Package 'gJLS'

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Type Package

Title Joint Location Scale (JLS) Test

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Description Joint Location Scale (JLS) test to simultaneously test for mean and variance differences between genotype groups.

License GPL-2

LazyData TRUE

RoxygenNote 5.0.1

Imports quantreg

URL http://github.com/dsoave/gJLS

BugReports http://github.com/dsoave/gJLS/issues

R topics documented:

`gJLS_test` *Joint Location Scale (JLS) Test*

Description

This function performs the Joint Location Scale (JLS) test (Soave et al. 2015) to simultaneously test for mean and variance differences between groups. The JLS test uses Fisher's combined p-value method to combine evidence from the individual locaiton (regression t-test) and scale (Levene's test of homogeneity of variances) tests.

Usage

```
gJLS_test(y, x.loc, x.scale)
```

Arguments

y	a qunatitative outcome variable
x.loc	a design matrix (or vector) for the location model
x.scale	a design matrix (or vector) for the scale model

Details

No missing data are allowed - function will return an "error". Absolute residuals, used in Levene's test (1960), are estimated using least absolute deviation (LAD) regression. LAD residuals correspond to deviations from group medians in the presence of a single categorical covariate. Outcome (phenotype) must be quantitative and covariate (genotype) must be discrete (categorical).

Value

p_L the location test (regression t-test) p-value

p_S the scale test (Levene's test) p-value

p_JLS the JLS test (Fisher's combined method) p-value

Author(s)

David Soave

References

Soave, D., Corvol, H., Panjwani, N., Gong, J., Li, W., Boelle, P.Y., Durie, P.R., Paterson, A.D., Rommens, J.M., Strug, L.J., and Sun, L. (2015). A Joint Location-Scale Test Improves Power to Detect Associated SNPs, Gene Sets, and Pathways. American journal of human genetics 97, 125-138.

Examples

```
#############################################################################
## Example simulating data from model [i] (Soave et al. 2015 AJHG)
#############################################################################

n<-2000  ## total sample size
pA<-0.3  ## MAF
pE1<-0.3  ## frequency of exposure E1

## Genotypes (XG)
genocount<-rmultinom(1,size=n,prob=c(pA*pA, 2*pA*(1-pA), (1-pA)*(1-pA)))
XG<-c(rep(0, genocount[1]), rep(1, genocount[2]), rep(2,genocount[3]))
XG<-sample(XG,size=length(XG),replace=FALSE)

## Exposures (E1)
E1<-rbinom(n,1,prob=pE1)

## Phenotype (y)
y<-0.01*XG+0.3*E1+0.5*XG*E1+rnorm(n,0,1)

# Additive model (will work with dosages)
JLS_test(y,XG,XG)
# Genotypic model (will not work with dosages --> factor() will create many groups)
JLS_test(y,factor(XG),factor(XG))
```

```
X2=round(cbind(XG==1,XG==2)) #convert to 2 columns

# Genotypic model --> same result as results above using JLS_test(y,factor(X),factor(X))
# This is how genotype probabilities will be analyzed (using a 2 column design matrix)
JLS_test(y,X2,X2)
```

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