

Package ‘Qtools’

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Description This is a collection of functions for unconditional and conditional quantiles. These include methods for transformation-based quantile regression, quantile-based measures of location, scale and shape, methods for quantiles of discrete variables, quantile-based multiple imputation, and restricted quantile regression.

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Description

This is a collection of functions for unconditional and conditional quantiles. These include methods for transformation-based quantile regression, quantile-based measures of location, scale and shape, methods for quantiles of discrete variables, quantile-based multiple imputation, and restricted quantile regression.

Details

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Author(s)

Marco Geraci

Maintainer: Marco Geraci <geraci@mailbox.sc.edu>

ao

Transformations

Description

Functions used in quantile regression transformation models

Usage

```

ao(theta, lambda, symm = TRUE, omega = 0.001)
invao(x, lambda, symm = TRUE, replace = TRUE)
bc(x, lambda)
invbc(x, lambda, replace = TRUE)
mcjI(x, lambda, symm = TRUE, dbounded = FALSE, omega = 0.001)
invmcjI(x, lambda, symm = TRUE, dbounded = FALSE)
mcjII(x, lambda, delta, dbounded = FALSE, omega = 0.001)
invmcjII(x, lambda, delta, dbounded = FALSE)
  
```

Arguments

x, theta	numeric vector of singly (x) or doubly (theta) bounded observations; theta must be between 0 and 1 (see map to map generic [a,b] intervals to [0,1]).
lambda, delta	transformation parameters.
symm	logical flag. If TRUE (default) a symmetric transformation is used.
dbounded	logical flag. If TRUE the argument x is assumed to be bounded between 0 and 1.
omega	small constant to avoid numerical problems when theta is exactly 0 or 1.
replace	logical flag. If TRUE (default), values that are outside the admissible range after the Box-Cox or the Aranda-Ordaz back-transformations are replaced by the range bounds.

Details

These functions transform (back-transform) x or θ conditional on the parameters λ and θ , using the Box–Cox (bc), Aranda-Ordaz (ao), Proposal I (mcjI) and Proposal II (mcjII) transformations.

Value

Transformed or back-transformed values.

Author(s)

Marco Geraci

References

- Aranda-Ordaz FJ. On two families of transformations to additivity for binary response data. *Biometrika* 1981;68(2):357-363.
- Box GEP, Cox DR. An analysis of transformations. *Journal of the Royal Statistical Society Series B-Statistical Methodology* 1964;26(2):211-252.
- Dehbi H-M, Cortina-Borja M, and Geraci M. Aranda-Ordaz quantile regression for student performance assessment. *Journal of Applied Statistics*. 2016;43(1):58-71.
- Geraci M and Jones MC. Improved transformation-based quantile regression. *Canadian Journal of Statistics* 2015;43(1):118-132.
- Jones MC. Connecting distributions with power tails on the real line, the half line and the interval. *International Statistical Review* 2007;75(1):58-69.

See Also

[tsrq](#), [tsrq2](#), [rcrq](#), [nlrq2](#)

Chemistry

A-level Chemistry Scores

Description

The Chemistry data frame has 31022 rows and 7 columns of the A-level scores in Chemistry for England and Wales students, 1997.

Format

This data frame contains the following columns:

lea school district ID.

school school ID.

id subject ID.

score a numeric vector of A-level scores in Chemistry.

sex a factor with levels male and female

age a numeric vector of ages of the subjects (months).

gcse a numeric vector of average GCSE scores.

Source

Fielding, A., Yang, M., and Goldstein, H. (2003) “Multilevel ordinal models for examination grades”. *Statistical Modelling*, 3, 127–53.

coef.rq.bin	<i>Extract Coefficients</i>
-------------	-----------------------------

Description

coef extracts model coefficients from rq.bin objects.

Usage

```
## S3 method for class 'rq.bin'  
coef(object, ...)  
## S3 method for class 'rq.bin'  
coefficients(object, ...)
```

Arguments

object	an rq.bin object.
...	not used.

Value

a vector for single quantiles or a matrix for multiple quantiles.

Author(s)

Marco Geraci

See Also

[rq.bin](#)

coef.rq.counts	<i>Extract Coefficients</i>
----------------	-----------------------------

Description

coef extracts model coefficients from rq.counts objects.

Usage

```
## S3 method for class 'rq.counts'  
coef(object, ...)  
## S3 method for class 'rq.counts'  
coefficients(object, ...)
```

Arguments

object	an rq.counts object.
...	not used.

Value

a vector for single quantiles or a matrix for multiple quantiles.

Author(s)

Marco Geraci

See Also

[rq.counts](#)

coef.rqt	<i>Extract Coefficients</i>
----------	-----------------------------

Description

coef extracts model coefficients from rqt objects.

Usage

```
## S3 method for class 'rqt'  
coef(object, all = FALSE, ...)  
## S3 method for class 'rqt'  
coefficients(object, all = FALSE, ...)
```

Arguments

object	an rqt object.
all	logical flag. If FALSE (default), only the regression coefficients are returned. If TRUE, the transformation parameter(s) too is returned.
...	not used.

Value

a vector for single quantiles or a matrix for multiple quantiles.

Author(s)

Marco Geraci

See Also

[tsrq](#)

confint.midquantile *Mid-distribution Functions*

Description

Compute mid-quantiles confidence intervals

Usage

```
## S3 method for class 'midquantile'  
confint(object, parm = NULL, level = 0.95, ...)
```

Arguments

object	an object of class midquantile.
parm	not used (included for consistency with confint.default).
level	nominal coverage level of the confidence interval.
...	not used.

Author(s)

Marco Geraci

References

- Ma Y., Genton M., and Parzen E. Asymptotic properties of sample quantiles of discrete distributions. *Annals of the Institute of Statistical Mathematics* 2011;63(2):227-243
- Parzen E. Quantile probability and statistical data modeling. *Statistical Science* 2004;19(4):652-62.

Examples

```
x <- rpois(100, lambda = 3)
mq <- midquantile(x)
confint(mq, level = 0.95)

# print standard errors
attributes(confint(mq, level = 0.95))$stderr
```

esterase

Esterase Essay Data

Description

The esterase data frame has 113 rows and 2 columns with the results of an essay for the concentration of an enzyme esterase.

Format

This data frame contains the following columns:

Esterase amount of esterase.

Count observed count.

Details

The esterase essay data were reported by Carroll and Ruppert (1988) and successively analyzed by Zhao (2000).

Source

R. J. Carroll and D. Ruppert, Transformation and Weighting in Regression. London: Chapman and Hall, 1988.

References

Zhao QS. Restricted regression quantiles. Journal of Multivariate Analysis 2000;72(1):78-99.

fitted.rq.bin	<i>Extract Fitted Values from Binary Quantile Regression Models</i>
---------------	---

Description

This function extracts fitted values from objects of class `rq.bin`.

Usage

```
## S3 method for class 'rq.bin'  
fitted(object, ...)
```

Arguments

<code>object</code>	an object of <code>class</code> <code>rq.bin</code> .
<code>...</code>	other arguments.

Value

a vector or a matrix or an array of fitted values.

Author(s)

Marco Geraci

See Also

[predict.rq.bin](#)

fitted.rq.counts	<i>Extract Fitted Values from Quantile Regression Models for Counts</i>
------------------	---

Description

This function extracts fitted values from objects of class `rq.counts`.

Usage

```
## S3 method for class 'rq.counts'  
fitted(object, ...)
```

Arguments

<code>object</code>	an object of <code>class</code> <code>rq.counts</code> .
<code>...</code>	other arguments.

Value

a vector or a matrix or an array of fitted values.

Author(s)

Marco Geraci

See Also

[predict.rq.counts](#)

fitted.rqt	<i>Extract Fitted Values from Quantile Regression Transformation Models</i>
------------	---

Description

This function extracts fitted values from objects of class `rqt`.

Usage

```
## S3 method for class 'rqt'  
fitted(object, ...)
```

Arguments

<code>object</code>	an object of <code>class</code> <code>rqt</code> .
<code>...</code>	other arguments.

Value

a vector or a matrix or an array of fitted values.

Author(s)

Marco Geraci

See Also

[predict.rqt](#)

Description

This function calculates a goodness-of-fit test for quantile regression models.

Usage

```
GOFTest(object, type = "cusum", alpha = 0.05, B = 100, seed = NULL)
```

Arguments

object	an object of <code>class</code> "rq", "rqs", "rqt", "rrq", or "rq.counts".
type	the type of the test. See details.
alpha	the significance level for the test. This argument is relevant for type = "cusum" only.
B	the number of Monte Carlo samples. This argument is relevant for type = "cusum" only.
seed	see for random numbers. This argument is relevant for type = "cusum" only.

Details

This function provides goodness-of-fit tests for quantile regression. Currently, there is only one method available (type = "cusum"), for a test based on the cusum process of the gradient vector (He and Zhu, 2013). The critical value at level alpha is obtained by resampling. Other methods will be implemented in future versions of the package.

Value

GOFTest returns an object of `class` GOFtest.

Author(s)

Marco Geraci

References

He XM, Zhu LX. A lack-of-fit test for quantile regression. *Journal of the American Statistical Association* (2003);98:1013-1022.

