Package ‘rvinecopulib’

October 7, 2021

Type Package

Title High Performance Algorithms for Vine Copula Modeling

Version 0.6.1.1.1

Description Provides an interface to 'vinecopulib', a C++ library for vine copula modeling. The 'vinecopulib' package implements the core features of the popular 'VineCopula' package, in particular inference algorithms for both vine copula and bivariate copula models. Advantages over 'VineCopula' are a sleeker and more modern API, improved performances, especially in high dimensions, nonparametric and multi-parameter families, and the ability to model discrete variables. The 'rvinecopulib' package includes 'vinecopulib' as header-only C++ library (currently version 0.6.1). Thus users do not need to install 'vinecopulib' itself in order to use 'rvinecopulib'. Since their initial releases, 'vinecopulib' is licensed under the MIT License, and 'rvinecopulib' is licensed under the GNU GPL version 3.

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Encoding UTF-8

NeedsCompilation yes

Imports assertthat, graphics, grDevices, kde1d (>= 1.0.2), lattice, Rcpp (>= 0.12.12), stats, utils

Suggests igraph, ggplot2, ggraph, testthat

LinkingTo BH, Rcpp, RcppEigen, RcppThread, wdm, kde1d

BugReports https://github.com/vinecopulib/rvinecopulib/issues

SystemRequirements C++11

RoxygenNote 7.1.1

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as_rvine_structure Coerce various kind of objects to R-vine structures and matrices

Description

`as_rvine_structure` and `as_rvine_matrix` are new S3 generics allowing to coerce objects into R-vine structures and matrices (see `rvine_structure()` and `rvine_matrix()`).

Usage

```r
as_rvine_structure(x, ...)

as_rvine_matrix(x, ...)
```

## S3 method for class 'rvine_structure'
as_rvine_structure(x, ..., validate = FALSE)

## S3 method for class 'rvine_structure'
as_rvine_structure

as_rvine_matrix(x, ..., validate = FALSE)

## S3 method for class 'list'
as_rvine_structure(x, ..., is_natural_order = FALSE)

## S3 method for class 'list'
as_rvine_matrix(x, ..., is_natural_order = FALSE)

## S3 method for class 'rvine_matrix'
as_rvine_structure(x, ..., validate = FALSE)

## S3 method for class 'rvine_matrix'
as_rvine_matrix(x, ..., validate = FALSE)

## S3 method for class 'matrix'
as_rvine_structure(x, ..., validate = TRUE)

## S3 method for class 'matrix'
as_rvine_matrix(x, ..., validate = TRUE)

Arguments

x An object of class rvine_structure, rvine_matrix, matrix or list that can be coerced into an R-vine structure or R-vine matrix (see Details).

... Other arguments passed on to individual methods.

validate When ‘TRUE‘, verifies that the input is a valid rvine-structure (see Details). You may want to suppress this when you know that you already have a valid structure and you want to save some time, or to explicitly enable it if you have a structure that you want to re-check.

is_natural_order A flag indicating whether the struct_array element of x is assumed to be provided in natural order already (a structure is in natural order if the anti-diagonal is 1, ... d from bottom left to top right).

Details

The coercion to rvine_structure and rvine_matrix can be applied to different kind of objects. Currently, rvine_structure, rvine_matrix, matrix and list are supported.

For as_rvine_structure:

- rvine_structure: the main use case is to re-check an object via validate = TRUE.
- rvine_matrix and matrix: allow to coerce matrices into R-vine structures (see rvine_structure() for more details). The main difference between rvine_matrix and matrix is the nature of the validity checks.
- list: must contain named elements order and struct_array to be coerced into an R-vine structure (see rvine_structure() for more details).

For as_rvine_matrix:
• `rvine_structure` : allow to coerce an `rvine_structure` into an R-vine matrix (useful e.g. for printing).
• `rvine_matrix` : similar to `as_rvine_structure` for `rvine_structure`, the main use case is to re-check an object via `validate = TRUE`.
• `matrix` : allow to coerce matrices into R-vine matrices (mainly by checking that the matrix defines a valid R-vine, see `rvine_matrix()` for more details).
• `list` : must contain named elements `order` and `struct_array` to be coerced into an R-vine matrix (see `rvine_structure()` for more details).

**Value**

Either an object of class `rvine_structure` or of class `rvine_matrix` (see `rvine_structure()` or `rvine_matrix()`).

**See Also**

`rvine_structure` `rvine_matrix`

**Examples**

```r
# R-vine structures can be constructed from the order vector and struct_array
rvine_structure(order = 1:4, struct_array = list(
  c(4, 4, 4),
  c(3, 3),
  2
))

# ... or a similar list can be coerced into an R-vine structure
as_rvine_structure(list(order = 1:4, struct_array = list(
  c(4, 4, 4),
  c(3, 3),
  2
)))

# similarly, standard matrices can be coerced into R-vine structures
mat <- matrix(c(4, 3, 2, 1, 4, 3, 2, 0, 4, 3, 0, 0, 4, 0, 0, 0), 4, 4)
apine_matrix(mat)

# or truncate and construct the structure
mat[3, 1] <- 0
as_rvine_structure(mat)

# throws an error
mat[3, 1] <- 5
try(as_rvine_structure(mat))
```
bicop  

**Fit and select bivariate copula models**

**Description**

Fit a bivariate copula model for continuous or discrete data. The family can be selected automatically from a vector of options.

**Usage**

```r
bicop(
  data,
  var_types = c("c", "c"),
  family_set = "all",
  par_method = "mle",
  nonpar_method = "quadratic",
  mult = 1,
  selcrit = "aic",
  weights = numeric(),
  psi0 = 0.9,
  presel = TRUE,
  keep_data = FALSE,
  cores = 1
)
```

**Arguments**

- **data**
  - a matrix or data.frame with at least two columns, containing the (pseudo-)observations for the two variables (copula data should have approximately uniform margins). More columns are required for discrete models, see *Details*.
- **var_types**
  - variable types, a length 2 vector; e.g., c("c", "c") for both continuous (default), or c("c", "d") for first variable continuous and second discrete.
- **family_set**
  - a character vector of families; see *Details* for additional options.
- **par_method**
  - the estimation method for parametric models, either "mle" for maximum likelihood or "itau" for inversion of Kendall's tau (only available for one-parameter families and "t").
- **nonpar_method**
  - the estimation method for nonparametric models, either "constant" for the standard transformation estimator, or "linear"/"quadratic" for the local-likelihood approximations of order one/two.
- **mult**
  - multiplier for the smoothing parameters of nonparametric families. Values larger than 1 make the estimate more smooth, values less than 1 less smooth.
- **selcrit**
  - criterion for family selection, either "loglik", "aic", "bic", "mbic". For vinecop() there is the additional option "mbicv".
- **weights**
  - optional vector of weights for each observation.
- **psi0**
  - see mBICV().
presel whether the family set should be thinned out according to symmetry characteristics of the data.

keep_data whether the data should be stored (necessary for using `fitted()`).

cores number of cores to use; if more than 1, estimation for multiple families is done in parallel.

Details

Discrete variables:
When at least one variable is discrete, more than two columns are required for data: the first $n \times 2$ block contains realizations of $F_{X_1}(x_1), F_{X_2}(x_2)$. The second $n \times 2$ block contains realizations of $F_{X_1}(x_1^-), F_{X_1}(x_1^-)$. The minus indicates a left-sided limit of the cdf. For, e.g., an integer-valued variable, it holds $F_{X_1}(x_1^-) = F_{X_1}(x_1 - 1)$. For continuous variables the left limit and the cdf itself coincide. Respective columns can be omitted in the second block.

