Package ‘vines’

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Type Package

Title Multivariate Dependence Modeling with Vines

Version 1.1.3

Description Implementation of the vine graphical model for building high-dimensional distributions as a factorization of bivariate copulas and marginal density functions. This package provides S4 classes for vines (C-vines and D-vines) and methods for inference, goodness-of-fit tests, density/distribution function evaluation, and simulation.

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URL https://github.com/yasserglez/vines

Depends methods, copula

Imports ADGofTest, cubature, TSP

       vineIter.R vineFit.R vineFitML.R vinePIT.R vineGoF.R

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Methods for the h-functions

Description

The $h$ function represents the conditional distribution function of a bivariate copula and it should be defined for every copula used in a pair-copula construction. It is defined as the partial derivative of the distribution function of the copula w.r.t. the second argument $h(x, v) = F(x|v) = \frac{\partial C(x, v)}{\partial v}$.

Usage

$h(copula, x, v)$

Arguments

copula A bivariate copula object.

x Numeric vector with values in [0, 1].

v Numeric vector with values in [0, 1].

Methods

signature(copula = "copula") Default definition of the $h$ function for a bivariate copula. This method is used if no particular definition is given for a copula. The partial derivative is calculated numerically using the numericDeriv function.

signature(copula = "indepCopula") The $h$ function of the independence copula.

$$h(x, v) = x$$

signature(copula = "normalCopula") The $h$ function of the normal copula.

$$h(x, v; \rho) = \Phi \left( \frac{\Phi^{-1}(x) - \rho \Phi^{-1}(v)}{\sqrt{1 - \rho^2}} \right)$$
signature(copula = "tCopula") The $h$ function of the t copula.

$$h(x, v; \rho, \nu) = t_{\nu+1}^{-1} \left( \frac{t_{\nu}^{-1}(x) - \rho \ t_{\nu}^{-1}(v)}{\sqrt{(1+(t_{\nu}^{-1}(v))^2)(1-\rho^2)}} \right)$$

signature(copula = "claytonCopula") The $h$ function of the Clayton copula.

$$h(x, v; \theta) = v^{-\theta-1}(x^{-\theta} + v^{-\theta} - 1)^{-1-1/\theta}$$

signature(copula = "gumbelCopula") The $h$ function of the Gumbel copula.

$$h(x, v; \theta) = C(x, v; \theta) \frac{1}{v} (-\log v)^{\theta-1} \left( (-\log x)^{\theta} + (-\log v)^{\theta} \right)^{1/\theta-1}$$

signature(copula = "fgmCopula") The $h$ function of the Farlie-Gumbel-Morgenstern copula.

$$h(x, v; \theta) = (1 + \theta (-1 + 2v) (-1 + x)) x$$

signature(copula = "frankCopula") The $h$ function of the Frank copula.

$$h(x, v; \theta) = \frac{e^{-\theta v}}{1 - e^{-\theta} + e^{-\theta v} - 1}$$

signature(copula = "galambosCopula") The $h$ function of the Galambos copula.

$$h(x, v; \theta) = \frac{C(x, v; \theta)}{v} \left( 1 - \left[ 1 + \left( -\log v \right)^{\theta} \right]^{-1-1/\theta} \right)$$

References


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**hinverse-methods**  
*Methods for the Inverse of the $h$-functions*

**Description**

The $h^{-1}$ function represents the inverse of the $h$ function with respect to its first argument. It should be defined for every copula used in a pair-copula construction (or it will be evaluated numerically).

**Usage**

`hinverse(copula, u, v)`
Arguments

- **copula**: A bivariate copula object.
- **u**: Numeric vector with values in [0, 1].
- **v**: Numeric vector with values in [0, 1].