Examples

```
## Not run:
data(barro, package = "quantreg")
fit <- quantreg::rq(y.net ~ lgdp2 + fse2 + gedy2 + Iy2 + gcony2, data = barro, tau = c(.1, .5, .9))
GOFTest(fit)

## End(Not run)
```

KhmaladzeFormat	<i>Khmaladze Test</i>
-----------------	-----------------------

Description

This function provides significance levels of the Khmaladze Test using a (hard-coded) table of asymptotic critical values.

Usage

```
KhmaladzeFormat(object, epsilon)
```

Arguments

`object` an object of class "KhmaladzeTest".
`epsilon` trimming value. One of $c(0.05, 0.10, 0.15, 0.20, 0.25, 0.30)$.

Details

This function is applied to an object produced by `KhmaladzeTest`. The Khmaladze test is used to test for location–shift and location–scale–shift hypotheses (Koenker, 2005). The test statistic is computed over the interval $[\epsilon, 1 - \epsilon]$, where ϵ is the trimming value.

Author(s)

Marco Geraci

References

Appendix B in Koenker R. Quantile regression. New York, NY: Cambridge University Press; 2005.
Koenker R. and Xiao Z. Inference on the quantile regression process. Available at <http://www.econ.uiuc.edu/~roger/research/inference/khmal6ap.pdf>.

Examples

```
data(barro, package = "quantreg")
eps <- 0.05
kt <- quantreg::KhmaldzeTest( y.net ~ lgdp2 + fse2 + gedy2 + Iy2 + gcony2,
  data = barro, taus = seq(.05,.95,by = .01), trim = c(eps, 1 - eps))
class(kt)
KhmaldzeFormat(kt, epsilon = eps)
```

labor

Labor Pain Data

Description

The labor data frame has 358 rows and 4 columns of the change in pain over time for several 83 women in labor.

Format

This data frame contains the following columns:

subject an ordered factor indicating the subject on which the measurement was made. The levels are labelled 1 to 83.

pain a numeric vector of self-reported pain scores on a 100mm line.

treatment a dummy variable with values 1 for subjects who received a pain medication and 0 for subjects who received a placebo.

time a numeric vector of times (minutes since randomization) at which pain was measured.

Details

The labor pain data were reported by Davis (1991) and successively analyzed by Jung (1996) and Geraci and Bottai (2007). The data set consists of repeated measurements of self-reported amount of pain on $N = 83$ women in labor, of which 43 were randomly assigned to a pain medication group and 40 to a placebo group. The response was measured every 30 min on a 100–mm line, where 0 means no pain and 100 means extreme pain. A nearly monotone pattern of missing data was found for the response variable and the maximum number of measurements for each woman was six.

Source

Davis CS (1991). Semi-parametric and non-parametric methods for the analysis of repeated measurements with applications to clinical trials. *Statistics in Medicine* 10, 1959–80.

References

Geraci M and Bottai M (2007). Quantile regression for longitudinal data using the asymmetric Laplace distribution. *Biostatistics* 8(1), 140–154.

Jung S (1996). Quasi-likelihood for median regression models. *Journal of the American Statistical Association* 91, 251–7.

maref.rqt	<i>Marginal Effects</i>
-----------	-------------------------

Description

This function computes marginal effects for `rqt` and `rq.counts` objects.

Usage

```
maref(object, namevec)
## S3 method for class 'rqt'
maref(object, namevec)
## S3 method for class 'rq.counts'
maref(object, namevec)
```

Arguments

<code>object</code>	an <code>rqt</code> or an <code>rq.counts</code> object.
<code>namevec</code>	character giving the name of the covariate with respect to which the marginal effect is to be computed.

Details

Given the τ th conditional quantile function $Q_{h(Y)|X}(\tau) = \eta = Xb$, where Y is the response variable, X a design matrix, and h is a one-parameter transformation with inverse $h^{-1} = g$, `maref` computes the marginal effect:

$$\frac{dQ_{Y|X}(\tau)}{dx_j} = \frac{dg\{Q_{h(Y)|X}(\tau)\}}{dx_j}$$

where x_j is the j -th covariate with respect to which the marginal effect is to be computed and its name is given in the argument `namevec`.

The derivative of the quantile function is the the product of two components

$$\frac{dQ_{Y|X}(\tau)}{dx_j} = \frac{dg(\eta)}{d\eta} \cdot \frac{d\eta}{dx_j}$$

The derivative w.r.t. the linear predictor η is calculated symbolically after parsing the object's formula and is evaluated using the object's model frame. The function that parses formulae has a limited scope. It recognizes interactions and basic operators (e.g., `log`, `exp`, etc.). Therefore, it is recommended to use simple expressions for the model's formula.

This function can be applied to models of class `rqt` and `rq.counts`. Note that marginal effects can be similarly obtained using `predict.rqt` or `predict.rq.counts` with argument `type = "maref"` which, in addition, allows for an optional data frame to be specified via `newdata`.

Value

a vector for single quantiles or a matrix for multiple quantiles of marginal effects.

Author(s)

Marco Geraci

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

```
## Not run:
# Box-Cox quantile regression model (dataset trees from package 'datasets')
fit <- tsrq(Volume ~ Height, data = trees, tsf = "bc", tau = 0.9)

# Coefficients (transformed scale)
coef(fit)

# Design matrix
head(fit$x)

# Marginal effect of 'Height'
maref(fit, namevec = "Height")

# Predict marginal effects over grid of values for Height
nd <- data.frame(Height = seq(min(trees$Height), max(trees$Height), length = 100))
x <- predict(fit, newdata = nd, type = "maref", namevec = "Height")

# Plot
plot(nd$Height, x, xlab = "Height", ylab = "Marginal effect on volume")

# Include 'Girth' and interaction between 'Height' and 'Girth'
fit <- tsrq(Volume ~ Height * Girth, data = trees, tsf = "bc", tau = 0.5)
head(fit$x)

# Predict marginal effects over grid of values for Height (for fixed girth)
nd$Girth <- rep(mean(trees$Girth), 100)
x <- predict(fit, newdata = nd, type = "maref", namevec = "Height")
plot(nd$Height, x, xlab = "Height", ylab = "Marginal effect on volume")

# Quantile regression for counts (log transformation)
data(esterase)
fit <- rq.counts(Count ~ Esterase, tau = 0.25, data = esterase, M = 50)
maref(fit, namevec = "Esterase")

## End(Not run)
```


Description

This function is used to multiply impute missing values using quantile regression imputation models.

Usage

```
mice.impute.rq(y, ry, x, tsf = "none", symm = TRUE, dbounded = FALSE,
lambda = NULL, epsilon = 0.001, method.rq = "fn", ...)
mice.impute.rrq(y, ry, x, tsf = "none", symm = TRUE, dbounded = FALSE,
lambda = NULL, epsilon = 0.001, method.rq = "fn", ...)
```

Arguments

y	numeric vector of length n with nmi s missing values.
ry	missing data indicator. Logical vector of length n: FALSE if y is missing, TRUE if y is observed.
x	matrix n x p of completely observed covariates.
tsf	transformation to be used. Possible options are mcjI for Proposal I, bc for Box-Cox and ao for Aranda-Ordaz transformation models. No transformation is used by default.
symm	logical flag. If TRUE (default) a symmetric transformation is used.
dbounded	logical flag. If TRUE the response y is assumed to be bounded between 0 and 1.
lambda	a numerical value for the transformation parameter. This is provided by the user or set to zero if not specified.
epsilon	constant used to trim the values of the sample space.
method.rq	linear programming algorithm (see rq).
...	additional arguments.

Details

This function implements the methods proposed by Geraci (2013) to impute missing values using quantile regression models. Uniform values are sampled from $[\epsilon, 1 - \epsilon]$, therefore allowing the interval to be bounded away from 0 and 1 (default is 0.001). It is possible to specify a quantile regression transformation model with parameter lambda (Geraci and Jones). The function `mice.impute.rrq` performs imputation based on restricted regression quantiles to avoid quantile crossing (see Geraci 2013 for details).

Value

A vector of length nmi s with imputations.

Author(s)

Marco Geraci

References

- Bottai M, Zhen H. Multiple imputation based on conditional quantile estimation. *Epidemiology, Biostatistics and Public Health* 2013;10(1):e8758-1.
- Geraci M. Estimation of regression quantiles in complex surveys with data missing at random: An application to birthweight determinants. *Statistical Methods in Medical Research* 2013. doi:10.1177/0962280213484401
- Geraci M and Jones MC. Improved transformation-based quantile regression. *Canadian Journal of Statistics* 2015;43(1):118-132.
- van Buuren S and Groothuis-Oudshoorn K (2011). *mice: Multivariate Imputation by Chained Equations in R*. *Journal of Statistical Software*, 45(3), 1-67. URL <http://www.jstatsoft.org/v45/i03/>.