Family collections:
The `family_set` argument accepts all families in `bicop_dist()` plus the following convenience definitions:

- "all" contains all the families,
- "parametric" contains the parametric families (all except "tll"),
- "nonparametric" contains the nonparametric families ("indep" and "tll")
- "onepar" contains the parametric families with a single parameter, ("gaussian", "clayton", "gumbel", "frank", and "joe"),
- "twopar" contains the parametric families with two parameters ("t", "bb1", "bb6", "bb7", and "bb8"),
- "elliptical" contains the elliptical families,
- "archimedean" contains the archimedean families,
- "BB" contains the BB families,
- "itau" families for which estimation by Kendall’s tau inversion is available ("indep", "gaussian", "t", "clayton", "gumbel", "frank", "joe").

Value
An object inheriting from classes `bicop` and `bicop_dist`. In addition to the entries contained in `bicop_dist()`, objects from the `bicop` class contain:

- data (optionally, if `keep_data = TRUE` was used), the dataset that was passed to `bicop()`.
- controls, a list with the set of fit controls that was passed to `bicop()`.
- loglik the log-likelihood.
- nobs, an integer with the number of observations that was used to fit the model.

See Also
`bicop_dist()`, `plot.bicop()`, `contour.bicop()`, `dbicop()`, `pbicop()`, `hbicop()`, `rbicop()`
bicop_dist

Examples

```r
## fitting a continuous model from simulated data
u <- rbicop(100, "clayton", 90, 3)
fit <- bicop(u, family_set = "par")
summary(fit)

## compare fit with true model
contour(fit)
contour(bicop_dist("clayton", 90, 3), col = 2, add = TRUE)

## fit a model from discrete data
x_disc <- qpois(u, 1) # transform to Poisson margins
plot(x_disc)
udisc <- cbind(ppois(x_disc, 1), ppois(x_disc - 1, 1))
fit_disc <- bicop(udisc, var_types = c("d", "d"))
summary(fit_disc)
```

bicop_dist

Bivariate copula models

**Description**

Create custom bivariate copula models by specifying the family, rotation, parameters, and variable types.

**Usage**

```r
bicop_dist(
  family = "indep",
  rotation = 0,
  parameters = numeric(0),
  var_types = c("c", "c")
)
```

**Arguments**

- `family`: the copula family, a string containing the family name (see Details for all possible families).
- `rotation`: the rotation of the copula, one of 0, 90, 180, 270.
- `parameters`: a vector or matrix of copula parameters.
- `var_types`: variable types, a length 2 vector; e.g., c("c", "c") for both continuous (default), or c("c", "d") for first variable continuous and second discrete.
Details

Implemented families:

<table>
<thead>
<tr>
<th>type</th>
<th>name</th>
<th>name in R</th>
</tr>
</thead>
<tbody>
<tr>
<td>-</td>
<td>Independence</td>
<td>&quot;indep&quot;</td>
</tr>
<tr>
<td>Elliptical</td>
<td>Gaussian</td>
<td>&quot;gaussian&quot;</td>
</tr>
<tr>
<td></td>
<td>Student t</td>
<td>&quot;student&quot;</td>
</tr>
<tr>
<td>Archimedean</td>
<td>Clayton</td>
<td>&quot;clayton&quot;</td>
</tr>
<tr>
<td></td>
<td>Gumbel</td>
<td>&quot;gumbel&quot;</td>
</tr>
<tr>
<td></td>
<td>Frank</td>
<td>&quot;frank&quot;</td>
</tr>
<tr>
<td></td>
<td>Joe</td>
<td>&quot;joe&quot;</td>
</tr>
<tr>
<td></td>
<td>Clayton-Gumbel (BB1)</td>
<td>&quot;bb1&quot;</td>
</tr>
<tr>
<td></td>
<td>Joe-Gumbel (BB6)</td>
<td>&quot;bb6&quot;</td>
</tr>
<tr>
<td></td>
<td>Joe-Clayton (BB7)</td>
<td>&quot;bb7&quot;</td>
</tr>
<tr>
<td></td>
<td>Joe-Frank (BB8)</td>
<td>&quot;bb8&quot;</td>
</tr>
<tr>
<td>Nonparametric</td>
<td>Transformation kernel</td>
<td>&quot;tll&quot;</td>
</tr>
</tbody>
</table>

Value

An object of class bicop_dist, i.e., a list containing:

- family, a character indicating the copula family.
- rotation, an integer indicating the rotation (i.e., either 0, 90, 180, or 270).
- parameters, a numeric vector or matrix of parameters.
- npars, a numeric with the (effective) number of parameters.
- var_types, the variable types.

See Also

bicop_dist(), plot.bicop(), contour.bicop(), dbicop(), pbicop(), hbicop(), rbicop()

Examples

```r
## Clayton 90° copula with parameter 3
cop <- bicop_dist("clayton", 90, 3)
cop
str(cop)

## visualization
plot(cop)
contour(cop)
plot(rbicop(200, cop))

## BB8 copula model for discrete data
cop_disc <- bicop_dist("bb8", 0, c(2, 0.5), var_types = c("d", "d"))
cop_disc
```
bicop_distributions  Bivariate copula distributions

Description

Density, distribution function, random generation and h-functions (with their inverses) for the bivariate copula distribution.

Usage

\[
dbicop(u, \text{family}, \text{rotation}, \text{parameters}, \text{var_types} = \text{c(“c”, “c”)})
\]

\[
 pbicop(u, \text{family}, \text{rotation}, \text{parameters}, \text{var_types} = \text{c(“c”, “c”)})
\]

\[
 rbicop(n, \text{family}, \text{rotation}, \text{parameters}, \text{qrng} = \text{FALSE})
\]

\[
 hbicop(
   u,
   \text{cond_var},
   \text{family},
   \text{rotation},
   \text{parameters},
   \text{inverse} = \text{FALSE},
   \text{var_types} = \text{c(“c”, “c”)}
)
\]

Arguments

- **u**: evaluation points, a matrix with at least two columns, see Details.
- **family**: the copula family, a string containing the family name (see bicop for all possible families).
- **rotation**: the rotation of the copula, one of 0, 90, 180, 270.
- **parameters**: a vector or matrix of copula parameters.
- **var_types**: variable types, a length 2 vector; e.g., c("c", "c") for both continuous (default), or c("c", "d") for first variable continuous and second discrete.
- **n**: number of observations. If `length(n) > 1`, the length is taken to be the number required.
- **qrng**: if TRUE, generates quasi-random numbers using the bivariate Generalized Halton sequence (default qrng = FALSE).
- **cond_var**: either 1 or 2; cond_var = 1 conditions on the first variable, cond_var = 2 on the second.
- **inverse**: whether to compute the h-function or its inverse.
Details

See `bicop` for the various implemented copula families.

The copula density is defined as joint density divided by marginal densities, irrespective of variable types.

H-functions (`hbicop()` are conditional distributions derived from a copula. If $C(u, v) = P(U \leq u, V \leq v)$ is a copula, then

$$h_1(u, v) = P(V \leq v | U = u) = \frac{\partial C(u, v)}{\partial u},$$

$$h_2(u, v) = P(U \leq u | V = v) = \frac{\partial C(u, v)}{\partial v}.$$

In other words, the H-function number refers to the conditioning variable. When inverting H-functions, the inverse is then taken with respect to the other variable, that is $v$ when `cond_var = 1` and $u$ when `cond_var = 2`.

