

# Package ‘QRank’

January 20, 2025

**Type** Package

**Title** A Novel Quantile Regression Approach for eQTL Discovery

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**Description**

A Quantile Rank-score based test for the identification of expression quantitative trait loci.

**License** GPL (>= 2)

**Imports** quantreg

**NeedsCompilation** no

**Repository** CRAN

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QRank-package	<i>A Novel Quantile Regression Tool for eQTL Discovery</i>
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## Description

A Quantile Rank-score (QRank) based test for the identification of expression quantitative trait loci (eQTLs).

**Details**

We use a Quantile Rank-score (QRank) based test to identify the expression quantitative trait loci (eQTLs) that are associated with the conditional quantile function of gene expressions.

**Author(s)**

Xiaoyu Song

Maintainer: Xiaoyu Song <xs2148@cumc.columbia.edu>

**References**

Xiaoyu Song, Gen Li, Zhenwei Zhou, Xianling Wang, Iuliana Ionita-Laza and Ying Wei (2016). QRank: A Novel Quantile Regression Tool for eQTL Discovery. *Under revision for Bioinformatics*.

**Examples**

```

set.seed(123) #
n=300 #
x=rbinom(n, 2, 0.2) #
y=rnorm(n, mean=0, sd=1) #
z=cbind(rbinom(n, 1, 0.3), rnorm(n, mean=2, sd=2)) #
taus=c( 0.25, 0.5, 0.75) #

# - run the proposed QRank approach #
QRank(gene=y, snp=x, cov=z, tau=taus) #

# - output #
#Composite.pvalue: #
#[1] 0.2241873 #

#Quantile.specific.pvalue: #
# 0.25 0.5 0.75 #
#0.5452044 0.1821452 0.5938421 #

```

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heter.QRank	<i>Heterogeneity index for "QRank"</i>
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**Description**

Calculate the heterogeneity index of quantile regression coefficients at multiple quantile levels. It measures the variation of the quantile coefficients across quantile levels.

$$heterogeneity = \log(sd(\beta)/abs(mean(\beta)))$$

where  $\beta$  is the vector of quantile regression coefficients at multiple quantile levels.

**Usage**

```
heter.QRank(object, newtaus=NULL)
```

**Arguments**

object            Object returned from "QRank"  
 newtaus          a vector of quantile levels based on which heterogeneity index are calculated. Default is NULL, in which case the quantile levels inherited from "QRank" will be used.

**Value**

heterogeneity index  
                          one heterogeneity index

**See Also**

[QRank](#)

**Examples**

```
# continued from "QRank"

taus=c( 0.25, 0.5, 0.75)
q = QRank(gene=y, snp=x, cov=z, tau=taus)
heter.QRank(q) # default uses taus inherited from "QRank"
# - output
#Heterogeneity index:
#[1] 2.474184
heter.QRank(q,newtaus = 1:9/10) # calculate based on new taus values
# - output
#Heterogeneity index:
#[1] 2.69242
```

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print.QRank                      *Print a QRank object*

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**Description**

Print the object of QRank

**Usage**

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

**Arguments**

x                      Object returned from QRank.  
 ...                    Optional arguments

**See Also**[QRank](#)


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```
print.QRank.heter      Print a QRank.heter object
```

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**Description**

Print the object of heter.QRank

**Usage**

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

**Arguments**

x	Object returned from heter.QRank.
...	Optional arguments

**See Also**[heter.QRank](#)


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QRank	<i>A new Quantile Rank-score (QRank) based test for the eQTL identification.</i>
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**Description**

A function to obtain the p-value on the association between a gene expression and a genetic variant based on quantile rank-score test.

**Usage**

```
QRank(gene, snp, cov = NULL, tau)
```

**Arguments**

gene	a gene expression level from a selected gene. No parametric assumption is needed for underlying distribution.
snp	a selected SNP.
cov	a vector or matrix of covariates. Default is NULL.
tau	the quantile levels to be estimated. Tau can be a single value or a vector of quantile levels.

**Details**

This function conducts Quantile Rank-score (QRank) based test for the continuous traits. It can be used to identify expression quantitative trait loci (eQTLs) that are associated with the conditional quantile functions of gene expression.

**Value**

`composite.pvalue`  
a single p-value for across all quantile levels under consideration, testing  $H_0$ : No genetic association at the selected quantile levels.

`quantile.specific.pvalue`  
p-values of each quantile level, testing  $H_0$ : The genetic variant and gene expression are not associated at this quantile level.

**Author(s)**

Xiaoyu Song

**References**

Xiaoyu Song, Gen Li, Zhenwei Zhou, Xianling Wang, Iuliana Ionita-Laza and Ying Wei (2016). QRank: A Novel Quantile Regression Tool for eQTL Discovery. *Under revision for Bioinformatics*.

**Examples**

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# - run the proposed QRank approach #
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# - output #
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#[1] 0.2241873 #

#Quantile.specific.pvalue: #
# 0.25 0.5 0.75 #
#0.5452044 0.1821452 0.5938421 #

```

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