See Also

[ao](#), [tsrq](#)

Examples

```
## Not run:

# Load package 'mice'
require(mice)

# Load data nhanes
data(nhanes)
nhanes2 <- nhanes
nhanes2$hyp <- as.factor(nhanes2$hyp)

# Impute continuous variables using quantile regression
set.seed(199)
imp <- mice(nhanes2, meth = c("polyreg", "rq", "logreg", "rrq"), m = 5)

# estimate linear regression and pool results
fit <- lm.mids(bmi ~ hyp + chl, data = imp)
pool(fit)

# Impute using restricted quantile regression
set.seed(199)
imp <- mice(nhanes2, meth = c("polyreg", "rrq", "logreg", "rrq"), m = 5)
fit <- lm.mids(bmi ~ hyp + chl, data = imp)
pool(fit)

# Impute using quantile regression + Box-Cox transformation with parameter
# lambda = 0 (ie, log transformation)

set.seed(199)
imp <- mice(nhanes2, meth = c("polyreg", "rq", "logreg", "rrq"), m = 5, tsf = "bc", lambda = 0)
fit <- lm.mids(bmi ~ hyp + chl, data = imp)
pool(fit)
```

```
## End(Not run)
```

midquantile *Mid-distribution Functions*

Description

Compute mid-cumulative probabilities and mid-quantiles

Usage

```
midecdf(x, na.rm = FALSE)
midquantile(x, probs = 1:3/4, na.rm = FALSE)
```

Arguments

x	numeric vector of observations used to estimate the mid-cumulative distribution or the mid-quantiles.
probs	numeric vector of probabilities with values in [0,1].
na.rm	logical value indicating whether NA values should be stripped before the computation proceeds.

Value

An object of class `class` `midecdf` or `midquantile` with mid-cumulative probabilities and mid-quantiles. For `midecdf`, this is a list that contains:

x	unique values of the vector x at which mid-cumulative probabilities are calculated.
y	estimated mid-cumulative probabilities.
fn	interpolating function of the points (x, y).
data	input values.

For `midquantile`, this is a list that contains:

x	probabilities probs at which mid-quantiles are calculated.
y	estimated mid-cumulative probabilities.
fn	interpolating function of the points (x, y).
data	input values.

Author(s)

Marco Geraci

References

Ma Y., Genton M., and Parzen E. Asymptotic properties of sample quantiles of discrete distributions. *Annals of the Institute of Statistical Mathematics* 2011;63(2):227-243

Parzen E. Quantile probability and statistical data modeling. *Statistical Science* 2004;19(4):652-62.

See Also

[confint.midquantile](#), [plot.midquantile](#)

Examples

```
x <- rpois(100, lambda = 3)
midquantile(x)
```

Orthodont

Growth curve data on an orthodontic measurement

Description

The Orthodont data frame has 108 rows and 4 columns of the change in an orthodontic measurement over time for several young subjects.

Format

This data frame contains the following columns:

distance a numeric vector of distances from the pituitary to the pterygomaxillary fissure (mm). These distances are measured on x-ray images of the skull.

age a numeric vector of ages of the subject (yr).

Subject an ordered factor indicating the subject on which the measurement was made. The levels are labelled M01 to M16 for the males and F01 to F13 for the females. The ordering is by increasing average distance within sex.

Sex a factor with levels Male and Female

Details

Investigators at the University of North Carolina Dental School followed the growth of 27 children (16 males, 11 females) from age 8 until age 14. Every two years they measured the distance between the pituitary and the pterygomaxillary fissure, two points that are easily identified on x-ray exposures of the side of the head.

Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.17)

Potthoff, R. F. and Roy, S. N. (1964), “A generalized multivariate analysis of variance model useful especially for growth curve problems”, *Biometrika*, 51, 313–326.

Jose Pinheiro, Douglas Bates, Saikat DebRoy, Deepayan Sarkar and the R Development Core Team (2011). nlme: Linear and Nonlinear Mixed Effects Models. R package version 3.1-100. <http://CRAN.R-project.org/package=nlme>

plot.midquantile *Plot Mid-distribution Functions*

Description

Plot an object generated by `midecdf` or `midquantile`.

Usage

```
## S3 method for class 'midecdf'
plot(x, ..., ylab = "p", main = "Ordinary and Mid-ECDF", verticals = FALSE,
     col.01line = "gray70", col.steps = "gray70", col.midline = "black", cex.points = 1,
     lty.midline = 2, lwd = 1, jumps = FALSE)
## S3 method for class 'midquantile'
plot(x, ..., xlab = "p", ylab = "Quantile", main = "Ordinary and Mid-Quantiles",
     col.steps = "gray70", col.midline = "black", cex.points = 1, lty.midline = 2,
     lwd = 1, jumps = FALSE)
```

Arguments

<code>x</code>	a <code>midecdf</code> or a <code>midquantile</code> object.
<code>...</code>	additional arguments for <code>plot.default</code> .
<code>xlab</code>	a label for the x axis.
<code>ylab</code>	a label for the y axis.
<code>main</code>	a main title for the plot.
<code>verticals</code>	logical. If TRUE, draw vertical lines at steps.
<code>col.01line</code>	numeric or character specifying the color of the horizontal lines at $y = 0$ and 1 .
<code>col.steps</code>	the color for the steps of ordinary quantiles.
<code>col.midline</code>	the color for the mid-ecdf or the mid-quantile line.
<code>cex.points</code>	amount by which plotting characters and symbols should be scaled relative to the default.
<code>lty.midline</code>	line type for the mid-ecdf or the mid-quantile line.
<code>lwd</code>	line width of the mid-ecdf or the mid-quantile line.
<code>jumps</code>	logical flag. Should values at jumps be marked (with the convention that, at the point of discontinuity or 'jump', the function takes its value corresponding to the ordinate of the filled circle as opposed to that of the hollow circle)?

Author(s)

Marco Geraci

See Also[midecdf](#), [midquantile](#)

`plot.qlss`*Quantile-based Summary Statistics for Location, Scale and Shape*

Description

This function plots location, scale and shape of a conditional distribution.

Usage

```
## S3 method for class 'qlss'  
plot(x, z, which = 1, interval = FALSE, type = "l", ...)
```

Arguments

<code>x</code>	an object of class <code>qlss</code> as returned by qlss.formula .
<code>z</code>	numeric vector of values against which LSS measures are plotted. This argument is required.
<code>which</code>	when <code>probs</code> in <code>qlss</code> is a vector, the argument which specifies which element of the vector should be used for plotting.
<code>interval</code>	logical flag. If <code>TRUE</code> , confidence intervals for the predictions are plotted.
<code>type</code>	1-character string giving the type of plot desired. See plot.default .
<code>...</code>	other arguments for plot.default .

Details

This function plots a `qlss` object from [qlss](#) or [predict.qlss](#).

Author(s)

Marco Geraci

See Also[qlss](#)

Examples

```

trees2 <- trees[order(trees$Height),]
fit <- qlss(Volume ~ Height, data = trees2, probs = c(.05, .1))
# Plot the results for probs = 0.1
plot(fit, z = trees2$Height, which = 2, xlab = "height")

```

predict.qlss

Predictions from Conditional LSS Objects

Description

This function computes predictions based on fitted conditional QLSS objects.

Usage

```

## S3 method for class 'qlss'
predict(object, newdata, interval = FALSE, level = 0.95, R = 200,
na.action = na.pass, trim = 0.05, ...)

```

Arguments

object	an object as returned by qlss.formula .
newdata	an optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
interval	logical flag. If TRUE, confidence intervals for predictions are computed by bootstrap.
level	nominal coverage level of the confidence interval.
R	number of bootstrap replications used to compute confidence intervals.
na.action	function determining what should be done with missing values in newdata. The default is to predict NA.
trim	proportion of extreme bootstrap replications to be trimmed before standard errors are computed.
...	not used.

Author(s)

Marco Geraci

See Also

[qlss.formula](#)

Examples

```

# Fit QLSS object
trees2 <- trees[order(trees$Height),]
fit <- qlss(Volume ~ Height, data = trees2)

## Predict using newdata. Calculate confidence intervals using 200 bootstrap replications

xx <- seq(min(trees2$Height), max(trees2$Height), length = 100)
new <- data.frame(Height = xx)
set.seed(121)
fit.pred <- predict(fit, newdata = new, interval = TRUE, level = 0.95, R = 200)
plot(fit.pred, z = xx, interval = TRUE, xlab = "height")
# large confidence intervals for shape index due
# to small IQR at low values of height

# Restrict range for Height

xx <- seq(65, 87, length = 100)
new <- data.frame(Height = xx)
set.seed(121)
fit.pred <- predict(fit, newdata = new, interval = TRUE, level = 0.95, R = 200)
plot(fit.pred, z = xx, interval = TRUE, xlab = "height") # better

```

predict.rq.bin

Predictions from rq.bin Objects

Description

This function computes predictions based on fitted binary quantile models.

Usage

```

## S3 method for class 'rq.bin'
predict(object, newdata, na.action = na.pass,
        type = "latent", grid = TRUE, ...)

```

Arguments

object	an rq.counts object.
newdata	an optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
na.action	function determining what should be done with missing values in newdata. The default is to predict NA.
type	the type of prediction required. See details.

grid	either a vector of breakpoints or a logical flag. If TRUE, the breakpoints are set to <code>seq(0.05, 0.95, by = 0.05)</code> . If FALSE, the breakpoints are extracted from <code>object\$tau</code> . At least 2 breakpoints must be provided.
...	not used.

Details

If `type = "latent"` (default), the predictions are for the conditional quantiles of the latent response variable; if `type = "probability"`, the predictions are for the conditional probabilities of the observable response. Note that `type = "probability"` is possible only when `normalize = "last"` in `rq.bin` call. The probabilities are predicted over a grid of values.