Discrete variables:

When at least one variable is discrete, more than two columns are required for $u$: the first $n \times 2$ block contains realizations of $F_X(x_1), F_X(x_2)$. The second $n \times 2$ block contains realizations of $F_X(x_1^{-1}), F_X(x_1^{-1})$. The minus indicates a left-sided limit of the cdf. For, e.g., an integer-valued variable, it holds $F_X(x_1^{-1}) = F_X(x_1 - 1)$. For continuous variables the left limit and the cdf itself coincide. Respective columns can be omitted in the second block.

Value

dbicop() gives the density, pbicop() gives the distribution function, rbicop() generates random deviates, and hbicop() gives the h-functions (and their inverses).

The length of the result is determined by $n$ for rbicop(), and the number of rows in $u$ for the other functions.

The numerical arguments other than $n$ are recycled to the length of the result.

Note

The functions can optionally be used with a `bicop_dist` object, e.g., `dbicop(c(0.1, 0.5), bicop_dist("indep"))`.

See Also

bicop_dist(), bicop()

Examples

```r
## evaluate the copula density
dbicop(c(0.1, 0.2), "clay", 90, 3)
dbicop(c(0.1, 0.2), bicop_dist("clay", 90, 3))

## evaluate the copula cdf
pbicop(c(0.1, 0.2), "clay", 90, 3)

## simulate data
plot(rbicop(500, "clay", 90, 3))
```
bicop_predict_and_fitted

Predictions and fitted values for a bivariate copula model

Description

Predictions of the density, distribution function, h-functions (with their inverses) for a bivariate copula model.

Usage

## S3 method for class 'bicop_dist'
predict(object, newdata, what = "pdf", ...)

## S3 method for class 'bicop'
fitted(object, what = "pdf", ...)

Arguments

object      a bicop object.
newdata     points where the fit shall be evaluated.
what         what to predict, one of "pdf", "cdf", "hfunc1", "hfunc2", "hinv1", "hinv2".
...         unused.

Details

fitted() can only be called if the model was fit with the keep_data = TRUE option.

Discrete variables:

When at least one variable is discrete, more than two columns are required for newdata: the first \( n \times 2 \) block contains realizations of \( F_{X_1}(x_1), F_{X_2}(x_2) \). The second \( n \times 2 \) block contains realizations of \( F_{X_1}(x_1^-), F_{X_1}(x_1^-) \). The minus indicates a left-sided limit of the cdf. For, e.g., an integer-valued variable, it holds \( F_{X_1}(x_1^-) = F_{X_1}(x_1 - 1) \). For continuous variables the left limit and the cdf itself coincide. Respective columns can be omitted in the second block.
**Value**

fitted() and logLik() have return values similar to `dbicop()`, `pbicop()`, and `hbicop()`.

**Examples**

```r
# Simulate and fit a bivariate copula model
u <- rbicop(500, "gauss", 0, 0.5)
fit <- bicop(u, family = "par", keep_data = TRUE)

# Predictions
all.equal(predict(fit, u, "hfunc1"), fitted(fit, "hfunc1"),
          check.environment = FALSE)
```

---

**getters**

Extracts components of `bicop_dist` and `vinecop_dist` objects

**Description**

Extracts either the structure matrix (for `vinecop_dist` only), or pair-copulas, their parameters, Kendall’s taus, or families (for `bicop_dist` and `vinecop_dist`).

**Usage**

```r
get_structure(object)
get_pair_copula(object, tree = NA, edge = NA)
get_parameters(object, tree = NA, edge = NA)
get_ktau(object, tree = NA, edge = NA)
get_family(object, tree = NA, edge = NA)
get_all_pair_copulas(object, trees = NA)
get_all_parameters(object, trees = NA)
get_all_ktaus(object, trees = NA)
get_all_families(object, trees = NA)
```

**Arguments**

- `object` a `bicop_dist`, `vinecop_dist` or `vine_dist` object.
- `tree` tree index (not required if object is of class `bicop_dist`).
- `edge` edge index (not required if object is of class `bicop_dist`).
- `trees` the trees to extract from object (trees = NA extracts all trees).
getters

Details

#' The `get_structure` method (for `vinecop_dist` or `vine_dist` objects only) extracts the structure (see `rvine_structure` for more details).

The `get_matrix` method (for `vinecop_dist` or `vine_dist` objects only) extracts the structure matrix (see `rvine_structure` for more details).

The other `get_xyz` methods for `vinecop_dist` or `vine_dist` objects return the entries corresponding to the pair-copula indexed by its tree and edge. When object is of class `bicop_dist`, tree and edge are not required.

- `get_pair_copula()` = the pair-copula itself (see `bicop`).
- `get_parameters()` = the parameters of the pair-copula (i.e., a numeric scalar, vector, or matrix).
- `get_family()` = a character for the family (see `bicop` for implemented families).
- `get_ktau()` = a numeric scalar with the pair-copula Kendall's tau.

The `get_all_xyz` methods (for `vinecop_dist` or `vine_dist` objects only) return lists of lists, with each element corresponding to a tree in `trees`, and then elements of the sublists correspond to edges. The returned lists have two additional attributes:

- "d" = the dimension of the model.
- "trees" = the extracted trees.

Value

The structure matrix, or pair-copulas, their parameters, Kendall’s taus, or families.

Examples

```r
# specify pair-copulas
bicop <- bicop_dist("bb1", 90, c(3, 2))
pcs <- list(
  list(bicop, bicop), # pair-copulas in first tree
  list(bicop) # pair-copulas in second tree
)

# specify R-vine matrix
mat <- matrix(c(1, 2, 3, 1, 2, 0, 1, 0, 0), 3, 3)

# set up vine copula model
vc <- vinecop_dist(pcs, mat)

# get the structure
get_structure(vc)
all(get_matrix(vc) == mat)

# get pair-copulas
get_pair_copula(vc, 1, 1)
get_all_pair_copulas(vc)
```
all.equal(get_all_pair_copulas(vc), pcs, 
    check.attributes = FALSE, check.environment = FALSE)

mBICV

Modified vine copula Bayesian information criterion (mBICv)

Description

Calculates the modified vine copula Bayesian information criterion.

Usage

mBICV(object, psi0 = 0.9, newdata = NULL)

Arguments

  object        a fitted vinecop object.
  psi0          baseline prior probability of a non-independence copula.
  newdata       optional; a new data set.

Details

The modified vine copula Bayesian information criterion (mBICv) is defined as

\[ BIC = -2\loglik + \nu \log(n) - 2 \sum_{t=1}^{d-1} (q_t \log(\psi_0^t) - (d - t - q_t) \log(1 - \psi_t^0)) \]

where \( \loglik \) is the log-likelihood and \( \nu \) is the (effective) number of parameters of the model, \( t \) is the tree level \( \psi_0 \) is the prior probability of having a non-independence copula and \( q_t \) is the number of non-independence copulas in tree \( t \). The mBICv is a consistent model selection criterion for parametric sparse vine copula models.

