Package 'QRKM'

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Type Package

Title Quantile Regression Kernel Machine

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Depends R(>= 3.1.0)

Imports MASS,quadprog,linprog,quantreg,PearsonDS

Author Xiang Zhan, Dehan Kong, Arnab Maity, Fang-Chi Hsu, Jung-Ying Tzeng and Michael C. Wu

Maintainer Xiang Zhan <xiangzhan9@gmail.com>

Description This package fits quantile regression for a partial linear model and tests the overall effect of a genetic marker set using kernel machines within the quantile regression framework.

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R topics documented:

| fKMQR.test | *Fast Kernel Machine Quantile Regression test* |

Description

Testing the overall effect of a genetic marker set on a outcome of interest via kernel machine quantile regression in a fast permutation-free manner.

Usage

```
fKMQR.test(Y, X, Z, tau)
```

Arguments

Y	An outcome of interest
X	A n by p matrix for the genetic marker set
Z	A n by q matrix for the covariates
tau	A quantile

Details

It first fits the null kernel machine quantile regression model without genetic markers (modeling the outcome with covariates only). A n-vector ω of tau and (tau-1) is formed based on the quantile regression residuals. In particular, the ith coordinate ω_i is tau if the residual for the ith sample is poistive and (tau-1) of the residual is negative. If the residual is zero, then we set the $\omega_i =$ tau with probability (1-tau) and as $\omega_i =$ tau-1 with probability tau. On the other hand, a kernel matrix (e.g., IBS kernel) K is constructed based on the genetic marker set. A RV coeffcient test comparing two $n \times n$ matrices (kernel matrix K and product matrix $\omega\omega^t$) is conducted for evaluating the association between the market set and outcome of interest after accounting for covariates. More details can be found in Josse et al., (2008).

Value

A p-value between 0 and 1

References

Josse, J. et al. (2008). Testing the significance of the RV coeffcient. Computational Statistics & Data Analysis, 53, 82–91

Kong, D. et al. (2016). Testing and estimation in marker-set association study using semiparametric quantile regression kernel machine. Biometrics, 72, 364–371.

See Also

KMQR.test

Examples

```
n<-50
p<-5
q<-2
tau<-0.5
X<-matrix(0,n,p)
Z<-matrix(0,n,q)
y<-rep(0,n)
epsilon<-rep(0,n)
freq=matrix(NA,3,p)
freq[2,]=runif(p,min=0,max=0.3)
freq[3,]=runif(p,min=0,max=0.3)
freq[1,]=1-freq[2,]-freq[3,]
for (j in 1:p){
tempfrequency<-freq[,j]
randomnumber<-runif(n)
X[,j]<-(randomnumber>tempfrequency[1])+(randomnumber>tempfrequency[1]+tempfrequency[2])
}
for (i in 1:n) {
Z[i,]<-rnorm(q,0,1)
```

```
epsilon[i]<-rnorm(1,0,1)
}
y = matrix(epsilon, ncol=1)
fKMQR.test(y,X,Z,tau)
```

IBS.kernel *IBS Kernel*

Description

Calculating the IBS kernel matrix of the genotypes

Usage

```
IBS.kernel(X)
```

Arguments

X A n by p matrix of genotypes of the genetic marker set

Details

The (i,j)-entry of the kernel matrix measures the similarity of genotype profiles of ith subject and jth subject.

Value

A n by n matrix

KMQR *Kernal Machine Quantile Regression*

Description

Fitting the kernel machine quantile regression model by minimizing the penalized check loss function

Usage

```
KMQR(Y, X, Z, tau, lambda.grid = 10^seq(-3, 3, len = 30), nboot = 50)
```

Arguments

Y	An outcome of interest
X	A n by p matrix for the genetic marker set
Z	A n by q matrix for the covariates
tau	A quantile
lambda.grid	A grid of regularization parameters for the kernel machine quantile regression model
nboot	The number of bootstrap samples used in selecting the tuning parameter

Details

This function fits the kernel machine quantile regression model with varied regularization parameters. More details can be found in Theorem 1 and Web Appendix C of Kong et al., (2016).

Value

result   A full list of the fitted kernal machine quantile regression model, including coefficients, fitted marker set effect and residuals.

beta.cov.mat   Covariance matrix of the covariate coefficients

lambda.opt   Optimal lambda value such that the model fitting criterion is minimized

opt.crit   The minimum value of the model fitting criterion, which is the sum of trace of beta.cov.mat and the check loss function

References

Kong, D. et al. (2016). Testing and estimation in marker-set association study using semiparametric quantile regression kernel machine. Biometrics, 72, 364–371.