Value

a vector or a matrix of predictions.

Author(s)

Marco Geraci

See Also

[rq.bin](#), [coef.rq.bin](#)

predict.rq.counts *Predictions from rq.counts Objects*

Description

This function computes predictions based on fitted linear quantile models.

Usage

```
## S3 method for class 'rq.counts'
predict(object, newdata, offset,
na.action = na.pass, type = "response",
namevec = NULL, ...)
```

Arguments

object	an <code>rq.counts</code> object.
newdata	an optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
offset	an offset to be used with <code>newdata</code> .
na.action	function determining what should be done with missing values in <code>newdata</code> . The default is to predict NA.

type	the type of prediction required. The default "response" is on the scale of the response variable, i.e. the values are back-transformed using the inverse of the transformation $h^{-1}(Xb)$; the alternative "link" is on the scale of the linear predictors $h(y) = Xb$; finally, predictions for marginal effects are given with "maref".
namevec	character giving the name of the covariate with respect to which the marginal effect is to be computed. If type = "maref", this argument is required. See maref.rq.counts .
...	not used.

Value

a vector or a matrix or an array of predictions.

Author(s)

Marco Geraci

See Also

[residuals.rq.counts](#), [rq.counts](#), [coef.rq.counts](#), [maref.rq.counts](#)

Examples

```
# Esterase data
data(esterase)

# Fit quantiles 0.25 and 0.75
fit <- rq.counts(Count ~ Esterase, tau = 0.5, data = esterase, M = 50)
cbind(fit$fitted.values, predict(fit, type = "response"))
```

predict.rqt

Predictions from Quantile Regression Transformation Models

Description

This function computes predictions based on fitted quantile regression transformation models.

Usage

```
## S3 method for class 'rqt'
predict(object, newdata, na.action = na.pass,
        type = "response", namevec = NULL, ...)
```

Arguments

object	an object of <code>class</code> <code>rqt</code> .
newdata	an optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
na.action	function determining what should be done with missing values in newdata. The default is to predict NA.
type	the type of prediction required. The default "response" is on the scale of the response variable, i.e. the values are back-transformed using the inverse of the transformation $h^{-1}(Xb)$; the alternative "link" is on the scale of the linear predictors $h(y) = Xb$; finally, predictions for marginal effects are given with "meref".
namevec	character giving the name of the covariate with respect to which the marginal effect is to be computed. If <code>type = "meref"</code> , this argument is required. See meref.rqt .
...	not used.

Value

a vector or a matrix or an array of predictions.

Author(s)

Marco Geraci

See Also

[residuals.rqt](#), [tsrq](#), [coef.rqt](#), [meref.rqt](#)

predict.rrq

Predictions from Restricted Quantile Regression Models

Description

This function computes predictions based on fitted restricted quantile regression models.

Usage

```
## S3 method for class 'rrq'  
predict(object, newdata, na.action = na.pass, ...)
```

Arguments

object	an object of <code>class</code> <code>rrq</code> .
newdata	an optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
na.action	function determining what should be done with missing values in newdata. The default is to predict NA.
...	not used.

Value

a vector or a matrix or an array of predictions.

Author(s)

Marco Geraci

print.GOFTest *Print Goodness-of-Fit Test for Quantile Regression Models*

Description

Print an object generated by `GOFTest`.

Usage

```
## S3 method for class 'GOFTest'  
print(x, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

x	an <code>GOFTest</code> object.
digits	a non-null value for digits specifies the minimum number of significant digits to be printed in values.
...	not used.

Author(s)

Marco Geraci

See Also

[GOFTest](#)

print.midquantile *Print Mid-distribution Functions*

Description

Print an object generated by [midecdf](#) or [midquantile](#).

Usage

```
## S3 method for class 'midecdf'  
print(x, ...)  
## S3 method for class 'midquantile'  
print(x, ...)
```

Arguments

x a midecdf or a midquantile object.
... not used.

Author(s)

Marco Geraci

See Also

[midecdf](#), [midquantile](#)

print.qlss *Print Quantile-based Summary Statistics for Location, Scale and Shape*

Description

Print an object generated by [qlss](#).

Usage

```
## S3 method for class 'qlss'  
print(x, ...)
```

Arguments

x an qlss object.
... not used.

Author(s)

Marco Geraci

See Also

[qlss](#)

print.rq.bin

Print Binary Quantile Regression Models

Description

Print an object of class `rq.bin`.

Usage

```
## S3 method for class 'rq.bin'  
print(x, digits = max(6, getOption("digits")), ...)
```

Arguments

<code>x</code>	an object of class <code>rq.bin</code> .
<code>digits</code>	a non-null value for <code>digits</code> specifies the minimum number of significant digits to be printed in values.
<code>...</code>	not used.

Author(s)

Marco Geraci

See Also

[rq.bin](#)

print.rq.counts	<i>Print rq.counts</i>
-----------------	------------------------

Description

Print an object generated by [rq.counts](#).

Usage

```
## S3 method for class 'rq.counts'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

x	an rq.counts object.
digits	a non-null value for digits specifies the minimum number of significant digits to be printed in values.
...	not used.

Author(s)

Marco Geraci

See Also

[rq.counts](#)

print.rqt	<i>Print Transformation Models</i>
-----------	------------------------------------

Description

Print an object of class rqt or summary.rqt.

Usage

```
## S3 method for class 'rqt'
print(x, ...)
## S3 method for class 'summary.rqt'
print(x, ...)
```

Arguments

x	an object of class rqt or summary.rqt.
...	other arguments used by print.default .

Author(s)

Marco Geraci

See Also

[tsrq](#), [rcrq](#), [tsrq2](#) or [nlrq2](#)

print.rrq

Print Restricted Quantile Regression Models

Description

Print an object of class `rrq` or `summary.rrq`.

Usage

```
## S3 method for class 'rrq'  
print(x, ...)  
## S3 method for class 'summary.rrq'  
print(x, ...)
```

Arguments

`x` an object of `class` `rrq` or `summary.rrq`.
`...` other arguments used by `print.default`.

Author(s)

Marco Geraci

See Also

[rrq](#)

qlss

*Quantile-based Summary Statistics for Location, Scale and Shape***Description**

This function calculates quantile-based summary statistics for location, scale and shape of a distribution, unconditional or conditional.

Usage

```
qlss(...)
## Default S3 method:
qlss(fun = "qnorm", probs = 0.1, ...)
## S3 method for class 'numeric'
qlss(x, probs = 0.1, ...)
## S3 method for class 'formula'
qlss(formula, probs = 0.1, data = sys.frame(sys.parent()), subset, weights,
na.action, contrasts = NULL, method = "fn", type = "rq", tsf = "mcjI",
symm = TRUE, dbounded = FALSE, lambda = NULL, conditional = FALSE, ...)
```

Arguments

fun	quantile function.
x	a numeric vector.
formula	an object of class <code>formula</code> : a symbolic description of the model to be fitted. The details of model specification are given under "Details".
probs	a vector of probabilities.
data	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. By default the variables are taken from the environment from which the call is made.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of weights to be used in the fitting process. Should be <code>NULL</code> or a numeric vector.
na.action	a function which indicates what should happen when the data contain NAs.
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
method	the algorithm used to solve the linear program. See <code>rq</code> for further details. The Frisch-Newton interior point method is the default.
type	possible options are <code>rq</code> for linear quantile regression (default) or <code>rqt</code> for transformation-based quantile regression.
tsf	transformation to be used. Possible options are <code>mcjI</code> for Proposal I transformation models (default), <code>bc</code> for Box-Cox and <code>ao</code> for Aranda-Ordaz transformation models. See <code>tsrq</code> for further details.

<code>symm</code>	logical flag. If TRUE (default) a symmetric transformation is used.
<code>dbounded</code>	logical flag. If TRUE the response is assumed to be doubly bounded on [a,b]. If FALSE the response is assumed to be singly bounded (ie, strictly positive).
<code>lambda</code>	values of transformation parameters for grid search.
<code>conditional</code>	logical flag. If TRUE, the transformation parameter is assumed to be known and this must be provided via the arguments <code>lambda</code> using a vector of length $3 + 2 \times \text{length}(\text{probs})$ (see details).
<code>...</code>	other arguments for <code>fun</code> , <code>rq</code> or <code>tsrq</code> .

Details

This function computes a number of quantile-based summary statistics for location (median), scale (inter-quartile range and inter-quantile range), and shape (Bowley skewness and shape index) of a distribution. These statistics can be computed for unconditional and conditional distributions.

Let Y be a continuous random variable and let $Q(p)$ be its p th quantile. The function `qlss` computes the median $Q(0.5)$, the inter-quartile range $IQR = Q(0.75) - Q(0.25)$, the inter-quantile range $IPR(p) = Q(1 - p) - Q(p)$, the Bowley skewness index $A(p) = (Q(1 - p) + Q(p) - 2Q(0.5))/IPR(p)$, and the shape index $T(p) = IPR(p)/IQR(p)$, for $0 < p < 0.25$.

The default `qlss` function computes the summary statistics of a standard normal distribution or any other theoretical distribution via the argument `fun`. The latter must be a function with `p` as its probability argument (see for example `qnorm`, `qt`, `qchisq`, `qgamma`, etc.). When a variable `x` is provided, LSS measures are computed using empirical (sample) quantiles.

