

Package ‘qrmix’

July 22, 2025

Type Package

Title Quantile Regression Mixture Models

Version 0.9.0

Date 2017-04-24

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Description Implements the robust algorithm for fitting finite mixture models based on quantile regression proposed by Emir et al., 2017 (unpublished).

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LazyData TRUE

Imports MASS, quantreg

RoxygenNote 6.0.1

NeedsCompilation no

Repository CRAN

Date/Publication 2017-05-03 21:49:24 UTC

Contents

Bisquare	2
blood.pressure	2
Huber	3
plot.qrmix	4
predict.qrmix	5
qrmix	6
summary.qrmix	7
Index	9

Bisquare

Tukey's Bisquare Loss

Description

"Bisquare" evaluates Tukey's Bisquare function defined as

$$f(r) = \begin{cases} 1 - (1 - (\frac{r}{c})^2)^3 & |r| \leq c \\ 1 & |r| > c \end{cases}$$

Usage

```
Bisquare(r, c = 4.685)
```

Arguments

r a real number or vector.

c a positive number. If the value is negative, it's absolute value will be used.

Examples

```
set.seed(1)
x = rnorm(200, mean = 3)
y = Bisquare(x)
plot(x, y)
```

blood.pressure

Blood Pressure Data for qrmix

Description

Simulated blood pressure data created for usage in qrmix examples.

Usage

```
blood.pressure
```

Format

A data frame with 500 observations on the following 7 variables.

bmi a numeric vector referring to body mass index

age a numeric vector

systolic a numeric vector referring to systolic blood pressure

diastolic a numeric vector referring to diastolic blood pressure

gender a factor with levels female and male

race a factor with levels white, black, and other

smoking a factor with levels yes and no

Note

This data does not include any real patient information.

Huber	<i>Huber Loss</i>
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Description

Evaluates the Huber loss function defined as

$$f(r) = \begin{cases} \frac{1}{2}|r|^2 & |r| \leq c \\ c(|r| - \frac{1}{2}c) & |r| > c \end{cases}$$

Usage

```
Huber(r, c = 1.345)
```

Arguments

r a real number or vector.

c a positive number. If the value is negative, it's absolute value will be used.

Examples

```
set.seed(1)
x = rnorm(200, mean = 1)
y = Huber(x)
plot(x, y)
abline(h = (1.345)^2/2)
```

plot.qrmix

*Plot Method for a qrmix Object***Description**

Three types of plots (chosen with `type`) are currently available: density of the response variable by cluster, plots of the response variable against each covariate included in the model (scatterplots with the `k` fitted lines for continues variables and boxplots by cluster for the categorical variables), and boxplots of the residuals by cluster.

Usage

```
## S3 method for class 'qrmix'
plot(x, data = NULL, type = c(1,2,3), lwd = 2, bw = "SJ", adjust = 2, ...)
```

Arguments

<code>x</code>	a fitted object of class "qrmix".
<code>data</code>	the data used to fit the model object. It is only necessary when the when the parameter <code>xy</code> was set to <code>FALSE</code> when fitting the <code>qrmix</code> model.
<code>type</code>	a numeric vector with values chosen from 1:3 to specify a subset of types of plots required.
<code>lwd</code>	the line width for the first type of plot (density plot), a positive number. If a negative number is given, <code>lwd = 1</code> will be used instead. See par .
<code>bw</code>	the smoothing bandwidth to be used to obtain the density for the first type of plot. See density for details.
<code>adjust</code>	the bandwidth used is <code>adjust*bw</code> . See density for details.
<code>...</code>	other argumets passed to other methods.

Examples

```
data(blood.pressure)

#qrmix model using default function values:
mod1 = qrmix(bmi ~ ., data = blood.pressure, k = 3)
plot(mod1)
plot(mod1, type = c(1,3), lwd = 1)
```

predict.qrmix	<i>Predict Method for qrmix Fits</i>
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Description

Obtains clusters, predictions, or residuals from a fitted qrmix object.

Usage

```
## S3 method for class 'qrmix'
predict(object, newdata = NULL, type = "clusters", ...)
```

Arguments

object	a fitted object of class "qrmix".
newdata	optional data frame for which clusters, predictions, or residuals will be obtained from the qrmix fitted object. If omitted, the training values will be used.
type	the type of prediction. type = "clusters" (default value) for predicted clusters, "yhat" for the response predicted value corresponding to the predicted clusters, "residuals" for the residuals corresponding to the response predicted values.
...	other arguments passed to other methods.

Value

A vector with predicted clusters, responses, or residuals, depending on type.