See Also

KMQR.test

Examples

```
n<-50
p<-5
q<-2
tau<-0.5
X<-matrix(0,n,p)
Z<-matrix(0,n,q)
y<-rep(0,n)
epsilon<-rep(0,n)
freq=matrix(NA,3,p)
freq[2,]=runif(p,min=0,max=0.3)
freq[3,]=runif(p,min=0,max=0.3)
freq[1,]=1-freq[2,]-freq[3,]
for (j in 1:p){
tempfrequency<-freq[,j]
randomnumber<-runif(n)
X[,j]<-(randomnumber>tempfrequency[1])+(randomnumber>tempfrequency[1]+tempfrequency[2])
}
for (i in 1:n) {
Z[i,]<-rnorm(q,0,1)
epsilon[i]<-rnorm(1,0,1)
}
y = matrix(epsilon, ncol=1)
KMQR(y,X,Z,tau,lambda.grid=10^seq(-1,1,len=10),nboot=30)
```

| KMQR.internal | *Kernel Machine Quantile Regression with fixed regularization parameter* |

Description

Fitting the kernel machine quantile regression model by minimizing the penalized check loss function with a fixed regularization parameter

Usage

```
KMQR.internal(Y, K, Z, tau, lambda)
```

Arguments

Y	An outcome of interest
K	A n by n kernel matrix on genotypes
Z	A n by q matrix for the covariates
tau	A qunatile
lambda	Regularization parameter

Details

This function fits the kernel machine quantile regression model under a given regularization parameter λ. More details can be found in Theorem 1 of Kong et al. (2016).

Value

beta0	Intercept of the kernal machine quantile regression model
beta	Beta coefficients of the kernal machine quantile regression model
fest	Estimated marker set effect
lambda	Regularization parameter
resid	Residuals of the kernal machine quantile regression model

References

Kong, D. et al. (2016). Testing and estimation in marker-set association study using semiparametric quantile regression kernel machine. Biometrics, 72, 364–371.

See Also

KMQR

Examples

```
n<-50
p<-5
q<-2
tau<-0.5
freq=matrix(NA,3,p)
freq[2,]=runif(p,min=0,max=0.3)
freq[3,]=runif(p,min=0,max=0.3)
freq[1,]=1-freq[2,]-freq[3,]
X<-matrix(0,n,p)
Z<-matrix(0,n,q)
y<-rep(0,n)
epsilon<-rep(0,n)

for (j in 1:p){
tempfrequency<-freq[,j]
randomnumber<-runif(n)
X[,j]<-(randomnumber>tempfrequency[1])+(randomnumber>tempfrequency[1]+tempfrequency[2])
}
K = IBS.kernel(X)
for (i in 1:n) {
Z[i,]<-rnorm(q,0,1)
epsilon[i]<-rnorm(1,0,1)
}
y = matrix(epsilon, ncol=1)
KMQR.internal(y, K, Z, tau, lambda=1)
```

KMQR.test   *Kernel Machine Quantile Regression Test*

Description

Testing the overall effect of a genetic marker set via the kernel machine quantile regression

Usage

```
KMQR.test(Y, X, Z, tau, simrep = 1000)
```

Arguments

Y	An outcome of interest
X	A n by p matrix for the genetic marker set
Z	A n by q matrix for the covariates
tau	A quantile
simrep	The number of permutations used to calculate the p-value

Details

Please see Section 3 of Kong et al. (2016).

Value

A p-value between 0 and 1

References

Kong, D. et al. (2016). Testing and estimation in marker-set association study using semiparametric quantile regression kernel machine. Biometrics, 72, 364–371.

See Also

KMQR, fKMQR.test

Examples

```
n<-50
p<-5
q<-2
tau<-0.5
freq=matrix(NA,3,p)
freq[2,]=runif(p,min=0,max=0.3)
freq[3,]=runif(p,min=0,max=0.3)
freq[1,]=1-freq[2,]-freq[3,]
X<-matrix(0,n,p)
Z<-matrix(0,n,q)
y<-rep(0,n)
epsilon<-rep(0,n)
for (j in 1:p){
tempfrequency<-freq[,j]
randomnumber<-runif(n)
X[,j]<-(randomnumber>tempfrequency[1])+(randomnumber>tempfrequency[1]+tempfrequency[2])
}
for (i in 1:n) {
Z[i,]<-rnorm(q,0,1)
epsilon[i]<-rnorm(1,0,1)
}
y = matrix(epsilon, ncol=1)
KMQR.test(y, X, Z, tau, simrep=100)
```

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