

# Package ‘vinereg’

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**Type** Package

**Title** D-Vine Quantile Regression

**Version** 0.9.2

**Maintainer** Thomas Nagler <mail@tnagler.com>

**Description** Implements D-vine quantile regression models with parametric or nonparametric pair-copulas. See Kraus and Czado (2017) <[doi:10.1016/j.csda.2016.12.009](https://doi.org/10.1016/j.csda.2016.12.009)> and Schallhorn et al. (2017) <[arXiv:1705.08310](https://arxiv.org/abs/1705.08310)>.

**License** GPL-3

**Imports** rvinecopulib (>= 0.6.1.1.2), kde1d (>= 1.0.2), Rcpp, assertthat

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

**RoxygenNote** 7.1.2

**Suggests** knitr, rmarkdown, ggplot2, AppliedPredictiveModeling, quantreg, tidyr, dplyr, purrr, scales, mgcv, testthat, covr

**VignetteBuilder** knitr

**URL** <https://tnagler.github.io/vinereg/>

**BugReports** <https://github.com/tnagler/vinereg/issues>

**Encoding** UTF-8

**NeedsCompilation** yes

**Author** Thomas Nagler [aut, cre],  
Dani Kraus [ctb]

**Repository** CRAN

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c1l	<i>Conditional log-likelihood</i>
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### Description

Calculates the conditional log-likelihood of the response given the covariates.

### Usage

```
c1l(object, newdata, cores = 1)
```

### Arguments

object	an object of class <code>vinereg</code> .
newdata	matrix of response and covariate values for which to compute the conditional distribution.
cores	integer; the number of cores to use for computations.

### Examples

```
# simulate data
x <- matrix(rnorm(500), 250, 2)
y <- x %*% c(1, -2)
dat <- data.frame(y = y, x = x, z = as.factor(rbinom(250, 2, 0.5)))

# fit vine regression model
fit <- vinereg(y ~ ., dat)

c1l(fit, dat)
fit$stats$c1l
```

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cpit	<i>Conditional probability integral transform</i>
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**Description**

Calculates the conditional distribution of the response given the covariates.

**Usage**

```
cpit(object, newdata, cores = 1)
```

**Arguments**

object	an object of class <code>vinereg</code> .
newdata	matrix of response and covariate values for which to compute the conditional distribution.
cores	integer; the number of cores to use for computations.

**Examples**

```
# simulate data
x <- matrix(rnorm(500), 250, 2)
y <- x %*% c(1, -2)
dat <- data.frame(y = y, x = x, z = as.factor(rbinom(250, 2, 0.5)))

# fit vine regression model
fit <- vinereg(y ~ ., dat)

hist(cpit(fit, dat)) # should be approximately uniform
```

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plot_effects	<i>Plot marginal effects of a D-vine regression model</i>
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**Description**

The marginal effects of a variable is the expected effect, where expectation is meant with respect to all other variables.

**Usage**

```
plot_effects(object, alpha = c(0.1, 0.5, 0.9), vars = object$order)
```

**Arguments**

object	a vinereg object
alpha	vector of quantile levels.
vars	vector of variable names.

**Examples**

```
# simulate data
x <- matrix(rnorm(200), 100, 2)
y <- x %*% c(1, -2)
dat <- data.frame(y = y, x = x, z = as.factor(rbinom(100, 2, 0.5)))

# fit vine regression model
fit <- vinereg(y ~ ., dat)
plot_effects(fit)
```

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predict.vinereg	<i>Predict conditional mean and quantiles from a D-vine regression model</i>
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**Description**

Predict conditional mean and quantiles from a D-vine regression model

**Usage**

```
## S3 method for class 'vinereg'
predict(object, newdata, alpha = 0.5, cores = 1, ...)

## S3 method for class 'vinereg'
fitted(object, alpha = 0.5, ...)
```

**Arguments**

object	an object of class vinereg.
newdata	matrix of covariate values for which to predict the quantile.
alpha	vector of quantile levels; NA predicts the mean based on an average of the 1:10 / 11-quantiles.
cores	integer; the number of cores to use for computations.
...	unused.

**Value**

A data.frame of quantiles where each column corresponds to one value of alpha.

