Package ‘someMTP’

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Some Multiple Testing Procedures

Description

It is a collection of functions for Multiplicity Correction and Multiple Testing.

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Author(s)

livio finos

Maintainer: <livio@stat.unipd.it>

References

For weighted methods:


For LSD test:


Examples

```r
set.seed(13)
y <- matrix(rnorm(5000),5,1000) #create toy data
ty[,1:100] <- y[,1:100]+3 #create toy data

p <- apply(y,2,function(y) t.test(y,p.value) #compute p-values
M2 <- apply(y^2,2,mean) #compute ordering criterion
```
fdr <- p.adjust(p, method="BH")  #(unweighted) procedure, fdr control
  sum(fdr<.05)

fdr.w <- p.adjust.w(p, method="BH", w=M2)  #weighted procedure, weighted fdr control
  sum(fdr.w<.05)

fwer  <- p.adjust(p, method="holm")  #(unweighted) procedure, fwer control
  sum(fwer<.05)

fwer.w <- p.adjust.w(p, method="BHfwe", w=M2)  #weighted procedure, weighted fwer (fwer) control
  sum(fwer.w<.05)

plot(M2,-log10(p))

---

**class *OrNULL**

Description

class * or Null

Objects from the Class

A virtual Class: No objects may be created from it.

Methods

No methods defined with class "*OrNULL" in the signature.

Examples

showClass("call0rNULL")

---

**draw**

Plots results of fdrOrd()

Description

Plots results of fdrOrd()

Usage

draw(object, what = c("all", "ordVsP", "stepVsR"), pdfName = NULL)
Arguments

object  a someMTP.object resulting from fdrOrd()
what  what to plot; "all" is the default
pdfName  it is the pdf filename where the plot will be saved. If pdfName is null (the default) the plot will show as window.

Value

No value is returned

Author(s)

Livio Finos

See Also

See Also fdrOrd.

Examples

set.seed(17)
x=matrix(rnorm(60),3,20)x[,1:10]=x[,1:10]+2 ##variables 1:10 have tests under H1ts=apply(x,2,function(x) t.test(x)$statistic)
ps=apply(x,2,function(x) t.test(x)$p.value)m2=apply(x^2,2,mean)pOrd <- fdrOrd(ps,q=.05,ord=m2)
draw(pOrd)

fdrOrd/kfweOrd

Controlling the False Discovery Rate and and the Generalized FWER in ordered Test

Description

Ordinal procedure controlling the FDR and the Generalized FWER

Usage

fdrOrd(p, q = .01, ord = NULL, GD=FALSE)
kfweOrd(p, k = 1, alpha = 0.01, ord = NULL, alpha.prime = alpha, J = qnbinom(alpha, k, alpha.prime), GD = FALSE)
Arguments

- **p**: vector of p-values
- **ord**: Values on the basis of which the procedure select the hypotheses (following decreasing order). The vector have the same length of p. If NULL the natural ordering is considered.
- **q**: average FDR level
- **alpha**: global significance level
- **k**: number of allowed errors in kFWE controls
- **J**: number of allowed jumps before stopping
- **alpha.prime**: univariate alpha for single step Guo and Romano procedure
- **GD**: Logic value. Should the correction for general dependence be applied?

Value

The function returns an object of class `someMTP.object`.

- **rej**: a logical vector indicating whenever the related hypothesis have been rejected.
- **p**: the vector of p-values used in the call
- **ord**: The vector used to sort the p-values (decreasing).
- **MTP**: "fdrOrd" or "kfweOrd"
- **GD**: A logical value indicating if the correction for General Dependence have been used or not.
- **q**: The level of controlled FDR.
- **alpha**: The level of controlled k-FWER
- **alphaprime**: The significance level of individual tests
- **k**: Number of allowed Errors
- **J**: Number of allowed Jumps

Author(s)