References


Examples

```
u <- sapply(1:5, function(i) runif(50))
fit <- vinecop(u, family = "par", keep_data = TRUE)
mBICV(fit, 0.9) # with a 0.9 prior probability of a non-independence copula
mBICV(fit, 0.1) # with a 0.1 prior probability of a non-independence copula
```
Exploratory pairs plot for copula data

Description

This function provides pair plots for copula data. It shows bivariate contour plots on the lower panel, scatter plots and correlations on the upper panel and histograms on the diagonal panel.

Usage

pairs_copula_data(data, ...)

Arguments

data the data (must lie in the unit hypercube).

... other parameters passed to pairs.default(), contour.bicop(), points.default(), hist.default(), or bicop().

Examples

u <- replicate(3, runif(100))
pairs_copula_data(u)

Conversion between Kendall’s tau and parameters

Description

Conversion between Kendall’s tau and parameters

Usage

par_to_ktau(family, rotation, parameters)
ktau_to_par(family, tau)

Arguments

family a copula family (see bicop_dist()) or a bicop_dist object.
rotation the rotation of the copula, one of 0, 90, 180, 270.
parameters vector or matrix of copula parameters, not used when family is a bicop_dist object.
tau Kendall’s $\tau$. 
Examples

# the following are equivalent
par_to_ktau(bicop_dist("clayton", 0, 3))
par_to_ktau("clayton", 0, 3)

ktau_to_par("clayton", 0.5)
ktau_to_par(bicop_dist("clayton", 0, 3), 0.5)

plot.bicop_dist  Plotting tools for bicop_dist and bicop objects

Description

There are several options for plotting bicop_dist 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).

Usage

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

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

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

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

Arguments

x  bicop_dist object.

type  plot type; either "surface" or "contour".

margins  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".

size  integer; the plot is based on values on a size x size grid, default is 100.

...  optional arguments passed to contour or wireframe.

See Also

bicop_dist(), graphics:::contour(), wireframe()
Examples

```r
## construct bicop_dist object for a student t copula
obj <- bicop_dist(family = "t", rotation = 0, parameters = c(0.7, 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
```

Description

Plot one or all trees of an R-vine structure.

Usage

```r
## S3 method for class 'rvine_structure'
plot(x, ...)

## S3 method for class 'rvine_matrix'
plot(x, ...)
```

Arguments

- `x` an `rvine_structure` or `rvine_matrix` object.
- `...` passed to `plot.vinecop_dist()`.

Examples

```r
plot(cvine_structure(1:5))
plot(rvine_structure_sim(5))
mat <- rbind(c(1, 1, 1), c(2, 2, 0), c(3, 0, 0))
plot(rvine_matrix(mat))
plot(rvine_matrix_sim(5))
```
plot.vinecop_dist

Plotting vinecop_dist and vinecop objects.

Description

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

Usage

```r
## S3 method for class 'vinecop_dist'
plot(x, tree = 1, var_names = "ignore", edge_labels = NULL, ...)

## S3 method for class 'vinecop'
plot(x, tree = 1, var_names = "ignore", edge_labels = NULL, ...)

## S3 method for class 'vinecop_dist'
contour(x, tree = "ALL", cex.nums = 1, ...)

## S3 method for class 'vinecop'
contour(x, tree = "ALL", cex.nums = 1, ...)
```

Arguments

- `x` vinecop_dist object.
- `tree"ALL" or integer vector; specifies which trees are plotted.
- `var_names` integer; specifies how to make use of variable names:
  - "ignore" = variable names are ignored,
  - "use" = variable names are used to annotate vertices,
  - "legend" = uses numbers in plot and adds a legend for variable names,
  - "hide" = no numbers or names, just the node.
- `edge_labels` character; options are:
  - "family" = pair-copula family (see bicop_dist()),
  - "tau" = pair-copula Kendall’s tau
  - "family_tau" = pair-copula family and Kendall’s tau,
  - "pair" = the name of the involved variables.
- `...` Unused for plot and passed to contour.bicop for contour.
- `cex.nums` numeric; expansion factor for font of the numbers.

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.

The plot() method returns an object that (among other things) contains the igraph representation of the graph; see Examples.
pseudo_obs

Author(s)

Thomas Nagler, Thibault Vatter

See Also

twinecop, plot.bicop

Examples

# set up vine copula model
u <- matrix(runif(20 * 10), 20, 10)
vc <- vinecop(u, family = "indep")

# plot
plot(vc, tree = c(1, 2))
plot(vc, edge_labels = "pair")

# extract igraph representation
plt <- plot(vc, edge_labels = "family_tau")
igr_obj <- get("g", plt$plot_env)[[1]]
igr_obj # print object
igraph::E(igr_obj)$name # extract edge labels

# set up another vine copula model
pcs <- lapply(1:3, function(j) # pair-copulas in tree j
  lapply(runif(4 - j), function(cor) bicop_dist("gaussian", 0, cor)))
mat <- rvine_matrix_sim(4)
vc <- vinecop_dist(pcs, mat)

# contour plot
contour(vc)

---

twinecop (Pseudo-Observations)

Description

Compute the pseudo-observations for the given data matrix.

Usage

twinecop(x, ties_method = "average", lower_tail = TRUE)

Arguments

x

vector or matrix random variates to be converted (column wise) to pseudo-observations.

ties_method

similar to ties.method of rank() (only "average", "first" and "random" currently available).
lower_tail logical which, if ‘FALSE’, returns the pseudo-observations when applying the empirical marginal survival functions.

Details

Given \( n \) realizations \( x_i = (x_{i1}, \ldots, x_{id}) \), \( i \in \{1, \ldots, n\} \) 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.

When \( \text{lower\_tail} = \text{FALSE} \), then \( \text{pseudo\_obs()} \) simply returns \( 1 - \text{pseudo\_obs()} \).

Value

a vector of matrix of the same dimension as the input containing the pseudo-observations.

Examples

```r
# pseudo-observations for a vector
pseudo_obs(rnorm(10))

# pseudo-observations for a matrix
pseudo_obs(cbind(rnorm(10), rnorm(10)))
```

---

**rosenblatt**  
*(Inverse) Rosenblatt transform*

Description

The Rosenblatt transform takes data generated from a model and turns it into independent uniform variates. The inverse Rosenblatt transform computes conditional quantiles and can be used to simulate from a stochastic model, see Details.

Usage

```r
rosenblatt(x, model, cores = 1)
inverse_rosenblatt(u, model, cores = 1)
```

Arguments

- **x** matrix of evaluation points; must be in \((0,1)^d\) for copula models.
- **model** a model object; classes currently supported are `bicop_dist()`, `vinecop_dist()`, and `vine_dist()`.
- **cores** if >1, computation is parallelized over cores batches (rows of \( u \)).
- **u** matrix of evaluation points; must be in \((0,1)^d\).
Details

The Rosenblatt transform (Rosenblatt, 1952) $U = T(V)$ of a random vector $V = (V_1, \ldots, V_d)$ $F$ is defined as

$$U_1 = F(V_1), U_2 = F(V_2|V_1), \ldots, U_d = F(V_d|V_1, \ldots, V_{d-1}),$$

where $F(v_k|v_1, \ldots, v_{k-1})$ is the conditional distribution of $V_k$ given $V_1, \ldots, V_{k-1}, k = 2, \ldots, d$. The vector $U$ are then independent standard uniform variables. The inverse operation

$$V_1 = F^{-1}(U_1), V_2 = F^{-1}(U_2|U_1), \ldots, V_d = F^{-1}(U_d|U_1, \ldots, U_{d-1}),$$

can be used to simulate from a distribution. For any copula $F$, if $U$ is a vector of independent random variables, $V = T^{-1}(U)$ has distribution $F$.

