

# Package ‘MultiKink’

May 4, 2020

**Type** Package

**Version** 0.1.0

**Title** Estimation and Inference for Multi-Kink Quantile Regression

**Description** Estimation and inference for multiple kink quantile regression. A bootstrap restarting iterative segmented quantile algorithm is proposed to estimate the multiple kink quantile regression model conditional on a given number of change points. The number of kinks is also allowed to be unknown. In such case, the backward elimination algorithm and the bootstrap restarting iterative segmented quantile algorithm are combined to select the number of change points based on a quantile BIC. A score-type based test statistic is also developed for testing the existence of kink effect. The package is based on the paper, “Wei Zhong, Chuang Wan and Wenyang Zhang (2020). Estimation and inference for multi-kink quantile regression, submitted”.

**Imports** quantreg, MASS

**Depends** R (>= 3.5.0)

**License** GPL

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.0.2

**NeedsCompilation** no

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## R topics documented:

fit.control . . . . .	2
kinkTest . . . . .	3
mkqr.bea . . . . .	4
mkqr.fit . . . . .	6
triceps . . . . .	7

**Index****9**


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fit.control	<i>Auxiliary parameters to control the model fitting.</i>
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**Description**

This is a user interface to control the auxiliary parameter in fitting multi-kink quantile regression.

**Usage**

```
fit.control(toll=1e-4,h=1,it.max=50,K.max=6,stop.if.error=TRUE,dev0=NULL,visual=FALSE,
            visualBoot=FALSE,pow=c(1,1),digits=NULL,grid=NULL,n.boot=20)
```

**Arguments**

toll	Positive convergence tolerance.
h	Positive factor (from zero to one) modifying the increments in kink parameter updates during the iterative process.
it.max	Positive integer for the maximal number of iterations.
K.max	Positive integer for the maximal given number of kink points.
stop.if.error	Logical indicating if the estimation algorithm should be stopped if some kink point estimators belong to the non-admissible set. Default is FALSE which suggests to remove the non-admissible change points automatically.
dev0	Initial objective value or deviance. Default is NULL which implies that the initial values is unknown.
visual	Logical indicating if the results of estimation process should be printed at each iteration.
visualBoot	Logical indicating if the results of estimation should be printed at each iteration in the bootstrap restarting process.
pow	The powers of the pseudo covariates employed by the algorithm.
digits	If specified it means the desired number of decimal points of the kink estimators to be used during the iterative algorithm.
grid	It measures how close between the two adjacent change points should be merged, default is NULL.
n.boot	Positive integer indicating the times of bootstrap re-sampling in the bootstrap restarting algorithm, default is 20.

**Value**

A list with the arguments as components to be used by 'mkqr.fit' and 'mkqr.bea'.

**Author(s)**

Chuang Wan

**References**

Wei Zhong, Chuang Wan and Wenyang Zhang. (2020) Estimation and inference for multi-kink quantile regression. working paper.

**See Also**

[mkqr.bea,mkqr.fit](#)

**Examples**

```
fit.control(K.max=8)
```

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kinkTest	<i>Test the existence of kink effect in the multi-kink quantile regression</i>
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**Description**

This function is used to calculate the score test statistics and its asymptotical p-value is obtained by using wild bootstrap.

**Usage**

```
kinkTest(y, thre.x, cont.z, tau, NB=200, sparsity="nid",
         bandwidth_type="Hall-Sheather")
```

**Arguments**

y	A vector of response.
thre.x	A scalar covariate with threshold effect.
cont.z	A vector of covariates with constant slopes.
tau	A given quantile level belongs to (0,1).
NB	Resampling times, 200 for default.
sparsity	The error term type. Specify one from "iid" and "nid". Default is "nid".
bandwidth_type	The bandwidth type. Specify one from "Hall-Sheather", "Bofinger", "Chamberlain". Default is "Hall-Sheather".

**Value**

A list with the elements

Tn	The statistic based on original data.
Tn.NB	The statistics by wild bootstrap.
pv	The p-value by wild bootstrap.

**Author(s)**

Chuang Wan

**References**

Wei Zhong, Chuang Wan and Wenyang Zhang. (2020) Estimation and inference for multi-kink quantile regression. working paper.

**Examples**

```
ptm <- proc.time()
##Simulated data
set.seed(123)
n <- 500
tau <- 0.5
x <- runif(n,-5,5)
z <- rnorm(n,1,1)
e <- rnorm(n,0,1)-qnorm(tau,0,1)
y <- 1+x-0.5*pmx(x-2,0)+z+e
obj <- kinkTest(y, x, z, tau, NB = 200, sparsity="nid", bandwidth_type="Hall-Sheather")
proc.time() - ptm
```

mkqr.bea

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*Fit the multi-kink quantile regression in absence of the number of change points.*

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**Description**

A quantile BIC combining the backward elimination algorithm to estimate the multi-kink quantile regression.

**Usage**

```
mkqr.bea(y, thre.x, cont.z, tau, Cn, bandwidth_type="Hall-Sheather", control=fit.control())
```

**Arguments**

y	A vector of response.
thre.x	A scalar covariate with threshold effect.
cont.z	A vector of covariates with constant slopes.
tau	The quantile level that belongs to (0,1).
Cn	A psotive number corresponding to different types of BIC.
bandwidth_type	The bandwidth type. Specify one from "Hall-Sheather", "Bofinger", "Chamberlain". Default is "Hall-Sheather".
control	A list returned by fit.control.