L. Finos and A. Farcomeni

References


See Also

See also `draw`
Examples

```r
set.seed(17)
x=matrix(rnorm(60),3,20)
x[,1:10]=x[,1:10]+2  # variables 1:10 have tests under H1
ts=apply(x,2,function(x) t.test(x)$statistic)
ps=apply(x,2,function(x) t.test(x)$p.value)  # compute p-values
m2=apply(x^2,2,mean)  # compute ordering criterion
pOrd <- fdrOrd(ps, q=.05, ord=m2)  # ordinal Procedure
pOrd
draw(pOrd)
sum(p.adjust(ps, method="BH")<=.05)  # rejections with BH

kOrd <- kfweOrd(ps, k=5, ord=m2)# ordinal procedure
kOrd
kOrdGD <- kfweOrd(ps, k=5, ord=m2, GD=TRUE)# ord. proc. (any dependence)
kOrdGD
```

lsd.object class

Class "lsd.object" for storing the result of the function lsd

Description

The class lsd.object is the output of a call to lsd.test

Slots

- **F**: the test statistic
- **df**: the degrees of freedom of F
- **globalP**: the associated p-value
- **D**: the matrix used in the test (it provides the influence of columns in resp to the test statistic)
- **call**: The matched call to lsd.
- **MTP**: The procedure used ("fdrOrd", "kfweOrd" or others).

Methods

- **p.value** (lsd.object): Extracts the p-values.
- **show** lsd.object: Prints the test results: p-value, test statistic, expected value of the test statistic under the null hypothesis, standard deviation of the test statistic under the null hypothesis, and number of covariates tested.
- **summary** lsd.object: Prints the test results: p-value, test statistic, expected value of the test statistic under the null hypothesis, standard deviation of the test statistic under the null hypothesis, and number of covariates tested.
- **weights** lsd.object: diagonal of matrix D used in the test (i.e. the influence of columns in resp to the test statistic)
Multivariate Left Spherically Distributed (LSD) linear scores test.

Description

It performs the multivariate Left Spherically Distributed linear scores test of L"auter et al. (The Annals of Statistics, 1998) (see also details below).

Usage

```r
lsd.test(resp, alternative = 1, null = NULL, D = NULL, data=NULL)
```

Arguments

- `resp` The response vector of the regression model. May be supplied as a vector or as a formula object. In the latter case, the right hand side of `Y` is passed on to `alternative` if that argument is missing, or otherwise to `null`.
- `alternative` The part of the design matrix corresponding to the alternative hypothesis. The covariates of the null model do not have to be supplied again here. May be given as a half formula object (e.g. `~a+b`). In that case the intercept is always suppressed.
- `null` The part of the design matrix corresponding to the null hypothesis. May be given as a design matrix or as a half formula object (e.g. `~a+b`). The default for `Z` is `~1`, i.e. only an intercept. This intercept may be suppressed, if desired, with `Z = ~0`.
- `data` Only used when `Y`, `X`, or `Z` is given in formula form. An optional data frame, list or environment containing the variables used in the formulae. If the variables in a formula are not found in `data`, the variables are taken from environment(formula), typically the environment from which `gt` is called.
lsd.test

D is a q x p matrix or it is a function with arguments `resp` and `null` returning the q x p transformation matrix. When D = NULL, then D = diag(t(resp)%*%IP0)%*%resp) with IP0 = diag(n) - null%*%solve(t(null)%*%null)%*%t(null)

Value

The function returns an object of class `lsd.object`.

F the test statistic
df the degrees of freedom of F
p the associated p-value
D the matrix used in the test (it provide information on the influence of columns in `resp` to the test)
call: The matched call to `lsd.test`.

Author(s)

Livio Finos

References


Examples

```r
set.seed(1)
# Standard multivariate LSD test for one sample case
X=matrix(rnorm(50),5,10)+2
lsd.test(resp=X,alternative=-1)

# Standard multivariate LSD test for two sample case
X2=X+matrix(c(0,0,1,1),5,10)*10
lsd.test(resp=X2,null=-1,alternative=c(0,0,1,1))

# General multivariate LSD test for linear predictor with covariates
lsd.test(resp=X2,null=cbind(rep(1,5),c(0,0,1,1)),alternative=1:5)
```
Description

Given a set of p-values, returns p-values adjusted using one of several (weighted) methods. It extends the method of \texttt{p.adjust(stats)}

Usage

\begin{verbatim}
\texttt{p.adjust.w(p, method = c("bonferroni","holm","BHfwe","BH","BY"), n = length(p), w=NULL)}
\end{verbatim}

Arguments

- \texttt{p}: vector of p-values (possibly with NAs)
- \texttt{method}: correction method
- \texttt{n}: number of comparisons, must be at least \texttt{length(p)}; only set this (to non-default) when you know what you are doing!
- \texttt{w}: weights to be used. \texttt{p.adjust.w(..., rep(1,length(p))))} produces the same results as in \texttt{p.adjust(...)} (i.e. the unweighted counterpart).

