

Package ‘JLS’

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Type Package

Title Joint Location Scale (JLS) Test

Version 0.1.0

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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/JLS>

BugReports <http://github.com/dsoave/JLS/issues>

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JLS_test	<i>Joint Location Scale (JLS) Test</i>
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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

```
JLS_test(y, x, locAdd = FALSE, scaleAdd = FALSE)
```

Arguments

y	a quantitative outcome variable
x	a categorical covariate
locAdd	TRUE/FALSE (default=FALSE). Whether the location model is additive (TRUE) or genotypic (FALSE).
scaleAdd	TRUE/FALSE (default=FALSE). Whether the scale model is additive (TRUE) or genotypic (FALSE).

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)
```

```
JLS_test(y=y,x=XG)
```

```
## or
```

```
JLS_test(y=y,x=XG,locAdd=TRUE,scaleAdd=TRUE)
```

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