Methods

- **signature(copula = "copula")**: Default definition of the $h^{-1}$ function for a bivariate copula. This method is used if no particular definition is given for a copula. The inverse is calculated numerically using the `uniroot` function.
- **signature(copula = "indepcopula")**: The $h^{-1}$ function of the Independence copula.
  \[ h^{-1}(u, v) = u \]
- **signature(copula = "normalCopula")**: The $h^{-1}$ function of the normal copula.
  \[ h^{-1}(u, v; \rho) = \Phi \left( \Phi^{-1}(u) \sqrt{1 - \rho^2} + \rho \Phi^{-1}(v) \right) \]
- **signature(copula = "tCopula")**: The $h^{-1}$ function of the t copula.
  \[ h^{-1}(u, v; \rho, \nu) = t_{\nu} \left( t_{\nu+1}^{-1}(u) \sqrt{\frac{(\nu + (t_{\nu}^{-1}(v)))^2}{\nu + 1} (1 - \rho^2) + \rho t_{\nu}^{-1}(v)} \right) \]
- **signature(copula = "claytonCopula")**: The $h^{-1}$ function of the Clayton copula.
  \[ h^{-1}(u, v; \theta) = \left( (u v^{\theta+1})^{-\frac{\theta}{\theta+1}} + 1 - v^{-\theta} \right)^{-1/\theta} \]
- **signature(copula = "frankCopula")**: The $h^{-1}$ function of the Frank copula.
  \[ h^{-1}(u, v; \theta) = -\log \left( 1 - \frac{1 - e^{-\theta}}{(u^{-1} - 1)e^{-\theta v} + 1} \right) / \theta \]

References

RVine-classes  

Classes for Regular Vines

Description

Extend the Vine class to represent regular vines.

Slots

See Vine for information about the inherited slots.

Methods

show signature(object = "CVine"): Print a textual representation of the C-vine.

show signature(object = "DVine"): Print a textual representation of the D-vine.

See Also

Vine.

Vine  

Create Vine Objects

Description

Functions to create Vine objects.

Usage

Vine(type, dimension = 2, trees = dimension - 1,  
copulas = matrix(list(indepCopula()),  
dimension - 1, dimension - 1))
CVine(dimension = 2, trees = dimension - 1,  
copulas = matrix(list(indepCopula()),  
dimension - 1, dimension - 1))
DVine(dimension = 2, trees = dimension - 1,  
copulas = matrix(list(indepCopula()),  
dimension - 1, dimension - 1))

Arguments

type        Type of vine. Supported values: "CVine" and "DVine".
dimension   See the documentation of the Vine slot.
trees       See the documentation of the Vine slot.
copulas     See the documentation of the Vine slot.
See Also

Vine, CVine, DVine.

Examples

dimension <- 3
copulas <- matrix(list(normalCopula(0.5),
claytonCopula(2.75),
tCopula(0.75, df = 2),
NULL),
ncol = dimension - 1,
nrow = dimension - 1,
byrow = TRUE)

Vine("DVine", dimension = dimension, trees = dimension - 1,
copulas = copulas)
DVine(dimension = dimension, trees = dimension - 1,
copulas = copulas)

Vine-class

Base Vine Class

Description

Base class of all classes that implement vine models in the package. It is a virtual class, no objects may be created from it.

Slots

type: Object of class "character". Descriptive name of the type of vine: Canonical vine or D-vine.
dimension: Object of class "numeric". Dimension of the vine.
dimensionNames: Object of class "character". Names of the variables of the vine. It is either an empty character vector or a vector with one element for each variable of the vine.
copulas: Object of class "matrix". It contains the copula objects for each copula in the pair-copula decomposition. The indexes of the matrix follow the notation used for the subscripts of $\Theta$ in (Aas et al., 2009).
trees: Object of class "numeric". Number of dependence trees of the vine. It should be an integer between 0 and dimension - 1, including both endpoints. Functions acting on vines assume that copulas in arcs of all trees greater than trees are independence copulas.

Methods

show signature(object = "Vine"): Print a textual representation of the vine.
dimnames signature(x = "Vine"): Retrieve the names of the variables of the vine.
dimnames<- signature(x = "Vine"): Set the names of the variables of the vine.
Vine-distribution

References

See Also
RVine, CVine, DVine.

