Package 'GeneF'

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Type Package

Title Package for Generalized F-statistics

Version 1.0

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Description This package implements several generalized F-statistics.
The current version includes a generalized F-statistic based on
the flexible isotonic/monotonic regression or order restricted
hypothesis testing.

License GPL (>= 2)

Repository CRAN

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NeedsCompilation no

R topics documented:

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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.

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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 correponding 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 t-test with lower bound `lambda`
alpha.adjacency	α level for the upper-tailed two-sample t-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 F-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)
```

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flexorhtest.pvalue   *Significance Assessment for the Flexible Order Restricted Hypothesis Testing*

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

m	a matrix of observed data, where samples are in columns and variables are in rows
y	a vector of observed data
x	a vector of ordinal group correponding to y or rows of m 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 t-test with lower bound lambda
alpha.adjacency	
	α level for the upper-tailed two-sample t-test to evaluate the magnitude of non-decreasing order
B	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

This package implements several generalized F-statistics. The current version includes a generalized F-statistic based on the flexible isotonic/monotonic regression or order restricted hypothesis testing.

Details

Package:	GeneF
Type:	Package
Version:	1.0
Date:	2007-07-18
License:	GPL version 2 or newer

Author(s)

Yinglei Lai

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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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