: it can be a function taking in parameter \((u1, u2, v1, v2, \text{gamma}, \text{alpha})\) or a name giving the kernel to use in the list:

- **gaussian**: Gaussian kernel \(k(x, y) = \exp(-\|\frac{x-y}{\gamma}\|^2)\)
- **exp.12**: \(k(x, y) = \exp(-\|\frac{x-y}{\gamma}\|_2)\)
- **exp.11**: \(k(x, y) = \exp(-\|\frac{x-y}{\gamma}\|_1)\)
- **inv.12**: \(k(x, y) = 1/(1 + \|\frac{x-y}{\gamma}\|^2)^{\alpha}\)
- **inv.11**: \(k(x, y) = 1/(1 + \|\frac{x-y}{\gamma}\|_1)^{\alpha}\)

Each of these names can receive the suffix ".Phi", such as "gaussian.Phi" to indicates that the kernel \(k(x, y)\) is replaced by \(k(\Phi^{-1}(x), \Phi^{-1}(y))\) where \(\Phi^{-1}\) denotes the quantile function of the standard Normal distribution.

gamma parameter \(\gamma\) to be used in the kernel.

alpha parameter \(\alpha\) to be used in the kernel, if any.

niter the stochastic gradient algorithm is composed of two phases: a first "burn-in" phase and a second "averaging" phase. If \(\text{niter}\) is of size 1, the same number of iterations is used for both phases of the stochastic gradient algorithm. If \(\text{niter}\) is of size 2, then \(\text{niter}[1]\) iterations are done for the burn-in phase and \(\text{niter}[2]\) for the averaging phase.

C_\eta a multiplicative constant controlling for the size of the gradient descent step. The step size is then computed as \(C_\eta / \sqrt{i_iter}\) where \(i_iter\) is the index of the current iteration of the stochastic gradient algorithm.

epsilon the differential of VineCopula::BiCopTau2Par() is computed thanks to a finite difference with increment \(\epsilon\).

method the method of computing the stochastic gradient:

- **MC**: classical Monte-Carlo with \(\text{ndrawings}\) replications.
- **QMCV**: usual Monte-Carlo on \(U\) with \(\text{ndrawings}\) replications, quasi Monte-Carlo on \(V\).

quasiRNG a function giving the quasi-random points in \([0, 1]^2\) or a name giving the method to use in the list:

- **sobol**: use of the Sobol sequence implemented in randtoolbox::sobol
BiCopEstMMD

- halton: use of the Halton sequence implemented in randtoolbox::halton
- torus: use of the Torus sequence implemented in randtoolbox::torus

ndrawings number of replicas of the stochastic estimate of the gradient drawn at each step. The gradient is computed using the average of these replicas.

Value

an object of class VineCopula::BiCop() containing the estimated copula.

References


See Also

VineCopula::BiCopEst() for other methods of estimation such as Maximum Likelihood Estimation or Inversion of Kendall's tau. BiCopGradMMD() for the computation of the stochastic gradient. BiCopEst.MO for the estimation of Marshall-Olkin copulas by MMD.

Examples

# Estimation of a bivariate Gaussian copula with correlation 0.5.
dataSampled = VineCopula::BiCopSim(N = 500, family = 1, par = 0.5)
estimator = BiCopEstMMD(u1 = dataSampled[,1], u2 = dataSampled[,2], family = 1, niter=10)
estimator$par

# Estimation of a bivariate Student copula with correlation 0.5 and 5 degrees of freedom
dataSampled = VineCopula::BiCopSim(N = 1000, family = 2, par = 0.5, par2 = 5)
estimator = BiCopEstMMD(u1 = dataSampled[,1], u2 = dataSampled[,2], family = 2)
estimator$par
estimator$par2

# Comparison with maximum likelihood estimation with and without outliers
dataSampled = VineCopula::BiCopSim(N = 500, family = 1, par = 0.5)
estimatorMLE = VineCopula::BiCopEst(u1 = dataSampled[,1], u2 = dataSampled[,2],
family = 1, method = "mle")
estimatorMLE$par
dataSampled[1:10,1] = 0.999
dataSampled[1:10,2] = 0.001
estimatorMLE = VineCopula::BiCopEst(u1 = dataSampled[,1], u2 = dataSampled[,2],
family = 1, method = "mle")
estimatorMLE$par
BiCopGradMMD

Computation of the gradient of the MMD criterion for parametric bivariate copulas models

Description

This function computes a stochastic estimate of the gradient of the MMD criterion for parametric estimation of bidimensional copula family. The main arguments are the two vectors of observations, and the copula family. The family is parametrized as in VineCopula::BiCop(), using the Kendall’s tau instead of the first parameter. This function is used by BiCopEstMMD() to perform parameter estimation via MMD minimization.

Usage

BiCopGradMMD(
  u1,  
u2,  
family,  
tau,  
par = NULL,  
par2 = 0,  
kernel = "gaussian.Phi",  
gamma = 0.95,  
alpha = 1,  
epsilon = 1e-04,  
method = "QMCV",  
quasiRNG = "sobol",  
ndrawings = 10
)

Arguments

  u1  
  vector of observations of the first coordinate, in \([0, 1]\).
  u2  
  vector of observations of the second coordinate, in \([0, 1]\).
  family  
  the chosen family of copulas (see the documentation of the class VineCopula::BiCop() for the available families).
  tau  
  the copula family can be parametrized by the parameter par or by Kendall’s tau. This function assumes a Kendall tau parametrization. Thus, the user can choose the value of Kendall tau at which the stochastic gradient should be computed.
par if different from NULL, the user must instead of tau specify the corresponding parameter par. The value of tau is then ignored.