---

Vine-distribution Vine Distribution Functions

Description
Density evaluation, distribution function evaluation, and random number generation.

Usage
dvine(vine, u)
pvine(vine, u)
rvine(vine, n)

Arguments

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>vine</td>
<td>A Vine object.</td>
</tr>
<tr>
<td>u</td>
<td>Vector of the same dimension of the vine or a matrix with one column for each variable of the vine.</td>
</tr>
<tr>
<td>n</td>
<td>Number of observations.</td>
</tr>
</tbody>
</table>

Details
The implementation of the dvine function for CVine and DVine objects is based on the Algorithms
3 and 4 of (Aas et al. 2009), respectively.

The pvine function is evaluated through the numerical integration of the density function (using the
cubature package). This is a computationally demanding procedure, even for small dimensions.

The implementation of the rvine function for CVine and DVine objects is based on the Algorithms
1 and 2 of (Aas et al. 2009), respectively.

Value
dnorm returns a vector with the evaluation of the density. pnorm returns a vector with the evaluation of
the distribution function. rvine returns a matrix with one column for each variable of the vine and
one row for each observation.
References


Examples

dimension <- 3
copulas <- matrix(list(normalCopula(0.5),
claytonCopula(2.75),
tCopula(0.75, df = 2),
NULL),
ncol = dimension - 1,
nrow = dimension - 1)
vine <- DVine(dimension = dimension, trees = dimension - 1,
copulas = copulas)
dimnames(vine) <- c("A", "B", "C")
data <- rvine(vine, 1)
dvine(vine, data)
pvine(vine, data)

---

**vineFit**

**Vine Inference**

**Description**

Estimate a vine model from multivariate data in the unit hypercube. Data can be pseudo-observations constructed from empirical or parametric marginal cumulative distribution functions.

**Usage**

`vineFit(type, data, method = "ml", ...)`

**Arguments**

- `type` Type of vine. Supported values: "CVine" and "DVine".
- `data` Data matrix of pseudo-observations.
- `method` Inference method. Supported values: "ml" (Maximum Likelihood).
- `...` Additional arguments for the inference method.
Details

The "ml" (Maximum Likelihood) method starts with the sequential estimation procedure described in (Aas et al., 2009) and then executes a numerical maximization of the full log-likelihood of the vine. The sequential procedure is used to determine the family and the initial values of the parameters of each bivariate copula in the decomposition. Additional arguments for this method are:

selectCopula Function provided by the user to select the copulas in the pair-copula construction. This function should return a copula object and expect the following arguments.
   
   - vine Vine object being constructed.
   - j, i Indexes of the copula under selection in the matrix of the copulas slot of the vine.
   - x, y Bivariate sample.

   The default value is function (vine, j, i, x, y) indepCopula() that assigns the independence copula to all the arcs of the vine.

trees Maximum number of dependence trees of the vine. Independence copulas will be used in all the arcs of the following trees. The final number of dependence trees could be smaller because of the use of a truncation method. The default value is ncol(data) - 1.

truncMethod Method used to automatically truncate the vine if enough dependence is captured in a given number of trees. Supported methods are "AIC" and "BIC". See (Brechmann, 2010; Brechmann et al., 2010) for information about these methods. The default value is "" that means no truncation.

optimMethod optim method used in the optimization of the log-likelihood function. If "" is specified the optimization is disabled and the vine calculated using the sequential estimation procedure is returned. The default value is "Nelder-Mead".

optimControl List of control parameters for optim. The default value is list().

Value

A vineFit object or a subclass with specific information about inference method used. The vine slot of this object contains the fitted Vine object.

References


See Also

CVine, DVine, vineFit, vineFitML.
Examples

```r
data <- matrix(runif(5 * 100), ncol = 5, nrow = 100)
colnames(data) <- c("A", "B", "C", "D", "E")

selectCopula <- function (vine, j, i, x, y) {
  data <- cbind(x, y)
  fit <- fitCopula(normalCopula(), data, method = "itau")
  fit@copula
}
fit <- vineFit("DVine", data, method = "ml",
  selectCopula = selectCopula,
  optimMethod = "")
show(fit)
show(fit@vine)
```

vineFit-class

Class for the Results of Vine Inference

Description

Base class of all classes providing information about vine inference. Objects of this class (or subclasses) are created by calling the `vinefit` function.

