

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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Author Yinglei Lai [aut, cre]

Maintainer Yinglei Lai <ylai@gwu.edu>

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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

<code>y</code>	a vector of observed data
<code>x</code>	a vector of ordinal group labels corresponding to <code>y</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

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

<code>groups</code>	A partition of sample groups
<code>estimates</code>	estimated population means
<code>statistic</code>	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)

Yinglei Lai ylai@gwu.edu

References

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

Examples

```

#generate ordinal group labels 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)

Yinglei Lai ylai@gwu.edu

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

Package: GeneF
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Author(s)

Yinglei Lai

Maintainer: ylai@gwu.edu

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

Author(s)

Yinglei Lai ylai@gwu.edu

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