Examples

```r
# simulate data with some dependence
x <- replicate(3, rnorm(200))
x[, 2:3] <- x[, 2:3] + x[, 1]
pairs(x)

# estimate a vine distribution model
fit <- vine(x, copula_controls = list(family_set = "par"))

# transform into independent uniforms
u <- rosenblatt(x, fit)
pairs(u)

# inversion
pairs(inverse_rosenblatt(u, fit))

# works similarly for vinecop models
vc <- fit$copula
rosenblatt(pseudo_obs(x), vc)
```

Description

Provides an interface to 'vinecopulib', a C++ library for vine copula modeling based on 'Boost' and 'Eigen'. The 'vinecopulib' package implements the core features of the popular 'VineCopula' package, in particular inference algorithms for both vine copula and bivariate copula models. Advantages over 'VineCopula' are a sleeker and more modern API, improved performances, especially in high dimensions, nonparametric and multi-parameter families. The 'vinecopulib' package includes 'vinecopulib' as header-only C++ library (currently version 0.5.5). Thus users do not need to install 'vinecopulib' itself in order to use 'vinecopulib'. Since their initial releases, 'vinecopulib' is licensed under the MIT License, and 'rvinecopulib' is licensed under the GNU GPL version 3.
Author(s)

Thomas Nagler, Thibault Vatter

Examples

```r
## bicop_dist objects
bicop_dist("gaussian", 0, 0.5)
str(bicop_dist("gauss", 0, 0.5))
bicop <- bicop_dist("clayton", 90, 3)

## bicop objects
u <- rbicop(500, "gauss", 0, 0.5)
fit1 <- bicop(u, family = "par")
fit1

## vinecop_dist objects
## specify pair-copulas
bicop <- bicop_dist("bb1", 90, c(3, 2))
pcs <- list(
  list(bicop, bicop), # pair-copulas in first tree
  list(bicop) # pair-copulas in second tree
)
## specify R-vine matrix
mat <- matrix(c(1, 2, 3, 1, 2, 0, 1, 0, 0), 3, 3)
## build the vinecop_dist object
vc <- vinecop_dist(pcs, mat)
summary(vc)

## vinecop objects
u <- sapply(1:3, function(i) runif(50))
vc <- vinecop(u, family = "par")
summary(vc)

## vine_dist objects
vc <- vine_dist(list(distr = "norm"), pcs, mat)
summary(vc)

## vine objects
x <- sapply(1:3, function(i) rnorm(50))
vc <- vine(x, copula_controls = list(family_set = "par"))
summary(vc)
```

Description

R-vine structures are compressed representations encoding the tree structure of the vine, i.e. the conditioned/conditioning variables of each edge. The functions [cvine_structure()] or [dvine_structure()] give a simpler way to construct C-vines (every tree is a star) and D-vines (every tree is a path), respectively (see Examples).
rvine_structure

Usage

rvine_structure(order, struct_array = list(), is_natural_order = FALSE)

cvine_structure(order, trunc_lvl = Inf)

dvine_structure(order, trunc_lvl = Inf)

rvine_matrix(matrix)

Arguments

order a vector of positive integers.

struct_array a list of vectors of positive integers. The vectors represent rows of the r-rvine structure and the number of elements have to be compatible with the order vector. If empty, the model is 0-truncated.

is_natural_order whether struct_array is assumed to be provided in natural order already (a structure is in natural order if the anti-diagonal is 1, ..., d from bottom left to top right).

trunc_lvl the truncation level

matrix an R-vine matrix, see Details.

Details

The R-vine structure is essentially a lower-triangular matrix/triangular array, with a notation that differs from the one in the VineCopula package. An example array is

```
4 4 4 4
3 3 3
2 2
1
```

which encodes the following pair-copulas:

<table>
<thead>
<tr>
<th>tree</th>
<th>edge</th>
<th>pair-copulas</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0</td>
<td>(1, 4)</td>
</tr>
<tr>
<td>0</td>
<td>1</td>
<td>(2, 4)</td>
</tr>
<tr>
<td>0</td>
<td>2</td>
<td>(3, 4)</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>(1, 3; 4)</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>(2, 3; 4)</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>(1, 2; 3, 4)</td>
</tr>
</tbody>
</table>

An R-vine structure can be converted to an R-vine matrix using as_rvine_matrix(), which encodes the same model with a square matrix filled with zeros. For instance, the matrix corresponding to the structure above is:

```
4 4 4 4 4
```
Similarly, an R-vine matrix can be converted to an R-vine structure using \texttt{as_rvine_structure()}. Denoting by $M[i,j]$ the array entry in row $i$ and column $j$ (the pair-copula index for edge $e$ in tree $t$ of a $d$ dimensional vine is $(M[d+1-e,e], M[t,e]; M[t-1,e], ..., M[1,e])$. Less formally,

1. Start with the counter-diagonal element of column $e$ (first conditioned variable).
2. Jump up to the element in row $t$ (second conditioned variable).
3. Gather all entries further up in column $e$ (conditioning set).

Internally, the diagonal is stored separately from the off-diagonal elements, which are stored as a triangular array. For instance, the off-diagonal elements off the structure above are stored as

4 4 4
3 3
2

for the structure above. The reason is that it allows for parsimonious representations of truncated models. For instance, the 2-truncated model is represented by the same diagonal and the following truncated triangular array:

4 4 4
3 3

A valid R-vine structure or matrix must satisfy several conditions which are checked when \texttt{rvine_structure()}, \texttt{rvine_matrix()}, or some coercion methods (see \texttt{as_rvine_structure()} and \texttt{as_rvine_matrix()}) are called:

1. It can only contain numbers between 1 and $d$ (and additionally zeros for R-vine matrices).
2. The anti-diagonal must contain the numbers 1, ..., $d$.
3. The anti-diagonal entry of a column must not be contained in any column further to the right.
4. The entries of a column must be contained in all columns to the left.
5. The proximity condition must hold: For all $t = 1, ..., d-2$ and $e = 1, ..., d-t$ there must exist an index $j > d$, such that $(M[t,e], {M[1,e], ..., M[t-1,e]})$ equals either $(M[d+1-j,j], {M[1,j], ..., M[t-1,j]})$ or $(M[t-1,j], {M[d+1-j,j], M[1,j], ..., M[t-2,j]})$.

Condition 5 already implies conditions 2-4, but is more difficult to check by hand.

\textbf{Value}

Either an \texttt{rvine_structure} or an \texttt{rvine_matrix}.