par2 value for the second parameter, if any. (Works only for Student copula).

kernel the kernel used in the MMD distance: it can be a function taking in parameter \((u_1, u_2, v_1, v_2, \gamma, \alpha)\) or a name giving the kernel to use in the list:

- gaussian: Gaussian kernel \(k(x, y) = \exp(-\frac{\| x-y \|^2}{\gamma})\)
- exp.12: \(k(x, y) = \exp(-\frac{\| x-y \|_2}{\gamma})\)
- exp.11: \(k(x, y) = \exp(-\frac{\| x-y \|_1}{\gamma})\)
- inv.12: \(k(x, y) = \frac{1}{(1 + \frac{\| x-y \|^2}{\gamma})^\alpha}\)
- inv.11: \(k(x, y) = \frac{1}{(1 + \frac{\| x-y \|_1}{\gamma})^\alpha}\)

Each of these names can receive the suffix ".Phi", such as "gaussian.Phi" to indicates that the kernel \(k(x, y)\) is replaced by \(k(\Phi^{-1}(x), \Phi^{-1}(y))\) where \(\Phi^{-1}\) denotes the quantile function of the standard Normal distribution.

gamma parameter \(\gamma\) to be used in the kernel.

alpha parameter \(\alpha\) to be used in the kernel, if any.

epsilon the differential of `VineCopula::BiCopEstMMD()` is computed thanks to a finite difference with increment epsilon.

method the method of computing the stochastic gradient:

- MC: classical Monte-Carlo with ndrawings replications.
- QMCV: usual Monte-Carlo on U with ndrawings replications, quasi Monte-Carlo on V.

quasiRNG a function giving the quasi-random points in \([0, 1]^2\) or a name giving the method to use in the list:

- sobol: use of the Sobol sequence implemented in randtoolbox::sobol
- halton: use of the Halton sequence implemented in randtoolbox::halton
- torus: use of the Torus sequence implemented in randtoolbox::torus

ndrawings number of replicas of the stochastic estimate of the gradient drawn at each step. The gradient is computed using the average of these replicas.

Value the value of the gradient.

References


See Also

`BiCopEstMMD()` for the estimation of parametric bivariate copulas by stochastic gradient descent on the MMD criteria.
Examples

# Simulation from a bivariate Gaussian copula with correlation 0.5.
dataSampled = VineCopula::BiCopSim(N = 500, family = 1, par = 0.5)

# computation of the gradient of the MMD criteria at different points
# Gradient is small at the true parameter
BiCopGradMMD(dataSampled[,1], dataSampled[,2], family = 1, par = 0.5)
# Gradient is negative when below the parameter
BiCopGradMMD(dataSampled[,1], dataSampled[,2], family = 1, par = 0.1)
# and positive when above
BiCopGradMMD(dataSampled[,1], dataSampled[,2], family = 1, par = 0.8)

BiCopParamDistLp

Compute the distance between 2 parametric copulas

Description

This function uses the numerical integration procedure cubature::hcubature() to numerical integrate the distance between the distribution or between the densities of two bivariate copulas.

Usage

BiCopParamDistLp(
  family,
  par,
  par_p,
  par2 = par,
  par2_p = par_p,
  family_p = family,
  p,
  type,
  maxEval = 0
)

Arguments

family family of the first copula.
par first parameter of the first copula.
par_p first parameter of the second copula.
par2 second parameter of the first copula (only useful for two-parameter families of copulas).
par2_p second parameter of the first copula (only useful for two-parameter families of copulas).
family_p family of the second copula.
p determines the $L_p$ distance that is used.
type type of the functions considered. Can be cdf for the distance between the two cumulative distribution functions or pdf for the distance between the two probability density functions.

maxEval maximum number of evaluation of the function be integrated. If 0, then no maximum limit is given.

Value

a list of four items

- distance the value of the distance
- integral the value of the integral, which is the $p$-th power of the distance.
- error the estimated relative error of the integral
- returnCode the integer return code of the C routine called by cubature::hcubature(). This should be 0 if there is no error.

Examples

```r
# Distance between the densities of a Gaussian copula with correlation 0.5 # and a Gaussian copula with correlation 0.2
BiCopParamDistLp(family = 1, par = 0.5, par_p = 0.2, p = 2, type = "cdf", maxEval = 10)

# Distance between the cdf of a Student copula # with correlation 0.5 and 4 degrees of freedom # and a Student copula with the same correlation but 20 degrees of freedom
BiCopParamDistLp(family = 2, par = 0.5, par_p = 0.5, par2 = 5, par2_p = 20, p = 2, type = "pdf", maxEval = 10)

# Distance between the densities of a Gaussian copula with correlation 0.5 # and of a Student copula with correlation 0.5 and 15 degrees of freedom
BiCopParamDistLp(family = 1, par = 0.5, par_p = 0.5, par2_p = 15, family_p = 2, p = 2, type = "pdf", maxEval = 10)
```

---

**BiCopSim.MO**  
*Simulation of Marshall-Olkin copula*

**Description**

This function simulates independent realizations from the Marshall-Olkin copula.

**Usage**

```r
BiCopSim.MO(n, alpha)
```

**Arguments**

- `n` number of samples
- `alpha` parameter of the Marshall-Olkin copula
Value

an $n \times 2$ matrix containing the samples

See Also

BiCopEst.MO for the estimation of Marshall-Olkin copulas.

Examples

# Simulation from a Marshall-Olkin copula with parameter alpha = 0.5
BiCopSim.MO(n = 100, alpha = 0.5)
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