The argument `formula` specifies a quantile function for Y conditional on predictors X . Linear models are fitted via standard quantile regression with `type = "rq"`. Nonlinear models are fitted via transformation-based quantile regression with `type = "rqt"` (proposal II transformation models are not available.). When `conditional = TRUE`, `lambda` is a vector of transformation parameters of length $3 + 2 \times \text{np}$, where `np = length(probs)` (3 quartiles, `np` quartiles at level p , `np` quartiles at level $1 - p$).

Value

`qlss` returns an object of `class` `qlss`. This is a list that contains at least three elements:

<code>location</code>	summary statistic(s) for location.
<code>scale</code>	summary statistic(s) for scale.
<code>shape</code>	summary statistic(s) for shape.

Author(s)

Marco Geraci

References

- Geraci M and Jones MC. Improved transformation-based quantile regression. *Canadian Journal of Statistics* 2015;43(1):118-132.
- Gilchrist W. *Statistical modelling with quantile functions*. Chapman and Hall/CRC; 2000.

See Also[predict.qlss](#), [plot.qlss](#)**Examples**

```
# Compute summary statistics of a normal distribution
qlss()

# Compute summary statistics of a t distribution with 3 df
qlss(fun = "qt", df = 3, probs = 0.05)

# Compute summary statistics for a sample using a sequence of probabilities
x <- rnorm(1000)
qlss(x, probs = c(0.1, 0.2, 0.3, 0.4))

# Compute summary statistics for Volume conditional on Height
trees2 <- trees[order(trees$Height),]
fit <- qlss(Volume ~ Height, data = trees2)
plot(fit, z = trees2$Height, xlab = "height")

# Use a quadratic model for Height
fit <- qlss(Volume ~ poly(Height,2), data = trees2)
plot(fit, z = trees2$Height, xlab = "height")
```

residuals.rq.counts *Residuals from an rq.counts Object*

Description

This function computes the residuals from a fitted linear quantile model for counts.

Usage

```
## S3 method for class 'rq.counts'
residuals(object, ...)
```

Arguments

object	an rq.counts object.
...	not used.

Value

a vector or matrix of residuals.

Author(s)

Marco Geraci

See Also[rq.counts](#)

`residuals.rqt`*Residuals from an rqt Objects*

Description

This function computes the residuals from a fitted quantile regression transformation model.

Usage

```
## S3 method for class 'rqt'  
residuals(object, ...)
```

Arguments

<code>object</code>	an rqt object.
<code>...</code>	not used.

Value

a vector or matrix of residuals.

Author(s)

Marco Geraci

See Also[tsrq](#)

rq.bin	<i>Binary Quantile Regression</i>
--------	-----------------------------------

Description

This function is used to fit a quantile regression model when the response is binary.

Usage

```
rq.bin(formula, tau = 0.5, data, weights = NULL, contrasts = NULL,  
normalize = "last", control = NULL, fit = TRUE)  
rqbin.fit(x, y, tau = 0.5, weights, control)
```

Arguments

formula	an object of class formula : a symbolic description of the model to be fitted.
x	the design matrix.
y	the response variable.
tau	quantile to be estimated.
data	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>lqm</code> is called.
weights	an optional vector of weights to be used in the fitting process. Should be <code>NULL</code> or a numeric vector - not yet implemented.
contrasts	an optional list. See the <code>contrasts.arg</code> of model.matrix.default .
normalize	character specifying the type of normalization of the coefficients: if "last" (default), the last coefficient is set equal to 1; if "all", the vector of all coefficients except the intercept has norm equal to 1.
control	list of control parameters of the fitting process. See rqbinControl .
fit	logical flag. If <code>FALSE</code> the function returns a list of arguments to be passed to rqbin.fit .

Details

A binary quantile regression model is fitted as linear specification of the quantile function of a latent response variable (Manski 1975, 1985). The function `rqbin.fit` calls the Fortran routine `simann.f` implementing the simulated annealing algorithm of Goffe et al (1994) – original code by William Goffe, modified by Gregory Kordas. Normalization is necessary for estimation to be possible. The normalization proposed by Horowitz (1992) assumes that there is a continuous regressor independent of the (latent) error and the corresponding regression coefficient is constrained to be equal to 1. Therefore, the user must ensure that the last term in `formula` or the last column in the matrix `x` corresponds to such regressor. If the argument `normalize = "all"`, then the normalization proposed by Manski (1975) is applied so that the norm of the vector with all the 'slopes' (i.e., excluding the intercept), is equal to 1.

Value

a list of class `rq.bin` containing the following components

<code>coefficients</code>	a vector of coefficients. <code>coefficients</code> is a named matrix of coefficients when <code>tau</code> is a vector of values.
<code>logLik</code>	the log-likelihood.
<code>opt</code>	details on optimization.
<code>call</code>	the matched call.
<code>term.labels</code>	names for theta.
<code>terms</code>	the terms object used.
<code>nobs</code>	the number of observations.
<code>edf</code>	the number of parameters (minus 1 if <code>normalize</code> is last).
<code>rdf</code>	the number of residual degrees of freedom.
<code>tau</code>	the estimated quantile(s).
<code>x</code>	the model matrix.
<code>y</code>	the model response.
<code>weights</code>	the weights used in the fitting process (a vector of 1's if <code>weights = NULL</code>).
<code>levels</code>	factors levels.
<code>control</code>	list of control parameters used for optimization (see <code>rqbinControl</code>).
<code>normalize</code>	type of normalization.

Author(s)

Marco Geraci

References

- Goffe WL, Ferrier GD, Rogers J. Global optimization of statistical functions with simulated annealing. *Journal of Econometrics* 1994;60(1):65-99. Code retrieved from <http://econpapers.repec.org/software/wpawuwppr/9406001.htm>.
- Kordas G. Smoothed binary regression quantiles. *Journal of Applied Econometrics* 2006;21(3):387-407. Code retrieved from <http://qed.econ.queensu.ca/jae/2006-v21.3/kordas/>.
- Horowitz JL. A Smoothed Maximum Score Estimator for the Binary Response Model. *Econometrica* 1992;60(3):505-531.
- Manski CF. Maximum score estimation of the stochastic utility model of choice. *Journal of Econometrics* 1975;3(3):205-228.
- Manski, CF. Semiparametric analysis of discrete response: Asymptotic properties of the maximum score estimator. *Journal of Econometrics* 1985;27(3):313-333.

Description

This function is used to fit a quantile regression model when the response is a count variable.

Usage

```
rq.counts(formula, data = sys.frame(sys.parent()), tau = 0.5, tsf = "bc", symm = TRUE,
          dbounded = FALSE, lambda = 0, subset, weights, na.action, contrasts = NULL,
          offset = NULL, method = "fn", M = 50, zeta = 1e-5, B = 0.999, cn = NULL,
          alpha = 0.05)
```

Arguments

formula	an object of class <code>formula</code> : a symbolic description of the model to be fitted.
data	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>rq.counts</code> is called.
tau	quantile to be estimated.
tsf	transformation to be used. Possible options are <code>mcjI</code> for Proposal I and <code>bc</code> for Box-Cox. The latter is the default, with <code>lambda = 0</code> , i.e. the logarithmic transformation.
symm	logical flag. If TRUE and <code>tsf = 'mcj'</code> , the symmetric Proposal I transformation is used.
dbounded	logical flag. If TRUE the response is assumed to be doubly bounded on $[a,b]$. If FALSE (default) the response is assumed to be singly bounded (ie, strictly positive).
lambda	a numerical value for the transformation parameter. This is provided by the user or set to zero if not specified.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of weights to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain NAs.
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
offset	an optional offset to be included in the model frame.
method	estimation method for the fitting process. See <code>rq</code> .
M	number of dithered samples.
zeta	small constant (see References).
B	right boundary for uniform random noise $U[0,B]$ to be added to the response variable (see References).
cn	small constant to be passed to <code>Fn</code> (see Theorem 3, Machado and Santos Silva).
alpha	significance level.

Details

A linear quantile regression model is fitted to the log–transformed response. The transformation of the response can be changed with arguments `tsf`, `symm`, `dbounded`, `lambda` (see `bc`). The notation used here follows closely that of Machado and Santos Silva (2005). This function is based on routines from package `quantreg` (Koenker, 2013). See also `lqm.counts` from package `lqmm` (Geraci, 2014) for Laplace gradient estimation.

Value

a list of class `rq.counts` containing the following components

<code>call</code>	the matched call.
<code>method</code>	the fitting algorithm for <code>rq</code> .
<code>x</code>	the model matrix.
<code>y</code>	the model response.
<code>tau</code>	the order of the estimated quantile(s).
<code>tsf</code>	transformation used (see also <code>attributes(tsf)</code>).
<code>coefficients</code>	regression quantile (on the log–scale).
<code>fitted.values</code>	fitted values (on the response scale).
<code>tTable</code>	coefficients, standard errors, etc.
<code>offset</code>	offset.
<code>M</code>	specified number of dithered samples for standard error estimation.
<code>Mn</code>	actual number of dithered samples used for standard error estimation that gave an invertible <code>D</code> matrix (Machado and Santos Silva, 2005).
<code>InitialPar</code>	starting values for coefficients.
<code>terms</code>	the terms object used.
<code>term.labels</code>	names of coefficients.
<code>rdf</code>	the number of residual degrees of freedom.