Examples

```
data(blood.pressure)

set.seed(8)
sampleInd = sort(sample(1:500, 400))
bpSample1 = blood.pressure[sampleInd,]
bpSample2 = blood.pressure[-sampleInd,]

mod1 = qrmix(bmi ~ ., data = bpSample1, k = 3)

#Cluster assigned to the training values
predict(mod1)

#Residuals corresponding to the response predicted values from mod1 for new data
predict(mod1, newdata = bpSample2, type = "residuals")
```

qrmix

*Quantile Regression Classification***Description**

qrmix estimates the components of a finite mixture model by using quantile regression to select a group of quantiles that satisfy an optimality criteria chosen by the user.

Usage

```
qrmix(formula, data, k, Ntau=50, alpha=0.03, lossFn="Squared", fitMethod="lm",
xy=TRUE, ...)
```

Arguments

formula	an object of class "formula".
data	an optional data frame that contains the variables in formula.
k	number of clusters.
Ntau	an optional value that indicates the number of quantiles that will be considered for quantile regression comparison. Ntau should be greater or equal than $2k$.
alpha	an optional value that will determine the minimum separation between the k quantiles that represent each of the k clusters. alpha should be smaller than $\frac{1}{2k}$.
lossFn	the loss function to be used to select the best combination of k quantiles. The available functions are "Squared", "Absolute", "Bisquare", and "Huber".
fitMethod	the method to be used for the final fitting. Use "lm" for OLS (default), "rlm" for robust regression, and "rq" to use fit from quantile regression.
xy	logical. If TRUE (the default), the data will be saved in the qrmix object.
...	additional arguments to be passed to the function determined in fitMethod.

Details

The optimality criteria is determined by the lossFn parameter. If, for example, the default value is used (lossFn = "Squared"), the k quantiles selected will minimize the sum of squared residuals. Use "Bisquare" or "Huber" to make the method less sensitive to outliers.

Value

qrmix returns an object of class "qrmix"

coefficients	a matrix with k columns that represent the coefficients for each cluster.
clusters	cluster assignment for each observation.
quantiles	the set of k quantiles that minimize the mean loss.
residuals	the residuals, response minus fitted values.
fitted.values	the fitted values.
call	the matched call.
xy	the data used if xy is set to TRUE.

References

Emir, B., Willke, R. J., Yu, C. R., Zou, K. H., Resa, M. A., and Cabrera, J. (2017), "A Comparison and Integration of Quantile Regression and Finite Mixture Modeling" (submitted).

Examples

```
data(blood.pressure)

#qrmix model using default function values:
mod1 = qrmix(bmi ~ ., data = blood.pressure, k = 3)
summary(mod1)

#qrmix model using Bisquare loss function and refitted with robust regression:
mod2 = qrmix(bmi ~ age + systolic + diastolic + gender, data = blood.pressure, k = 3,
Ntau = 25, alpha = 0.1, lossFn = "Bisquare", fitMethod = "rlm")
summary(mod2)
```

summary.qrmix

Summarizing qrmix Fits

Description

summary method for class "qrmix"

Usage

```
## S3 method for class 'qrmix'
summary(object, fitMethod=NULL, data=NULL, ...)
```

Arguments

object	an object of class "qrmix".
fitMethod	an optional refitting method if the user wants a method different than the one used to obtain "object" Use "lm" for OLS, "rlm" for robust regression, and "rq" to use fit from quantile regression.
data	data used to fit object if it is not contained in object.
...	other arguments passed to other methods.

Value

residuals	the residuals, response minus fitted values.
clusters	cluster assignment for each observation.
call	the matched call.

fitMethod	the fitting method used to obtain residuals and clusters.
quantiles	the set of k quantiles that minimize the mean loss.
clusters#	generic summary from function fitMethod for data in cluster #.

Examples

```
data(blood.pressure)

#qrmix model using default function values:
mod1 = qrmix(bmi ~ ., data = blood.pressure, k = 3)

#summary using fitMethod = "rlm" instead of the one used when fitting the model mod1
summary1 = summary(mod1, fitMethod = "rlm")

#Are the quantiles selected in this case the same as in the original model?
summary1$quantiles
mod1$quantiles
```

Index

* **datasets**

blood.pressure, [2](#)

Bisquare, [2](#)

blood.pressure, [2](#)

density, [4](#)

Huber, [3](#)

par, [4](#)

plot.qrmix, [4](#)

predict.qrmix, [5](#)

qrmix, [6](#)

summary.qrmix, [7](#)