

# Package ‘vinereg’

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**Type** Package

**Title** D-Vine Quantile Regression

**Version** 0.5.0

**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> and Schallhorn et al. (2017) <arXiv:1705.08310>.

**License** GPL-3

**LazyData** TRUE

**Imports** cctools, rvinecopulib (>= 0.3.0), future, furr, kde1d (>= 0.2.0),

**RoxygenNote** 6.1.0

**NeedsCompilation** no

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

**VignetteBuilder** knitr

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

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

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**Repository** CRAN

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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(300), 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, uscale = FALSE,
  ...)
```

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

**Arguments**

object	an object of class <code>vinereg</code> .
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.
uscale	if TRUE input (newdata) and output is on copula scale.
...	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(300), 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")))
```

## Description

Sequential estimation of a regression D-vine for the purpose of quantile prediction as described in Kraus and Czado (2017). If discrete variables are declared as `ordered()` or `factor()`, jittering is used to make them continuous (see `cctools::cont_conv()`). Although this may make the model estimate inconsistent, predictions are usually still reasonable.

## Usage

```
vinereg(formula, data, family_set = "parametric", selcrit = "loglik",
        order = NA, par_1d = list(), 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>cctools::cont_conv()</code> on the <code>model.frame()</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>cores</code>	integer; the number of cores to use for computations.
<code>uscale</code>	logical indicating whether the data are already on copula scale (no margins have to be fitted).
<code>...</code>	further arguments passed to <code>rvinecopulib::bicop()</code> .

## 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

## See Also

[predict.vinereg](#)

## Examples

```
# simulate data
x <- matrix(rnorm(300), 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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