

Package ‘GeneF’

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Title Package for Generalized F-Statistics

Version 1.0.1

Description Implementation of several generalized F-statistics. The current version includes a generalized F-statistic based on the flexible isotonic/monotonic regression or order restricted hypothesis testing. Based on: Y. Lai (2011) <[doi:10.1371/journal.pone.0019754](https://doi.org/10.1371/journal.pone.0019754)>.

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flexorhtest *A Flexible Order Restricted Hypothesis Testing*

Description

These functions test the hypothesis regarding population means from ordered sample groups. Restrictions like a weakly/general/strongly isotonic/monotonic order as well as a lower bound for the location can be imposed on the population means. A partition of sample groups and the corresponding estimates of population means are also provided.

Usage

```
flexisoreg(y, x, lambda = 0, alpha.location = 1, alpha.adjacency = 0.5)
flexisoreg.stat(y, x, lambda = 0, alpha.location = 1, alpha.adjacency = 0.5)
flexmonoreg(y, x, lambda = 0, alpha.location = 1, alpha.adjacency = 0.5)
flexmonoreg.stat(y, x, lambda = 0, alpha.location = 1, alpha.adjacency = 0.5)
```

Arguments

y	a vector of observed data
x	a vector of ordinal group labels corresponding to y but not necessarily sorted
lambda	a lower location bound for partitioned groups other than the first one
alpha.location	α level for the upper-tailed one-sample <i>t</i> -test with lower bound lambda
alpha.adjacency	α level for the upper-tailed two-sample <i>t</i> -test to evaluate the magnitude of non-decreasing order

Details

flexisoreg is used for flexible nondecreasing order restricted hypothesis testing. flexmonoreg is used for flexible nondecreasing or nonincreasing order restricted hypothesis testing. flexisoreg.stat and flexmonoreg.stat only return an *F*-statistic, which is convenient for multiple comparison.

Value

groups	A partition of sample groups
estimates	estimated population means
statistic	an <i>F</i> -type statistic from the test

Note

Since the *p*-value of test has to be evaluated by permutation method, these functions will not return any *p*-value. For the permutation *p*-value of an individual test, see flexisoreg.pvalue and flexmonoreg.pvalue. For the pooled permutation *p*-values of multiple tests, see flexisoreg.poolpvalues and flexmonoreg.poolpvalues.

Author(s)

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References

Yinglei Lai (2007) A flexible order restricted hypothesis testing and its application to gene expression data. Technical Report

Examples

```

#generate ordinal group lables x
x <- runif(100)*6
x <- round(x,0)/3
#generate true values z
z <- round(x^2,0)
#generate observed values y
y <- z + rnorm(100)

#print default results
print(rbind(x,z,y))
print(flexisoreg(y,x))
print(flexisoreg.stat(y,x))
print(flexisoreg(y,0-x))
print(flexisoreg.stat(y,0-x))
print(flexmonoreg(y,x))
print(flexmonoreg.stat(y,x))

#plots for illustration
par(mfrow=c(2,3), mai=c(0.6, 0.6, 0.3, 0.1))
plot(x,y, main="True Model",cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
lines(x, z, type="p", pch=15, col="black", cex=2.5)

results <- flexisoreg(y, x, lambda=1, alpha.location=0.05, alpha.adjacency=1)
plot(x,y, main="Location Restriction",cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
lines(x, results$estimate, type="p", pch=15, col="black", cex=2.5)

results <- flexisoreg(y, x, lambda=1, alpha.location=0.05, alpha.adjacency=0.05)
plot(x,y, main="Location and Strong Order Restrictions",
cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
lines(x, results$estimate, type="p", pch=15, col="black", cex=2.5)

results <- flexisoreg(y, x, lambda=0, alpha.location=1, alpha.adjacency=0.95)
plot(x,y, main="Weak Order Restriction",cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
lines(x, results$estimate, type="p", pch=15, col="black", cex=2.5)

results <- flexisoreg(y, x, lambda=0, alpha.location=1, alpha.adjacency=0.5)
plot(x,y, main="General Order Restriction",cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
lines(x, results$estimate, type="p", pch=15, col="black", cex=2.5)

results <- flexisoreg(y, x, lambda=0, alpha.location=1, alpha.adjacency=0.05)
plot(x,y, main="Strong Order Restriction",cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
lines(x, results$estimate, type="p", pch=15, col="black", cex=2.5)

```

Description

These functions evaluate the p -values from an individual or multiple flexible order restricted hypothesis testing.