**Details**

this function does not need to set the number of change points in advance. The number of change points will be estimated automatically.

**Value**

A list with the elements

<code>bet.est</code>	The estimated regression coefficients with intercept.
<code>bet.se</code>	The estimated standard error of the regression coefficients.
<code>psi.est</code>	The estimated change points.
<code>psi.se</code>	The estimated standard errors of threshold parameters.
<code>n.psi</code>	The estimated number of change points.

**Author(s)**

Chuang Wan

**References**

Wei Zhong, Chuang Wan and Wenyang Zhang. (2020) Estimation and inference for multi-kink quantile regression. working paper.

**See Also**

[mkqr.fit](#), [fit.control](#)

**Examples**

```
ptm <- proc.time()
set.seed(123)
n <- 500
tau <- 0.5
bet0 <- c(1,1,1,-3,4,4)
psi0 <- c(-3,0,3)
k <- length(psi0)
x <- runif(n, -5, 5)
z <- rnorm(n, 1, 1)
X <- matrix(rep(x,k),nrow=n)
PSI <- matrix(rep(psi0,rep(n,k)),ncol=k)
XZ <- cbind(1,z,x,pmax((X-PSI),0))
e <- rnorm(n,0,1) - qnorm(tau, 0,1)
y <- as.vector(XZ %*% bet0) + e
fit <- mkqr.bea(y,x,z,tau,Cn=log(n))
proc.time() - ptm
```

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mkqr.fit	<i>Fit the multi-kink quantile regression conditional on a given or pre-specified number of change points.</i>
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**Description**

The bootstrap restarting iterative segmented quantile algorithm for the multi-kink quantile regression.

**Usage**

```
mkqr.fit(y, thre.x, cont.z, psi, k, tau, bandwidth_type="Hall-Sheather", control=fit.control())
```

**Arguments**

y	A vector of response.
thre.x	A scalar covariate with threshold effect.
cont.z	A vector of covariates with constant slopes.
psi	numeric vector to indicate the starting values for the changepoints. When psi=NULL (default), k quantiles are assumed.
k	The pre-specified number of change points.
tau	The quantile level that belongs to (0,1).
bandwidth_type	The bandwidth type. Specify one from "Hall-Sheather", "Bofinger", "Chamberlain". Default is "Hall-Sheather".
control	A list returned by fit.control.

**Details**

either 'psi' or 'k' must be given.

**Value**

A list with the elements

bet.est	The estimated regression coefficients with intercept.
bet.se	The estimated standard error of the regression coefficients.
psi.est	The estimated change points.
psi.se	The estimated standard errors of threshold parameters.

**Author(s)**

Chuang Wan

## References

- Wood S.N. (2001) Minimizing model fitting objectives that contain spurious local minima by bootstrap restarting. *Biometrics*, 57(1): 240-244.
- Muggeo, V.M.R., Adelfio, G. (2011) Efficient change point detection in genomic sequences of continuous measurements. *Bioinformatics* 27, 161-166.
- Wei Zhong, Chuang Wan and Wenyang Zhang. (2020) Estimation and inference for multi-kink quantile regression. working paper.

## See Also

[mkqr.bea,fit.control](#)

## Examples

```
ptm <- proc.time()
set.seed(123)
n <- 500
tau <- 0.5
bet0 <- c(1,1,1,-3,4,4)
psi0 <- c(-3,0,3)
k <- length(psi0)
x <- runif(n, -5, 5)
z <- rnorm(n, 1, 1)
X <- matrix(rep(x,k),nrow=n)
PSI <- matrix(rep(psi0,rep(n,k)),ncol=k)
XZ <- cbind(1,z,x,pmax((X-PSI),0))
e <- rnorm(n,0,1) - qnorm(tau, 0,1)
y <- as.vector(XZ %*% bet0) + e
fit <- mkqr.fit(y,x,z,psi=NULL,k=3,tau)
proc.time() - ptm
```

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triceps

*Triceps skinfold thickness dataset*

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## Description

The data are derived from an anthropometric study of 892 females under 50 years in three Gambian villages in West Africa.

## Usage

```
data(triceps)
```

## Format

A data frame with 892 observations on the following 3 variables.

age Age of respondents.

Intriceps Log of the triceps skinfold thickness.

triceps Triceps skinfold thickness.

**Source**

Cole T.J., Green P.J. (1992). Smoothing reference centile curves: the LMS method and penalized likelihood. *Statistics in medicine*, 11(10): 1305-1319.

Perperoglou A, Sauerbrei W, Abrahamowicz M, et al (2019). A review of spline function procedures in R. *BMC medical research methodology*, 19(1): 46-52.

**References**

Cole T.J., Green P.J. (1992). Smoothing reference centile curves: the LMS method and penalized likelihood. *Statistics in medicine*, 11(10): 1305-1319.

Perperoglou A, Sauerbrei W, Abrahamowicz M, et al (2019). A review of spline function procedures in R. *BMC medical research methodology*, 19(1): 46-52.

**Examples**

```
data(triceps)
## maybe str(triceps) ...
```



# Index

\*Topic **datasets**

triceps, [7](#)

\*Topic **kinkTest**

kinkTest, [3](#)

\*Topic **mkqr.bea**

mkqr.bea, [4](#)

\*Topic **mkqr.fit**

mkqr.fit, [6](#)

fit.control, [2](#), [5](#), [7](#)

kinkTest, [3](#)

mkqr.bea, [3](#), [4](#), [7](#)

mkqr.fit, [3](#), [5](#), [6](#)

triceps, [7](#)