Author(s)

Marco Geraci

References

- Geraci M and Jones MC. Improved transformation-based quantile regression. *Canadian Journal of Statistics* 2015;43(1):118-132.
- Koenker R (2013). `quantreg`: Quantile Regression. R package version 5.05. URL <http://CRAN.R-project.org/package=quantreg>.
- Machado JAF and Santos Silva JMC (2005). Quantiles for counts. *Journal of the American Statistical Association*, 100(472), 1226–1237.

See Also

[residuals.rq.counts](#), [predict.rq.counts](#), [coef.rq.counts](#), [maref.rq.counts](#)

Examples

```
# Esterase data
data(esterase)

# Fit quantiles 0.25 and 0.75
fit1 <- rq.counts(Count ~ Esterase, tau = 0.25, data = esterase, M = 50)
coef(fit1)
fit2 <- rq.counts(Count ~ Esterase, tau = 0.75, data = esterase, M = 50)
coef(fit2)

# Plot
with(esterase, plot(Count ~ Esterase))
lines(esterase$Esterase, fit1$fitted.values, col = "blue")
lines(esterase$Esterase, fit2$fitted.values, col = "red")
legend(8, 1000, lty = c(1,1), col = c("blue", "red"), legend = c("tau = 0.25", "tau = 0.75"))
```

 rqbinControl

Control parameters for rqbin estimation

Description

A list of parameters for controlling the fitting process based on simulated annealing.

Usage

```
rqbinControl(theta = NULL, lower = NULL, upper = NULL, maximise = TRUE, rt = 0.15,
  tol = 1e-06, ns = 10, nt = 20, neps = 4, maxiter = 1e+05, sl = NULL, vm = NULL,
  seed1 = 1, seed2 = 2, temp = 10, sgn = 1)
```

Arguments

theta	starting values for the regression coefficients.
lower	lower bound for the regression coefficients.
upper	upper bound for the regression coefficients.
maximise	logical flag. If TRUE the algorithm maximises the objective function.
rt	parameter.
tol	tolerance expressed as absolute change of the log-likelihood.
ns	parameter.
nt	parameter.
neps	parameter.

maxiter	maximum number of iterations.
sl	parameter.
vm	parameter.
seed1	random numbers seed.
seed2	random numbers seed.
temp	temperature of the algorithm.
sgn	sign of the objective function.

Details

For more details on specific parameters, see Goffe et al (1994).

Author(s)

Marco Geraci

References

Goffe WL, Ferrier GD, Rogers J. Global optimization of statistical functions with simulated annealing. *Journal of Econometrics* 1994;60(1):65-99. Code retrieved from <http://econpapers.repec.org/software/wpawuwppr/9406001.htm>.

See Also

[rq.bin](#)

rrq

Restricted Regression Quantiles

Description

This function fits a restricted quantile regression model to avoid crossing of quantile curves.

Usage

```
rrq(formula, tau, data, subset, weights, na.action, method = "fn",
model = TRUE, contrasts = NULL, ...)
rrq.fit(x, y, tau, method = "fn", ...)
rrq.wfit(x, y, tau, weights, method = "fn", ...)
```

Arguments

formula	a formula object, with the response on the left of a \sim operator, and the terms, separated by + operators, on the right.
x	the design matrix.
y	the response variable.
tau	the quantile(s) to be estimated.
data	a data frame in which to interpret the variables named in the formula.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of weights to be used in the fitting process. Should be NULL or a numeric vector.
na.action	a function which indicates what should happen when the data contain NAs.
method	the algorithm used to compute the fit (see rq).
model	if TRUE then the model frame is returned. This is essential if one wants to call <code>summary</code> subsequently.
contrasts	a list giving contrasts for some or all of the factors default = NULL appearing in the model formula. The elements of the list should have the same name as the variable and should be either a contrast matrix (specifically, any full-rank matrix with as many rows as there are levels in the factor), or else a function to compute such a matrix given the number of levels.
...	optional arguments passed to <code>rq.fit</code> or <code>rq.wfit</code> .

Author(s)

Marco Geraci

References

He X. Quantile curves without crossing. *The American Statistician* 1997;51(2):186-192.

Koenker R (2013). `quantreg`: Quantile Regression. R package version 5.05. URL <http://CRAN.R-project.org/package=quantreg>.

Examples

```
data(esterase)

# Fit standard quantile regression
fit <- quantreg::rq(Count ~ Esterase, data = esterase, tau = c(.1,.25,.5,.75,.9))
yhat <- fit$fitted.values

# Fit restricted quantile regression
fitr <- rrq(Count ~ Esterase, data = esterase, tau = c(.1,.25,.5,.75,.9))
yhat2 <- predict(fitr)

# Plot results
```

```

par(mfrow = c(1, 2))

# Plot regression quantiles
with(esterase, plot(Count ~ Esterase, pch = 16, cex = .8))
apply(yhat, 2, function(y,x) lines(x,y,lwd = 1.5), x = esterase$Esterase)

# Plot restricted regression quantiles
with(esterase, plot(Count ~ Esterase, pch = 16, cex = .8))
apply(yhat2, 2, function(y,x) lines(x,y,lwd = 1.5), x = esterase$Esterase)

```

sparsity.rqt

Sparsity Estimation

Description

This function estimates the density and sparsity functions of the residuals from a rq or a rqt object.

Usage

```

sparsity(object, se = "nid", hs = TRUE)
## S3 method for class 'rq'
sparsity(object, se = "nid", hs = TRUE)
## S3 method for class 'rqs'
sparsity(object, se = "nid", hs = TRUE)
## S3 method for class 'rqt'
sparsity(object, se = "nid", hs = TRUE)

```

Arguments

object	a rq, rqs or rqt object.
se	"iid" if errors are assumed independent and identically distributed; "nid" (default) if independent but not identically distributed; "ker" which uses a kernel estimate of the sandwich as proposed by Powell (1991).
hs	logical flag. If TRUE (default) the Hall-Sheather rule is used. Otherwise, the Bofinger's rule is used.

Details

This function is based on the code from `quantreg::summary.rq` and `quantreg::bandwidth.rq` to estimate the sparsity function for linear quantile regression models (Koenker and Bassett, 1978) and transformation models of Geraci and Jones (2014).

Value

sparsity returns an object of `class` list that contains three elements:

density	estimate of the density of the residuals.
sparsity	estimate of the sparsity of the residuals.
bandwidth	bandwidth used for estimation.

Author(s)

Marco Geraci

References

Geraci M and Jones MC. Improved transformation-based quantile regression. *Canadian Journal of Statistics* 2015;43(1):118-132.

Koenker R (2013). *quantreg: Quantile Regression*. R package version 5.05. URL <http://CRAN.R-project.org/package=quantreg>.

Koenker R, Bassett G. Regression quantiles. *Econometrica*. 1978;46(1):33-50.

Powell JL. Estimation of monotonic regression models under quantile restrictions. In: Barnett W, Powell J, Tauchen G, editors. *Nonparametric and Semiparametric Methods in Econometrics and Statistics: Proceedings of the Fifth International Symposium on Economic Theory and Econometrics*. New York, NY: Cambridge University Press 1991. p. 357-84.

See Also

[rq](#)

Examples

```
## Not run:

data(trees)

# 'rqt' object

fit.rqt <- tsrq(Volume ~ Height, tsf = "bc", symm = FALSE, data = trees,
lambda = seq(-10, 10, by = 0.01), tau = 0.5)
sparsity(fit.rqt)

# 'rq' object

fit.rq <- rq(Volume ~ Height, data = trees)
sparsity(fit.rq, se = "iid")
sparsity(fit.rq, se = "nid")
sparsity(fit.rq, se = "ker")

## End(Not run)
```

Description

This functions gives a summary list for a quantile regression transformation model.

Usage

```
## S3 method for class 'rqt'
summary(object, alpha = 0.05, se = "boot", R = 50,
sim = "ordinary", stype = "i", conditional = FALSE, ...)
```

Arguments

object	an object of <code>class</code> <code>rqt</code> .
alpha	numeric value to determine the confidence level (1-alpha) of the required interval.
se	specifies the method used to compute standard errors. For conditional inference (<code>conditional = TRUE</code>), see argument <code>se</code> in <code>summary.rq</code> . For unconditional inference (<code>conditional = FALSE</code>), see details below.
R	number of bootstrap replications.
sim	see argument <code>sim</code> in <code>boot</code> .
stype	see argument <code>stype</code> in <code>boot</code> .
conditional	logical flag. If <code>TRUE</code> , the transformation parameter is assumed to be known and conditional inference is carried out.
...	if <code>conditional = TRUE</code> , additional arguments for <code>summary.rq</code> in package <code>quantreg</code> . If <code>conditional = FALSE</code> , additional arguments for <code>boot</code> in package <code>boot</code> .

Details

If inference is carried out conditionally on the transformation parameter (ie, assuming this is *known* rather than estimated), any type of summary for regression quantiles can be used (see `summary.rq`).