Usage

```
flexisoreg.pvalue(y, x, lambda=0, alpha.location=1, alpha.adjacency=0.5, B=100)
flexisoreg.poolpvalues(m, x, lambda=0, alpha.location=1, alpha.adjacency=0.5, B=100)
flexmonoreg.pvalue(y, x, lambda=0, alpha.location=1, alpha.adjacency=0.5, B=100)
flexmonoreg.poolpvalues(m, x, lambda=0, alpha.location=1, alpha.adjacency=0.5, B=100)
```

Arguments

<code>m</code>	a matrix of observed data, where samples are in columns and variables are in rows
<code>y</code>	a vector of observed data
<code>x</code>	a vector of ordinal group labels corresponding to <code>y</code> or rows of <code>m</code> but not necessarily sorted
<code>lambda</code>	a lower location bound for partitioned groups other than the first one
<code>alpha.location</code>	α level for the upper-tailed one-sample t -test with lower bound <code>lambda</code>
<code>alpha.adjacency</code>	α level for the upper-tailed two-sample t -test to evaluate the magnitude of non-decreasing order
<code>B</code>	the number of permutations for p -value assessment

Details

`flexisoreg.pvalue` and `flexmonoreg.pvalue` provide the permutation p -value for an individual flexible order restricted hypothesis testing. `flexisoreg.poolpvalues` and `flexmonoreg.poolpvalues` provide the pooled permutation p -values for multiple flexible order restricted hypothesis testing.

Value

`flexisoreg.pvalue` and `flexmonoreg.pvalue` return a permutation p -value. `flexisoreg.poolpvalues` and `flexmonoreg.poolpvalues` return a vector of pooled permutation p -values.

Note

These functions are used in conjunction with `flexisoreg`, `flexisoreg.stat`, `flexmonoreg` and `flexmonoreg.stat`.

Author(s)

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References

Yinglei Lai (2007) A flexible order restricted hypothesis testing and its application to gene expression data. Technical Report

Examples

```

#generate ordinal group lables x
x <- runif(100)*6
x <- round(x,0)/3
#generate true values z
z <- round(x^2,0)
#generate 6 vectors in a matrix for observed values, some noises and some not
m <- array(double(6*100), dim=c(6,100))
for(k in 1:3)
m[k,] <- rnorm(100)
for(k in 4:6)
m[k,] <- z + rnorm(100)

#print default results
par(mfrow=c(2,3))
for(k in 1:6){
print(paste("The ", k, "-th vector", sep=""))
y <- m[k,]
plot(x,y,main=k)
print(flexisoreg.stat(y,x))
print(flexisoreg.pvalue(y,x,B=20))
print(flexisoreg.stat(y,0-x))
print(flexisoreg.pvalue(y,0-x,B=20))
print(flexmonoreg.stat(y,x))
print(flexmonoreg.pvalue(y,x,B=20))
}

flexisoreg.poolpvalues(m, x, B=20)
flexmonoreg.poolpvalues(m, x, B=20)

```

GeneF

*Package for Generalized F-Statistics***Description**

Implementation of several generalized F -statistics. The current version includes a generalized F -statistic based on the flexible isotonic/monotonic regression or order restricted hypothesis testing. Based on: Y. Lai (2011) <doi:10.1371/journal.pone.0019754>.

Details

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Author(s)

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internal functions *Internal GeneF Functions*

Description

Internal functions to support generalized F -statistics.

Usage

```
get.numbers(x)
t1p1(v, n)
t1p2(v, n1, n2)
```

Arguments

x	a vector of ordered groups of numbers
v	a vector of real numbers
n	the sample size of one-sample data
n1	the first sample size of two-sample data
n2	the second sample size of two-sample data

Value

get.numbers	a vector of culmulative sample sizes from ordered groups
t1p1	a p -value from one-sample t -test
t1p2	a p -value from two-sample t -test

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