\textbf{See Also}

\texttt{as_rvine_structure()}, \texttt{as_rvine_matrix()}, \texttt{plot.rvine_structure()}, \texttt{plot.rvine_matrix()}, \texttt{rvine_structure_sim()}, \texttt{rvine_matrix_sim()}
Examples

```
# R-vine structures can be constructed from the order vector and struct_array
rvine_structure(order = 1:4, struct_array = list(
  c(4, 4, 4),
  c(3, 3),
  2
))

# R-vine matrices can be constructed from standard matrices
mat <- matrix(c(4, 3, 2, 1, 4, 3, 2, 0, 4, 3, 0, 0, 4, 0, 0, 0), 4, 4)
rvine_matrix(mat)

# coerce to R-vine structure
str(as_rvine_structure(mat))

# truncate and construct the R-vine matrix
mat[3, 1] <- 0
rvine_matrix(mat)

# or use directly the R-vine structure constructor
rvine_structure(order = 1:4, struct_array = list(
  c(4, 4, 4),
  c(3, 3)
))

# throws an error
mat[3, 1] <- 5
try(rvine_matrix(mat))

# C-vine structure
cvine <- cvine_structure(1:5)
cvine
plot(cvine)

# D-vine structure
dvine <- dvine_structure(c(1, 4, 2, 3, 5))
dvine
plot(dvine)
```

---

**rvine_structure_sim**  
*Simulate R-vine structures*

**Description**

Simulates from a uniform distribution over all R-vine structures on \(d\) variables. `rvine_structure_sim()` returns an `rvine_structure()` object, `rvine_matrix_sim()` an `rvine_matrix()`. 
Usage

rvine_structure_sim(d, natural_order = FALSE)
rvine_matrix_sim(d, natural_order = FALSE)

Arguments

d  the number of variables
natural_order  boolean; whether the structures should be in natural order (counter-diagonal is 1:d).

See Also

rvine_structure(), rvine_matrix(), plot.rvine_structure(), plot.rvine_matrix()

Examples

rvine_structure_sim(10)
rvine_structure_sim(10, natural_order = TRUE)  # counter-diagonal is 1:d
rvine_matrix_sim(10)

== truncate_model

Truncate a vine copula model

Description

Extracts a truncated sub-vine based on a truncation level supplied by user.

Usage

truncate_model(object, ...)

## S3 method for class 'rvine_structure'
truncate_model(object, trunc_lvl, ...)

## S3 method for class 'rvine_matrix'
truncate_model(object, trunc_lvl, ...)

## S3 method for class 'vinecop_dist'
truncate_model(object, trunc_lvl, ...)

## S3 method for class 'vine_dist'
truncate_model(object, trunc_lvl, ...)
Arguments

- **object**: a model object.
- **...**: further arguments passed to specific methods.
- **trunc_lvl**: tree level after which the vine copula should be truncated.

Details

While a vine model for a d-dimensional random vector contains at most d-1 nested trees, this function extracts a sub-model based on a given truncation level.

For instance, `truncate_model(object, 1)` results in a 1-truncated vine (i.e., a vine with a single tree). Similarly `truncate_model(object, 2)` results in a 2-truncated vine (i.e., a vine with two trees). Note that `truncate_model(truncate_model(object, 1), 2)` returns a 1-truncated vine.

Examples

```r
# specify pair-copulas
bicop <- bicop_dist("bb1", 90, c(3, 2))
pcs <- list(
  list(bicop, bicop), # pair-copulas in first tree
  list(bicop) # pair-copulas in second tree
)

# specify R-vine matrix
mat <- matrix(c(1, 2, 3, 1, 2, 0, 1, 0, 0), 3, 3)

# set up vine structure
structure <- as_rvine_structure(mat)

# truncate the model
truncate_model(structure, 1)

# set up vine copula model
vc <- vinecop_dist(pcs, mat)

# truncate the model
truncate_model(vc, 1)
```

---

**vine**  
*Vine copula models*

Description

Automated fitting or creation of custom vine copula models
Usage

vine(
data,
margins_controls = list(mult = NULL, xmin = NaN, xmax = NaN, bw = NA, deg = 2),
copula_controls = list(family_set = "all", structure = NA, par_method = "mle",
nonpar_method = "constant", mult = 1, selcrit = "aic", psi0 = 0.9, presel = TRUE,
trunc_lvl = Inf, tree_crit = "tau", threshold = 0, keep_data = FALSE, show_trace =
FALSE, cores = 1),
weights = numeric(),
keep_data = FALSE,
cores = 1)
)

vine_dist(margins, pair_copulas, structure)

Arguments

data a matrix or data.frame.
margins_controls a list with arguments to be passed to \texttt{kde1d::kde1d()}. Currently, there can be
• mult numeric vector of length one or d; all bandwidths for marginal kernel
density estimation are multiplied with \texttt{mult}. Defaults to $\log(1 + d)$ where
\texttt{d} is the number of variables after applying \texttt{rvinecopulib:::expand_factors()}.
• xmin numeric vector of length \texttt{d}; see \texttt{kde1d::kde1d()}.
• xmax numeric vector of length \texttt{d}; see \texttt{kde1d::kde1d()}. 
• bw numeric vector of length \texttt{d}; see \texttt{kde1d::kde1d()}. 
• deg numeric vector of length one or \texttt{d}; \texttt{kde1d::kde1d()}. 
copula_controls a list with arguments to be passed to \texttt{vinecop()}. 
weights optional vector of weights for each observation. 
keep_data whether the original data should be stored; if you want to store the pseudo-
observations used for fitting the copula, use the \texttt{copula_controls} argument. 
cores the number of cores to use for parallel computations. 
margins A list with with each element containing the specification of a marginal \texttt{stats::Distributions}. 
Each marginal specification should be a list with containing at least the distribution family ("distr") and optionally the parameters, e.g. \texttt{list(list(distr = "norm"),list(distr = "norm", mu = 1),list(distr = "beta", shape1 = 1, shape2 = 1))}. Note that parameters that have no default values have to be provided. 
Furthermore, if margins has length one, it will be recycled for every component. 
pair_copulas A nested list of 'bicop_dist' objects, where \texttt{pair_copulas[[t]][[e]]} corre-
sponds to the pair-copula at edge \texttt{e} in tree \texttt{t}. 
structure an \texttt{rvine_structure} object, namely a compressed representation of the vine
structure, or an object that can be coerced into one (see \texttt{rvine_structure()} and 
\texttt{as_rvine_structure()}). The dimension must be length\texttt{pair_copulas[[1]]} + 1.
vine

Details

vine_dist() creates a vine copula by specifying the margins, a nested list of bicop_dist objects and a quadratic structure matrix.

vine() provides automated fitting for vine copula models. margins_controls is a list with the same parameters as kde1d::kde1d() (except for x). copula_controls is a list with the same parameters as vinecop() (except for data).

Value

Objects inheriting from vine_dist for vine_dist(), and vine and vine_dist for vine().

Objects from the vine_dist class are lists containing:

- margins, a list of marginals (see below).
- copula, an object of the class vinecop_dist, see vinecop_dist().

For objects from the vine class, copula is also an object of the class vine, see vinecop(). Additionally, objects from the vine class contain:

- margins_controls, a list with the set of fit controls that was passed to kde1d::kde1d() when estimating the margins.
- copula_controls, a list with the set of fit controls that was passed to vinecop() when estimating the copula.
- data (optionally, if keep_data = TRUE was used), the dataset that was passed to vine().
- nobs, an integer containing the number of observations that was used to fit the model.

Concerning margins:

- For objects created with vine_dist(), it simply corresponds to the margins argument.
- For objects created with vine(), it is a list of objects of class kde1d, see kde1d::kde1d().

Examples

# specify pair-copulas
bicop <- bicop_dist("bb1", 90, c(3, 2))
pcs <- list(
  list(bicop, bicop), # pair-copulas in first tree
  list(bicop) # pair-copulas in second tree
)

# specify R-vine matrix
mat <- matrix(c(1, 2, 3, 1, 2, 0, 1, 0, 0), 3, 3)

# set up vine copula model with Gaussian margins
vc <- vine_dist(list(distr = "norm"), pcs, mat)

# show model
summary(vc)

# simulate some data
x <- vine(50, vc)

# estimate a vine copula model
fit <- vine(x, copula_controls = list(family_set = "par"))
summary(fit)

---

**vinecop**

_Fitting vine copula models_

**Description**

Automated fitting and model selection for vine copula models with continuous or discrete data. Selection of the structure is performed using the algorithm of Dissmann et al. (2013).