For unconditional inference (`conditional = FALSE`), there are three methods available: `boot` for bootstrap; `iid` for large- n approximation of the standard errors under IID assumptions; `nid` for large- n approximation of the standard errors under NID assumptions. See Powell (1991), Chamberlain (1994) and Geraci and Jones (2015).

Author(s)

Marco Geraci

References

Canty A and Ripley B (2014). `boot`: Bootstrap R (S-Plus) Functions. R package version 1.3-11.

Chamberlain G. Quantile regression, censoring, and the structure of wages. In: Sims C, editor. *Advances in Econometrics: Sixth World Congress*. 1. Cambridge, UK: Cambridge University Press; 1994.

Davison AC and Hinkley DV (1997). *Bootstrap Methods and Their Applications*. Cambridge University Press, Cambridge.

Geraci M and Jones MC. Improved transformation-based quantile regression. *Canadian Journal of Statistics* 2015;43(1):118-132.

Mu YM, He XM. Power transformation toward a linear regression quantile. *Journal of the American Statistical Association* 2007;102(477):269-279.

Powell JL. Estimation of monotonic regression models under quantile restrictions. In: Barnett W, Powell J, Tauchen G, editors. *Nonparametric and Semiparametric Methods in Econometrics and Statistics: Proceedings of the Fifth International Symposium on Economic Theory and Econometrics*. New York, NY: Cambridge University Press 1991. p. 357-84.

See Also

[tsrq](#), [rcrq](#), [tsrq2](#) or [nlrq2](#)

summary.rrq

Summary for Restricted Quantile Regression Models

Description

This functions gives a summary list for a restricted quantile regression model.

Usage

```
## S3 method for class 'rrq'
summary(object, alpha = 0.05, se = "boot", R = 50,
sim = "ordinary", stype = "i", ...)
```

Arguments

object	an object of class <code>rrq</code> .
alpha	numeric value to determine the confidence level (1-alpha) of the required interval.
se	specifies the method used to compute standard errors. Currently, bootstrap is the only method available.
R	number of bootstrap replications.
sim	see argument <code>sim</code> in boot .
stype	see argument <code>stype</code> in boot .
...	additional arguments for boot in package <code>boot</code> .

Details

A bootstrap approach is used for inference. Future developments of this function will include asymptotic standard errors.

Author(s)

Marco Geraci

References

- Canty A and Ripley B (2014). boot: Bootstrap R (S-Plus) Functions. R package version 1.3-15.
- Davison AC and Hinkley DV (1997). Bootstrap Methods and Their Applications. Cambridge University Press, Cambridge.
- He X (1997). Quantile Curves without Crossing. The American Statistician, 51(2), 186-192.

 tsrq

Quantile Regression Transformation Models

Description

These functions are used to fit quantile regression transformation models.

Usage

```
tsrq(formula, data = sys.frame(sys.parent()), tsf = "mcjI", symm = TRUE,
     dbounded = FALSE, lambda = NULL, conditional = FALSE, tau = 0.5,
     subset, weights, na.action, contrasts = NULL, method = "fn")
tsrq2(formula, data = sys.frame(sys.parent()), dbounded = FALSE, lambda = NULL,
     delta = NULL, conditional = FALSE, tau = 0.5, subset, weights, na.action,
     contrasts = NULL, method = "fn")
rcrq(formula, data = sys.frame(sys.parent()), tsf = "mcjI", symm = TRUE,
     dbounded = FALSE, lambda = NULL, tau = 0.5, subset, weights, na.action,
     contrasts = NULL, method = "fn")
nlrq2(formula, data = sys.frame(sys.parent()), par = NULL, dbounded = FALSE,
     tau = 0.5, subset, weights, na.action, contrasts = NULL)
```

Arguments

- | | |
|---------------|---|
| formula | an object of class " formula " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'. |
| data | an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. By default the variables are taken from the environment from which the call is made. |
| tsf | transformation to be used. Possible options are <code>mcjI</code> for Proposal I transformation models (default), <code>bc</code> for Box-Cox and <code>ao</code> for Aranda-Ordaz transformation models. |
| symm | logical flag. If TRUE (default) a symmetric transformation is used. |
| dbounded | logical flag. If TRUE the response is assumed to be doubly bounded on $[a,b]$. If FALSE (default) the response is assumed to be singly bounded (ie, strictly positive). |
| lambda, delta | values of transformation parameters for grid search. |

conditional	logical flag. If TRUE, the transformation parameter is assumed to be known and this must be provided via the arguments <code>lambda</code> , <code>delta</code> in vectors of the same length as <code>tau</code> .
par	vector of length $p + 2$ of initial values for the parameters to be optimized over. The first p values are for the regression coefficients while the last 2 are for the transformation parameters <code>lambda</code> and <code>delta</code> in <code>mcjII</code> . These initial values are passed to <code>optim</code> .
tau	the quantile(s) to be estimated. See <code>rq</code> .
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of weights to be used in the fitting process. Should be NULL or a numeric vector.
na.action	a function which indicates what should happen when the data contain NAs.
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
method	fitting algorithm for <code>rq</code> (default is Frisch-Newton interior point method "fn").

Details

These functions implement quantile regression transformation models as discussed by Geraci and Jones (see references). The general model is assumed to be $Q_{h(Y)|X}(\tau) = \eta = Xb$, where Q denotes the conditional quantile function, Y is the response variable, X a design matrix, and h is a monotone one- or two-parameter transformation. A typical model specified in `formula` has the form `response ~ terms` where `response` is the (numeric) response vector and `terms` is a series of terms which specifies a linear predictor for the quantile of the transformed response. The response, which is singly or doubly bounded, i.e. `response > 0` or `0 <= response <= 1` respectively, undergoes the transformation specified in `tsf`. If the response is bounded in the generic $[a, b]$ interval, the latter is automatically mapped to $[0, 1]$ and no further action is required. If, however, the response is singly bounded and contains negative values, it is left to the user to offset the response or the code will produce an error.

The functions `tsrq` and `tsrq2` use a two-stage (TS) estimator (Fitzenberger et al, 2010) for, respectively, one- and two-parameter transformations. The function `rcrq` (one-parameter transformations) is based on the residual cusum process estimator proposed by Mu and He (2007), while the function `n1rq2` (two-parameter transformations) is based on Nelder-Mead optimization (Geraci and Jones).

Value

`tsrq`, `tsrq2`, `rcrq`, `n1rq2` return an object of class `rqf`. This is a list that contains as typical components:

	the first <code>nt = length(tau)</code> elements of the list store the results from fitting linear quantile models on the transformed scale of the response.
<code>call</code>	the matched call.
<code>method</code>	the fitting algorithm for <code>rq</code> or <code>optim</code> .
<code>y</code>	the response – untransformed scale.
<code>theta</code>	if <code>dbounded = TRUE</code> , the response mapped to the unit interval.

x	the model matrix.
weights	the weights used in the fitting process (a vector of 1's if weights is missing or NULL).
tau	the order of the estimated quantile(s).
lambda	the estimated parameter lambda.
eta	the estimated parameters lambda and delta in the two-parameter Proposal II transformation.
lambda.grid	grid of lambda values used for estimation.
delta.grid	grid of delta values used for estimation.
tsf	transformation used (see also <code>attributes(tsf)</code>).
objective	values of the objective function minimised over the transformation parameter(s). This is an array of dimension $c(nl, nt)$ or $c(nl, nd, nt)$, where $nl = \text{length}(\text{lambda.grid})$, $nd = \text{length}(\text{delta.grid})$ and $nt = \text{length}(\text{tau})$.
optimum	value of the objective function at solution.
coefficients	quantile regression coefficients – transformed scale.
fitted.values	fitted values.
rejected	proportion of inadmissible observations (Fitzenberger et al, 2010).
terms	the terms used.
term.labels	names of coefficients.
rdf	residual degrees of freedom.

Author(s)

Marco Geraci

References

- Aranda-Ordaz FJ. On two families of transformations to additivity for binary response data. *Biometrika* 1981;68(2):357-363.
- Box GEP, Cox DR. An analysis of transformations. *Journal of the Royal Statistical Society Series B-Statistical Methodology* 1964;26(2):211-252.
- Dehbi H-M, Cortina-Borja M, and Geraci M. Aranda-Ordaz quantile regression for student performance assessment. *Journal of Applied Statistics*. 2016;43(1):58-71.
- Fitzenberger B, Wilke R, Zhang X. Implementing Box-Cox quantile regression. *Econometric Reviews* 2010;29(2):158-181.
- Geraci M and Jones MC. Improved transformation-based quantile regression. *Canadian Journal of Statistics* 2015;43(1):118-132.
- Jones MC. Connecting distributions with power tails on the real line, the half line and the interval. *International Statistical Review* 2007;75(1):58-69.
- Koenker R (2013). `quantreg`: Quantile Regression. R package version 5.05. URL <http://CRAN.R-project.org/package=quantreg>.
- Mu YM, He XM. Power transformation toward a linear regression quantile. *Journal of the American Statistical Association* 2007;102(477):269-279.