**See Also**[vinereg](#)**Examples**

```

# simulate data
x <- matrix(rnorm(200), 100, 2)
y <- x %*% c(1, -2)
dat <- data.frame(y = y, x = x, z = as.factor(rbinom(100, 2, 0.5)))

# fit vine regression model
(fit <- vinereg(y ~ ., dat))

# inspect model
summary(fit)
plot_effects(fit)

# model predictions
mu_hat <- predict(fit, newdata = dat, alpha = NA) # mean
med_hat <- predict(fit, newdata = dat, alpha = 0.5) # median

# observed vs predicted
plot(cbind(y, mu_hat))

## fixed variable order (no selection)
(fit <- vinereg(y ~ ., dat, order = c("x.2", "x.1", "z.1")))

```

vinereg

*D-vine regression models***Description**

Sequential estimation of a regression D-vine for the purpose of quantile prediction as described in Kraus and Czado (2017).

**Usage**

```

vinereg(
  formula,
  data,
  family_set = "parametric",
  selcrit = "aic",
  order = NA,
  par_1d = list(),
  weights = numeric(),
  cores = 1,
  ...,
  uscale = FALSE
)

```

## Arguments

<code>formula</code>	an object of class "formula"; same as <code>lm()</code> .
<code>data</code>	data frame (or object coercible by <code>as.data.frame()</code> ) containing the variables in the model.
<code>family_set</code>	see <code>family_set</code> argument of <code>rvinecopulib::bicop()</code> .
<code>selcrit</code>	selection criterion based on conditional log-likelihood. "loglik" (default) imposes no correction; other choices are "aic" and "bic".
<code>order</code>	the order of covariates in the D-vine, provided as vector of variable names (after calling <code>vinereg:::expand_factors(model.frame(formula, data))</code> ); selected automatically if <code>order = NA</code> (default).
<code>par_1d</code>	list of options passed to <code>kde1d::kde1d()</code> , must be one value for each margin, e.g. <code>list(xmin = c(0, 0, NaN))</code> if the response and first covariate have non-negative support.
<code>weights</code>	optional vector of weights for each observation.
<code>cores</code>	integer; the number of cores to use for computations.
<code>...</code>	further arguments passed to <code>rvinecopulib::bicop()</code> .
<code>uscale</code>	if TRUE, <code>vinereg</code> assumes that marginal distributions have been taken care of in a preliminary step.

## Details

If discrete variables are declared as `ordered()` or `factor()`, they are handled as described in Panagiotelis et al. (2012). This is different from previous version where the data was jittered before fitting.

## Value

An object of class `vinereg`. It is a list containing the elements

**formula** the formula used for the fit.

**selcrit** criterion used for variable selection.

**model\_frame** the data used to fit the regression model.

**margins** list of marginal models fitted by `kde1d::kde1d()`.

**vine** an `rvinecopulib::vinecop_dist()` object containing the fitted D-vine.

**stats** fit statistics such as conditional log-likelihood/AIC/BIC and p-values for each variable's contribution.

**order** order of the covariates chosen by the variable selection algorithm.

**selected\_vars** indices of selected variables.

Use `predict.vinereg()` to predict conditional quantiles. `summary.vinereg()` shows the contribution of each selected variable with the associated p-value derived from a likelihood ratio test.

## References

Kraus and Czado (2017), D-vine copula based quantile regression, *Computational Statistics and Data Analysis*, 110, 1-18

Panagiotelis, A., Czado, C., & Joe, H. (2012). Pair copula constructions for multivariate discrete data. *Journal of the American Statistical Association*, 107(499), 1063-1072.

## See Also

[predict.vinereg](#)

## Examples

```
# simulate data
x <- matrix(rnorm(200), 100, 2)
y <- x %*% c(1, -2)
dat <- data.frame(y = y, x = x, z = as.factor(rbinom(100, 2, 0.5)))

# fit vine regression model
(fit <- vinereg(y ~ ., dat))

# inspect model
summary(fit)
plot_effects(fit)

# model predictions
mu_hat <- predict(fit, newdata = dat, alpha = NA) # mean
med_hat <- predict(fit, newdata = dat, alpha = 0.5) # median

# observed vs predicted
plot(cbind(y, mu_hat))

## fixed variable order (no selection)
(fit <- vinereg(y ~ ., dat, order = c("x.2", "x.1", "z.1")))
```

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