**Usage**

```r
vinecop(
  data, 
  var_types = rep("c", NCOL(data)), 
  family_set = "all", 
  structure = NA, 
  par_method = "mle", 
  nonpar_method = "constant", 
  mult = 1, 
  selcrit = "aic", 
  weights = numeric(), 
  psi0 = 0.9, 
  presel = TRUE, 
  trunc_lvl = Inf, 
  tree_crit = "tau", 
  threshold = 0, 
  keep_data = FALSE, 
  show_trace = FALSE, 
  cores = 1
)
```

**Arguments**

data  
a matrix or data.frame with at least two columns, containing the (pseudo-)observations for the two variables (copula data should have approximately uniform margins). More columns are required for discrete models, see Details.

var_types  
variable types, a length d vector; e.g., c("c","c") for two continuous variables, or c("c","d") for first variable continuous and second discrete.

family_set  
a character vector of families; see `bicop()` for additional options.
structure: an rvine_structure object, namely a compressed representation of the vine structure, or an object that can be coerced into one (see rvine_structure() and as_rvine_structure()). The dimension must be length(pair_copulas[[1]]) + 1; structure = NA performs automatic selection based on Dissman’s algorithm. See Details for partial selection of the structure.

par_method: the estimation method for parametric models, either "mle" for maximum likelihood or "itau" for inversion of Kendall’s tau (only available for one-parameter families and "t").

nonpar_method: the estimation method for nonparametric models, either "constant" for the standard transformation estimator, or "linear"/"quadratic" for the local-likelihood approximations of order one/two.

mult: multiplier for the smoothing parameters of nonparametric families. Values larger than 1 make the estimate more smooth, values less than 1 less smooth.

selcrit: criterion for family selection, either "loglik", "aic", "bic", "mbic". For vinecop() there is the additional option "mbicv".

weights: optional vector of weights for each observation.

psi0: prior probability of a non-independence copula (only used for selcrit = "mbic" and selcrit = "mbicv").

presel: whether the family set should be thinned out according to symmetry characteristics of the data.

trunc_lvl: the truncation level of the vine copula; Inf means no truncation, NA indicates that the truncation level should be selected automatically by mBICV().

tree_crit: the criterion for tree selection, one of "tau", "rho", "hoeffd", "mcor", or "joe" for Kendall’s τ, Spearman’s ρ, Hoeffding’s D, maximum correlation, or logarithm of the partial correlation, respectively.

threshold: for thresholded vine copulas; NA indicates that the threshold should be selected automatically by mBICV().

keep_data: whether the data should be stored (necessary for using fitted()).

show_trace: logical; whether a trace of the fitting progress should be printed.

cores: number of cores to use; if more than 1, estimation of pair copulas within a tree is done in parallel.

Details

Discrete variables:
The dependence measures used to select trees (default: Kendall’s tau) are corrected for ties (see wdm::wdm).

Let n be the number of observations and d the number of variables. When at least one variable is discrete, two types of "observations" are required in data: the first n x d block contains realizations of \( F_{X_j}(X_j) \). The second n x d block contains realizations of \( F_{X_j}(X_j^-) \). The minus indicates a left-sided limit of the cdf. For, e.g., an integer-valued variable, it holds \( F_{X_j}(X_j^-) = F_{X_j}(X_j - 1) \). For continuous variables the left limit and the cdf itself coincide. Respective columns can be omitted in the second block.
**Partial structure selection:**
It is possible to fix the vine structure only in the first trees and select the remaining ones automatically. To specify only the first $k$ trees, supply a $k$-truncated `rvine_structure()` or `rvine_matrix()`. All trees up to `trunc_lvl` will then be selected automatically.

**Value**
Objects inheriting from `vinecop` and `vinecop_dist` for `vinecop()`. In addition to the entries provided by `vinecop_dist()`, there are:

- threshold, the (set or estimated) threshold used for thresholding the vine.
- data (optionally, if `keep_data = TRUE` was used), the dataset that was passed to `vinecop()`.
- controls, a list with fit controls that was passed to `vinecop()`.
- `nobs`, the number of observations that were used to fit the model.

**References**

**See Also**
`vinecop()`, `dvinecop()`, `pvinecop()`, `rvinecop()`, `plot.vinecop()`, `contour.vinecop()`

**Examples**
```r
## simulate dummy data
x <- rnorm(30) * matrix(1, 30, 5) + 0.5 * matrix(rnorm(30 * 5), 30, 5)
u <- pseudo_obs(x)

## fit and select the model structure, family and parameters
fit <- vinecop(u)
summary(fit)
plot(fit)
contour(fit)

## select by log-likelihood criterion from one-paramter families
fit <- vinecop(u, family_set = "onepar", selcrit = "bic")
summary(fit)

## Gaussian D-vine
fit <- vinecop(u, structure = dvine_structure(1:5), family = "gauss")
plot(fit)
contour(fit)

## Partial structure selection with only first tree specified
structure <- rvine_structure(order = 1:5, list(rep(5, 4)))
fit <- vinecop(u, structure = structure, family = "gauss")
plot(fit)
```
## 1-truncated model with random structure
fit <- vinecop(u, structure = rvine_structure_sim(5), trunc_lvl = 1)
contour(fit)

## Model for discrete data
x <- qpois(u, 1)  # transform to Poisson margins
# we require two types of observations (see Details)
u_disc <- cbind(pois(x, 1), ppois(x - 1, 1))
fit <- vinecop(u_disc, var_types = rep("d", 5))

## Model for mixed data
x <- qpois(u[, 1], 1)  # transform first variable to Poisson margin
# we require two types of observations (see Details)
u_disc <- cbind(pois(x, 1), u[, 2:5], ppois(x - 1, 1))
fit <- vinecop(u_disc, var_types = c("d", rep("c", 4)))

---

### vinecop_dist

**Vine copula models**

#### Description
Create custom vine copula models by specifying the pair-copulas, structure, and variable types.

#### Usage

```
vinecop_dist(pair_copulas, structure, var_types = rep("c", dim(structure)[1]))
```

#### Arguments

- `pair_copulas`: A nested list of `bicop_dist()` objects, where `pair_copulas[[t]][[e]]` corresponds to the pair-copula at edge `e` in tree `t`.
- `structure`: an `rvine_structure` object, namely a compressed representation of the vine structure, or an object that can be coerced into one (see `rvine_structure()` and `as_rvine_structure()`). The dimension must be `length(pair_copulas[[1]]) + 1`; `structure = NA` performs automatic selection based on Dissman’s algorithm. See `Details` for partial selection of the structure.
- `var_types`: variable types, a length `d` vector; e.g., `c("c","c")` for two continuous variables, or `c("c","d")` for first variable continuous and second discrete.

#### Value
Object of class `vinecop_dist`, i.e., a list containing:

- `pair_copulas`, a list of lists. Each element of `pair_copulas` corresponds to a tree, which is itself a list of `bicop_dist()` objects.
- `structure`, a compressed representation of the vine structure, or an object that can be coerced into one (see `rvine_structure()` and `as_rvine_structure()`).
- `npars`, a numeric with the number of (effective) parameters.
- `var_types` the variable types.
### vinecop_distributions

**Vine copula distributions**

**Description**

Density, distribution function and random generation for the vine copula distribution.