See Also

[predict.rqt](#), [summary.rqt](#), [coef.rqt](#), [maref.rqt](#)

Examples

```
#####
## Example 1 - singly bounded (from Geraci and Jones, 2014)

## Not run:

data(trees)
require(MASS)

dx <- 0.01

lambda0 <- boxcox(Volume ~ log(Height), data = trees,
lambda = seq(-0.9, 0.5, by = dx))
lambda0 <- lambda0$x[which.max(lambda0$y)]
trees$z <- bc(trees$Volume,lambda0)
trees$y <- trees$Volume
trees$x <- log(trees$Height)
trees$x <- trees$x - mean(log(trees$Height))

fit.lm <- lm(z ~ x, data = trees)
newd <- data.frame(x = log(seq(min(trees$Height),
max(trees$Height), by = 0.1)))
newd$x <- newd$x - mean(log(trees$Height))
ylm <- invbc(predict(fit.lm, newdata = newd), lambda0)

lambdas <- list(bc = seq(-10, 10, by=dx),
mcjIs = seq(0,10,by = dx), mcjIa = seq(0,20,by = dx))

taus <- 1:3/4
fit0 <- tsrq(y ~ x, data = trees, tsf = "bc", symm = FALSE,
lambda = lambdas$bc, tau = taus)
fit1 <- tsrq(y ~ x, data = trees, tsf = "mcjI", symm = TRUE,
dbounded = FALSE, lambda = lambdas$mcjIs, tau = taus)
fit2 <- tsrq(y ~ x, data = trees, tsf = "mcjI", symm = FALSE,
dbounded = FALSE, lambda = lambdas$mcjIa, tau = taus)

par(mfrow = c(1,3), mar = c(7.1, 7.1, 5.1, 2.1), mgp = c(5, 2, 0))

cx.lab <- 2.5
cx.ax <- 2
lw <- 2
cx <- 2
xb <- "log(Height)"
yb <- "Volume"
xl <- range(trees$x)
yl <- c(5,80)
```

```

yhat <- predict(fit0, newdata = newd)
plot(y ~ x, data = trees, xlim = xl, ylim = yl, main = "Box-Cox",
     cex.lab = cx.lab, cex.axis = cx.ax, cex.main = cx.lab,
     cex = cx, xlab = xb, ylab = yb)
lines(newd$x, yhat[,1], lwd = lw)
lines(newd$x, yhat[,2], lwd = lw)
lines(newd$x, yhat[,3], lwd = lw)
lines(newd$x, ylm, lwd = lw, lty = 2)

yhat <- predict(fit1, newdata = newd)
plot(y ~ x, data = trees, xlim = xl, ylim = yl, main = "Proposal I (symmetric)",
     cex.lab = cx.lab, cex.axis = cx.ax, cex.main = cx.lab,
     cex = cx, xlab = xb, ylab = yb)
lines(newd$x, yhat[,1], lwd = lw)
lines(newd$x, yhat[,2], lwd = lw)
lines(newd$x, yhat[,3], lwd = lw)
lines(newd$x, ylm, lwd = lw, lty = 2)

yhat <- predict(fit2, newdata = newd)
plot(y ~ x, data = trees, xlim = xl, ylim = yl, main = "Proposal I (asymmetric)",
     cex.lab = cx.lab, cex.axis = cx.ax, cex.main = cx.lab,
     cex = cx, xlab = xb, ylab = yb)
lines(newd$x, yhat[,1], lwd = lw)
lines(newd$x, yhat[,2], lwd = lw)
lines(newd$x, yhat[,3], lwd = lw)
lines(newd$x, ylm, lwd = lw, lty = 2)

## End(Not run)

#####
## Example 2 - doubly bounded

## Not run:

data(Chemistry)

Chemistry$gcse_gr <- cut(Chemistry$gcse, c(0,seq(4,8,by=0.5)))
with(Chemistry, plot(score ~ gcse_gr, xlab = "GCSE score",
                    ylab = "A-level Chemistry score"))

# The dataset has > 31000 observations and computation can be slow
set.seed(178)
chemsub <- Chemistry[sample(1:nrow(Chemistry), 2000), ]

# Fit symmetric Aranda-Ordaz quantile 0.9
tsrq(score ~ gcse, data = chemsub, tsf = "ao", symm = TRUE,
     lambda = seq(0,2,by=0.01), tau = 0.9)

# Fit symmetric Proposal I quantile 0.9
tsrq(score ~ gcse, data = chemsub, tsf = "mcjI", symm = TRUE,
     dbounded = TRUE, lambda = seq(0,2,by=0.01), tau = 0.9)

```

```

# Fit Proposal II quantile 0.9 (Nelder-Mead)
nlrq2(score ~ gcse, data = chemsub, dbounded = TRUE, tau = 0.9)

# Fit Proposal II quantile 0.9 (grid search)
# This is slower than nlrq2 but more stable numerically
tsrq2(score ~ gcse, data = chemsub, dbounded = TRUE,
lambda = seq(0, 2, by = 0.1), delta = seq(0, 2, by = 0.1),
tau = 0.9)

## End(Not run)

#####
## Example 3 - doubly bounded

data(labor)

new <- labor
new$y <- new$pain
new$x <- (new$time-30)/30
new$x_gr <- as.factor(new$x)

par(mfrow = c(2,2))

cx.lab <- 1
cx.ax <- 2.5
cx <- 2.5
yl <- c(0,0.06)

hist(new$y[new$treatment == 1], xlab = "Pain score", main = "Medication group",
freq = FALSE, ylim = yl)

plot(y ~ x_gr, new, subset = new$treatment == 1, xlab = "Time (min)",
ylab = "Pain score", axes = FALSE, range = 0)
axis(1, at = 1:6, labels = c(0:5)*30 + 30)
axis(2)
box()

hist(new$y[new$treatment == 0], xlab = "Pain score", main = "Placebo group",
freq = FALSE, ylim = yl)

plot(y ~ x_gr, new, subset = new$treatment == 0, xlab = "Time (min)",
ylab = "Pain score", axes = FALSE, range = 0)
axis(1, at = 1:6, labels = (0:5)*30 + 30)
axis(2)
box()

#

## Not run:

taus <- c(1:3/4)

```

```

ls <- seq(0,3.5,by=0.1)

fit.aos <- tsrq(y ~ x*treatment, data = new, tsf = "ao", symm = TRUE,
dbounded = TRUE, tau = taus, lambda = ls)
fit.aoa <- tsrq(y ~ x*treatment, data = new, tsf = "ao", symm = FALSE,
dbounded = TRUE, tau = taus, lambda = ls)
fit.mcjs <- tsrq(y ~ x*treatment, data = new, tsf = "mcjI", symm = TRUE,
dbounded = TRUE, tau = taus, lambda = ls)
fit.mcja <- tsrq(y ~ x*treatment, data = new, tsf = "mcjI", symm = FALSE,
dbounded = TRUE, tau = taus, lambda = ls)
fit.mcj2 <- tsrq2(y ~ x*treatment, data = new, dbounded = TRUE, tau = taus,
lambda = seq(0,2,by=0.1), delta = seq(0,1.5,by=0.3))
fit.nlrq <- nlrq2(y ~ x*treatment, data = new, par = coef(fit.mcj2, all = TRUE)[,1],
dbounded = TRUE, tau = taus)

sel <- 0 # placebo (change to sel == 1 for medication group)
x <- new$x
nd <- data.frame(x = seq(min(x), max(x), length=200), treatment = sel)
xx <- nd$x+1

par(mfrow = c(2,2))

fit <- fit.aos
yhat <- predict(fit, newdata = nd)

plot(y ~ x_gr, new, subset = new$treatment == sel, xlab = "",
ylab = "Pain score", axes = FALSE, main = "Aranda-Ordaz (s)",
range = 0, col = grey(4/5))
apply(yhat, 2, function(y,x) lines(x, y, lwd = 2), x = xx)
axis(1, at = 1:6, labels = (0:5)*30 + 30)
axis(2, at = c(0, 25, 50, 75, 100))
box()

fit <- fit.aoa
yhat <- predict(fit, newdata = nd)

plot(y ~ x_gr, new, subset = new$treatment == sel, xlab = "", ylab = "",
axes = FALSE, main = "Aranda-Ordaz (a)", range = 0, col = grey(4/5))
apply(yhat, 2, function(y,x) lines(x, y, lwd = 2), x = xx)
axis(1, at = 1:6, labels = (0:5)*30 + 30)
axis(2, at = c(0, 25, 50, 75, 100))
box()

fit <- fit.mcjs
yhat <- predict(fit, newdata = nd)

plot(y ~ x_gr, new, subset = new$treatment == sel, xlab = "Time (min)",
ylab = "Pain score", axes = FALSE, main = "Proposal I (s)",
range = 0, col = grey(4/5))
apply(yhat, 2, function(y,x) lines(x, y, lwd = 2), x = xx)
axis(1, at = 1:6, labels = (0:5)*30 + 30)
axis(2, at = c(0, 25, 50, 75, 100))
box()

```

```
fit <- fit.mcj2
yhat <- predict(fit, newdata = nd)

plot(y ~ x_gr, new, subset = new$treatment == sel, xlab = "Time (min)",
      ylab = "", axes = FALSE, main = "Proposal II", range = 0, col = grey(4/5))
apply(yhat, 2, function(y,x) lines(x, y, lwd = 2), x = xx)
axis(1, at = 1:6, labels = (0:5)*30 + 30)
axis(2, at = c(0, 25, 50, 75, 100))
box()

## End(Not run)
```

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