Package ‘QRank’

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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.
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QRank-package A Novel Quantile Regression Tool for eQTL Discovery

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

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References

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))
tau=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
```

Description
Heterogeneity index for "QRank"

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

\[
\text{heterogeneity} = \log(sd(\beta))/abs(mean(\beta))
\]

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
See Also

QRank

print.QRank.heter  

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

QRank  

A new Quantile Rank-score (QRank) based test for the eQTL identification.

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 H0: 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


Examples

```r
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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