**Usage**

- `dvinecop(u, vinecop, cores = 1)`
- `pvinecop(u, vinecop, n_mc = 10^4, cores = 1)`
- `rvinecop(n, vinecop, qrng = FALSE, cores = 1)`

**Arguments**

- **u**: matrix of evaluation points; must contain at least d columns, where d is the number of variables in the vine. More columns are required for discrete models, see Details.
- **vinecop**: an object of class "vinecop_dist".

---

**Examples**

```r
# specify pair-copulas
bicop <- bicop_dist("bb1", 90, c(3, 2))
pcs <- list(
  list(bicop, bicop), # pair-copulas in first tree
  list(bicop) # pair-copulas in second tree
)

# specify R-vine matrix
mat <- matrix(c(1, 2, 3, 1, 2, 0, 1, 0, 0), 3, 3)

# set up vine copula model
vc <- vinecop_dist(pcs, mat)

# visualization
plot(vc)
contour(vc)

# simulate from the model
pairs(rvinecop(200, vc))
```
cores number of cores to use; if larger than one, computations are done in parallel on cores batches.
n_mc number of samples used for quasi Monte Carlo integration.
n number of observations.
qrng if TRUE, generates quasi-random numbers using the multivariate Generalized Halton sequence up to dimension 300 and the Generalized Sobol sequence in higher dimensions (default qrng = FALSE).

Details

See vinecop() for the estimation and construction of vine copula models.

The copula density is defined as joint density divided by marginal densities, irrespective of variable types.

Discrete variables:
When at least one variable is discrete, two types of "observations" are required in u: the first \( n \times d \) block contains realizations of \( F_{X_j}(X_j) \). The second \( n \times d \) block contains realizations of \( F_{X_j}(X_j^-) \). The minus indicates a left-sided limit of the cdf. For, e.g., an integer-valued variable, it holds \( F_{X_j}(X_j^-) = F_{X_j}(X_j - 1) \). For continuous variables the left limit and the cdf itself coincide. Respective columns can be omitted in the second block.

Value
dvinecop() gives the density, pvinecop() gives the distribution function, and rvinecop() generates random deviates.

The length of the result is determined by n for rvinecop(), and the number of rows in u for the other functions.

The vinecop object is recycled to the length of the result.

See Also

vinecop_dist(), vinecop(), plot.vinecop(), contour.vinecop()

Examples

```r
## simulate dummy data
x <- rnorm(30) * matrix(1, 30, 5) + 0.5 * matrix(rnorm(30 * 5), 30, 5)
u <- pseudo_obs(x)

## fit a model
vc <- vinecop(u, family = "clayton")

# simulate from the model
u <- rvinecop(100, vc)
pairs(u)

# evaluate the density and cdf
dvinecop(u[1, ], vc)
pvinecop(u[1, ], vc)
```
## Discrete models
vc$var_types <- rep("d", 5)  # convert model to discrete

# with discrete data we need two types of observations (see Details)
x <- qpois(u, 1)  # transform to Poisson margins
u_disc <- cbind(ppois(x, 1), ppois(x - 1, 1))

dvinecop(u_disc[1:5, ], vc)
pvinecop(u_disc[1:5, ], vc)

# simulated data always has uniform margins
pairs(rvinecop(200, vc))
**Discrete variables:**
When at least one variable is discrete, two types of "observations" are required in newdata: the first \( n \times d \) block contains realizations of \( F_{X_j}(X_j) \). The second \( n \times d \) block contains realizations of \( F_{X_j}(X_j^-) \). The minus indicates a left-sided limit of the cdf. For, e.g., an integer-valued variable, it holds \( F_{X_j}(X_j^-) = F_{X_j}(X_j - 1) \). For continuous variables the left limit and the cdf itself coincide. Respective columns can be omitted in the second block.

**Value**

`fitted()` and `predict()` have return values similar to `dvinecop()` and `pvinecop()`.

**Examples**

```r
u <- sapply(1:5, function(i) runif(50))
fit <- vinecop(u, family = "par", keep_data = TRUE)
all.equal(predict(fit, u), fitted(fit), check.environment = FALSE)
```

---

**vine_distributions**

<table>
<thead>
<tr>
<th>Vine based distributions</th>
</tr>
</thead>
</table>

**Description**

Density, distribution function and random generation for the vine based distribution.

**Usage**

- `dvine(x, vine, cores = 1)`
- `pvine(x, vine, n_mc = 10^4, cores = 1)`
- `rvine(n, vine, qrng = FALSE, cores = 1)`

**Arguments**

- `x` evaluation points, either a length \( d \) vector or a \( d \)-column matrix, where \( d \) is the number of variables in the vine.
- `vine` an object of class "vine_dist".
- `cores` number of cores to use; if larger than one, computations are done in parallel on cores batches.
- `n_mc` number of samples used for quasi Monte Carlo integration.
- `n` number of observations.
- `qrng` if TRUE, generates quasi-random numbers using the multivariate Generalized Halton sequence up to dimension 300 and the Generalized Sobol sequence in higher dimensions (default `qrng = FALSE`).
Details

See vine for the estimation and construction of vine models. Here, the density, distribution function and random generation for the vine distributions are standard.

The functions are based on dvinecop(), pvinecop() and rvinecop() for vinecop objects, and either kde1d::dkde1d(), kde1d::pkde1d() and kde1d::qkde1d() for estimated vines (i.e., output of vine()), or the standard d/p/q-xxx from stats::Distributions for custom vines (i.e., output of vine_dist()).

Value

dvine() gives the density, pvine() gives the distribution function, and rvine() generates random deviates.

The length of the result is determined by n for rvine(), and the number of rows in u for the other functions.

The vine object is recycled to the length of the result.

Examples

# specify pair-copulas
bicop <- bicop_dist("bb1", 90, c(3, 2))
pcs <- list(
    list(bicop, bicop), # pair-copulas in first tree
    list(bicop) # pair-copulas in second tree
)

# set up vine copula model
mat <- rvine_matrix_sim(3)
vc <- vine_dist(list(distr = "norm"), pcs, mat)

# simulate from the model
x <- rvine(200, vc)
pairs(x)

# evaluate the density and cdf
dvine(x[1, ], vc)
pvine(x[1, ], vc)
Usage

```r
## S3 method for class 'vine'
predict(object, newdata, what = "pdf", n_mc = 10^4, cores = 1, ...)

## S3 method for class 'vine'
fitted(object, what = "pdf", n_mc = 10^4, cores = 1, ...)
```

Arguments

- `object`: a vine object.
- `newdata`: points where the fit shall be evaluated.
- `what`: what to predict, either "pdf" or "cdf".
- `n_mc`: number of samples used for quasi Monte Carlo integration when `what = "cdf"`.
- `cores`: number of cores to use; if larger than one, computations are done in parallel on cores batches.
- `...`: unused.

Value

`fitted()` and `predict()` have return values similar to `dvine()` and `pvine()`.

Examples

```r
x <- sapply(1:5, function(i) rnorm(50))
fit <- vine(x, copula_controls = list(family_set = "par"), keep_data = TRUE)
all.equal(predict(fit, x), fitted(fit), check.environment = FALSE)
```
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