Slots

- `vine`: Object of class `Vine`. Fitted vine.
- `observations`: Object of class `numeric`. Number of observations in the sample.
- `method`: Object of class `character`. Inference method.

Methods

- `show` signature(object = "vineFit"): Print the result of the vine inference.

See Also

`vineFit, vineFitML`
vineFitML-class

Class for the Results of Vine Inference by Maximum Likelihood

Description

Extends the vineFit class to include information about the Maximum Likelihood inference.

Slots

See vineFit for information about inherited slots.

- optimMethod: Object of class character. optim method.
- optimConv: Object of class numeric. optim convergence code (0 indicates successful completion).
- startParams: Object of class numeric. Vector with the parameters of the copulas in the pair-copula construction calculated using the sequential estimation procedure.
- finalParams: Object of class numeric. Vector with the parameters of the copulas in the pair-copula construction after the maximization of the log-likelihood.

Methods

- show signature(object = "vineFitML"): Print information about the fitted vine.

See Also

vineFit, vineFit, vineParameters.

vineGoF

Vine Goodness-of-fit Tests

Description

Goodness-of-fit tests to verify whether the dependence structure of a sample is appropriately modeled by vine model.

Usage

vineGoF(vine, data, method = "PIT", ...)

Arguments

- vine: A Vine object.
- data: Data matrix of pseudo-observations.
- ... Additional arguments for the goodness-of-fit method.
Details

The "PIT" (Probability Integral Transform) method uses the `vinePIT` function to transform the data into variables which are independent and Uniform(0,1) and then use a hypothesis test to verify whether the resulting variables are independent and Uniform(0,1). The additional parameter `statistic` specifies the test to be applied for this purpose.

`statistic` Statistic used to verify if the transformed variables are independent and Uniform(0,1). The default value is "Breymann" and supported methods are:

"Breymann" Test proposed in the Section 7.1 of (Aas et al., 2009). See (Breymann et al., 2003) for more information.

Value

A `vineGoF` or a subclass with specific information about the goodness-of-fit method used. The `statistic` slot of this object contains the value of the statistic and `pvalue` the p-value.

References


See Also

`vineGoF`, `vinePIT`.

Examples

```r
copula <- normalCopula(c(-0.25, -0.21, 0.34, 0.51, -0.07, -0.18), dispstr = "un", dim = 4)
data <- rCopula(100, copula)

selectCopula <- function (vine, j, i, x, y) {
  data <- cbind(x, y)
  fit <- fitCopula(normalCopula(), data, method = "itau")
  fit@copula
}

normalCVine <- vineFit("CVine", data, method = "ml",
selectCopula = selectCopula,
optimMethod = "]"}@vine

normalDVine <- vineFit("DVine", data, method = "ml",
selectCopula = selectCopula,
optimMethod = "]"}@vine

show(normalCVine)
show(normalDVine)

normalCVineGof <- vineGoF(normalCVine, data, method = "PIT",
statistic = "Breymann")
normalDVineGof <- vineGoF(normalDVine, data, method = "PIT",
```
vineGoF-class

Class for the Results of Vine Goodness-of-fit Tests

Description

Base class of all classes containing information about vine goodness-of-fit tests. Objects of this class (or subclasses) are created by calling the `vineGoF` function.

Slots

- `statistic`: Object of class numeric. Value of the test statistic.
- `pvalue`: Object of class numeric. P-value.

Methods

- `show` signature(object = "vineGoF"): Print the result of the goodness-of-fit test.

See Also

- `vineGoF`.

vineLogLik

Vine Log-likelihood Evaluation

Description

Evaluate the log-likelihood of a Vine.