Value

A vector of corrected p-values (same length as \texttt{p}) having two attributes: \texttt{attributes(...)$w}} is the vector of used weights and \texttt{attributes(...)$method}} is the method used.

Author(s)

Livio Finos

References


See Also

\texttt{p.adjust}
someMTP.object class

Class "someMTP.object" for storing the result of the function fdrOrd

Description

The class someMTP.object is the output of a call to fdrOrd. It also stores the information needed for related plots.

Slots

- rej: a logical vector indicating whenever the related hypothesis have been rejected.
- p: The vector of (raw) p-values used in the procedure.
- ord: The vector used to sort the p-values (decreasing).
- idOrd: The vector of indices used in sorting.
- MTP: The type of procedure used.
- GD: A logical value incating if the correction for General Dependence have been used or not.
- q: The level of contrelled FDR when MTP=="fdrOrd".
- k: The number of false rejection when MTP=="kfweOrd"
- J: The number of allowed Jumps when MTP=="kfweOrd"
- alpha: The significance level when MTP=="kfweOrd"
- alphaprime: The significance level of individual tests.
- call: The cal that generates the object.
Methods

- **show** someMTP.object: Prints the test results.
- **summary** someMTP.object: Prints the test results (as show).
- **draw** someMTP.object: Plots results; what = c("all", "ordVsP", "stepVsR")
- **sort** signature(x = "someMTP.object"): Sorts the p-values to decreasing order of ord.
- **length** signature(x = "someMTP.object"): The number of tests performed.
- **names** signature(x = "someMTP.object"): Extracts the row names of the results matrix.
- **names<-** signature(x = "someMTP.object"): Changes the row names of the results matrix.
  Duplicate names are not allowed, but see alias.

Author(s)

Livio Finos: <livio@stat.unipd.it>

See Also

someMTP.object

Examples

```r
# Simple examples with random data
set.seed(17)
x = matrix(rnorm(60), 3, 20)
x[, 1:10] = x[, 1:10] + 2  # variables 1:10 have tests under H1
t = apply(x, 2, function(x) t.test(x)$statistic)
p = apply(x, 2, function(x) t.test(x)$p.value)
m2 = apply(x^2, 2, mean)
pOrd <- fdrOrd(p, q = .05, ord = m2)
pOrd
length(pOrd)
names(pOrd) <- paste("V", 1:20, sep="")
names(pOrd)
```

---

**step.adj**

*Multiplicity correction for Stepwise Selected models*

Description

Corrects the p-value due to model selection. It works with models of class glm and selected with function step {stats}.

Usage

```r
step.adj(object, MC = 1000, scope = NULL, scale = 0,
direction = c("both", "backward", "forward"),
trace = 0, keep = NULL, steps = 1000, k = 2)
```
Arguments

object object of class glm. Note that formula have to write by variables name like y~var1+var2+var3, data is a data.frame (see example below), offset is not yet implemented, avoid its use, glm(formula, data, family=gaussian) produce the same result of lm(formula, data), then linear model can be allways performed

MC number of random permutations for the dependent variable

scope as in function step

scale as in function step

direction as in function step

trace as in function step

keep as in function step

steps as in function step

k as in function step, other arguments are not implemented yet.

Details

It performs anova function (stats library) on the model selected by function step vs the null model with the only intercept and it corrects for multiplicity. For lm models and gaussian glm models it computes a F-test, form other models it uses Chisquare-test (see also anova.glm and anova.lm help).

Value

An anova table with an extra column reporting the corrected p-value

Author(s)

Livio Finos and Chiara Brombin

References


See Also

glm, anova

Examples

set.seed(17)
y=rnorm(10)
x=matrix(rnorm(50),10,5)
#define a data.frame to be used in the glm function
DATA=data.frame(y,x)
#fit the model on a toy dataset
mod=glm(y~X1+X2+X3+X4+X5, data=DATA)

#select the model using function step
mod.step=step(mod, trace=0)
#test the selected model vs the null model
anova(glm(y~1, data=DATA), mod.step, test="F")

#step.adj do the same, but it also provides multiplicity control
step.adj(mod, MC=101, trace=0)
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