Usage

`vineLogLik(vine, data)`

Arguments

- `vine`: A Vine object.
- `data`: Data matrix of pseudo-observations.
Examples

```r
dimension <- 3
copulas <- matrix(list(normalCopula(0.5),
                          claytonCopula(2.75),
                          NULL, NULL),
                  ncol = dimension - 1,
                  nrow = dimension - 1,
                  byrow = TRUE)
vine <- DVine(dimension = dimension, trees = 1,
              copulas = copulas)
data <- matrix(runif(dimension * 100),
                ncol = dimension, nrow = 100)
vineLogLik(vine, data)
```

**Description**

Select an order of the variables. The order of the variables determines the bivariate dependencies that will be explicit modeled in the first tree of the vine.

**Usage**

```r
vineOrder(type, data, method = "greedy", ...)
```

**Arguments**

- `type` : Type of vine. Supported values: "CVine" and "DVine".
- `data` : Data matrix of pseudo-observations.
- `method` : Ordering method. Supported values: "random", "greedy".
- `...` : Additional arguments for the order method.

**Details**

In D-vines, the order of the variables determines the structure of all the trees of the vine. This is not the case for C-vines where the root node of each tree can be selected. The "random" method returns a random permutation of the variables. The "greedy" method returns an order of the variables that intends to capture as much dependence as possible in the first tree of the vine. The method finds the order of the variables that defines a tree that maximizes a given dependence measure used as edge weights. For C-vines, it is determined iteratively checking each variable as root node. For D-vines, it is equivalent to solve the traveling salesman problem (TSP), see (Brechmann, 2010) for details. The TSP is solved using the cheapest insertion algorithm implemented by the `solve_TSP` function of the `TSP` package. The following are additional parameters for this method.
vineParameters

Parameters of a Vine

Description
Retrieve or set the parameters of a Vine.

Usage
vineParameters(vine)
vineParameters(vine) <- value

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>vine</td>
<td>A Vine object.</td>
</tr>
<tr>
<td>value</td>
<td>Vector with the parameters of the copulas in the pair-copula construction. This vector is the result of the concatenation of the parameters slots of the copula objects in the copulas slot of the Vine object (by rows).</td>
</tr>
</tbody>
</table>
Examples

dimension <- 5
copulas <- matrix(c(tCopula(-0.25, df = 2),
                   tCopula(-0.5, df = 4),
                   tCopula(0.25, df = 6),
                   tCopula(0.5, df = 8)),
                   rep(list(NULL), 12)),
ncol = dimension - 1,
nrow = dimension - 1,
byrow = TRUE)
vine <- DVine(dimension = dimension, trees = 1,
copulas = copulas)
dimnames(vine) <- c("A", "B", "C", "D", "E")

vineParameters(vine)
show(vine)

vineParameters(vine) <- c(-0.25, 3, -0.5, 5, 0.25, 7, 0.5, 9)

vineParameters(vine)
show(vine)

Description

Probability integral transform (PIT) of (Rosenblatt, 1952) for vine models. The PIT converts a set
of dependent variables into a new set of variables which are independent and uniformly distributed
in (0, 1) under the hypothesis that the data follows a given multivariate distribution.

Usage

vinePIT(vine, u)

Arguments

  vine A Vine object.

  u Vector with one component for each variable of the vine or a matrix with one
column for each variable of the vine.

Value

A matrix with one column for each variable of the vine and one row for each observation.
Methods

signature(vine = "CVine") PIT algorithm for CVine objects based on the Algorithm 5 of (Aas et al., 2009).

signature(vine = "DVine") PIT algorithm for DVine objects based on the Algorithm 6 of (Aas et al., 2009).

References


See Also

vinePIT.

Examples

dimension <- 3
copulas <- matrix(list(normalCopula(0.5),
claytonCopula(2.75),
NULL, NULL),
col = dimension - 1,
nrow = dimension - 1,
byrow = TRUE)
vine <- CVine(dimension = dimension, trees = 1,
copulas = copulas)
data <- matrix(runif(dimension * 100),
ncol = dimension, nrow = 100)
vinePIT(vine, data)
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