

Package ‘multmod’

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Title Testing of multiple outcomes

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LazyData yes

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Author Christian B. Pipper <pipper@life.ku.dk>, Christian Ritz
<ritz@life.ku.dk>, Signe M. Jensen <smj@life.ku.dk>

Maintainer Christian B. Pipper <pipper@life.ku.dk>

Description Testing of multiple outcomes using i.i.d. decompositions

License GPL (>= 2)

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amtest

*Testing multiple outcomes***Description**

Testing multiple endpoints or outcomes measures by providing a corrected significance level to assess the uncorrected, marginal p-values against.

Usage

```
amtest(modellist, varName, vcov. = c("sandwich", "model-based"),
       sig.level = 0.05, display = TRUE, adjp=FALSE)
```

Arguments

modellist	list of model fits. The fits may be obtained using <code>lm</code> , <code>glm</code> , or <code>coxph</code> . The fits should all be based on exactly the same dataset (data frame) and missing values should be handled using <code>na.omit</code> . All models should contain the explanatory variable of interest.
varName	string specifying the name of the explanatory variable for which the effect is to be assessed.
vcov.	string specifying the type of estimated variance-covariance matrix to use for calculating the test statistics. Two options are available model-based estimated standard errors or robust estimated sandwich standard errors, which is the default.
sig.level	numeric specifying the nominal significance level or type I error rate (default is 0.05).
display	logical indicating whether or not the results should be shown at the command line.
adjp	logical indicating whether or not the correction should be reported in terms of adjusted p-values.

Details

The function calculates a corrected overall significance level that asymptotically reaches the desired type I error using i.i.d. decompositions of parameter estimates by means of score components. The details are provided by Pipper and Ritz (2011).

The implemented method is less conservative than the practically identical Bonferroni/Slepian corrections and it flexibly adapts to the correlation structure between outcomes. Different types of outcome measures such as continuous, binomial, and event times, as well as missing values in outcome measures and explanatory variables can be handled by the procedure.

Value

The corrected significance level as well as the Slepian correction $1 - (1 - \text{Nominal significance level})^{(1/\text{Number of tests})}$ and the marginal p-values are shown by default (can be switched off using the argument 'display').

These values are also returned invisibly in a list.

Author(s)

Christian B. Pipper and Christian Ritz

References

Pipper, C. B., Ritz, C., Bisgaard, H. (2011). A versatile method for confirmatory evaluation of the effects of a covariate in multiple models. *To appear in JRSSC*.

Examples

```
##Example from: McCullagh, P. and Nelder, J.A. (1989,p. 239). Generalized Linear Models.  
##Second Edition. Chapman & Hall/CRC.
```

```
model1 <- glm(y1~group, family=binomial,na.action=na.omit,data=mn6.9)  
model2 <- glm(y2~group, family=binomial,na.action=na.omit,data=mn6.9)  
model3 <- glm(y3~group, family=binomial,na.action=na.omit,data=mn6.9)  
model4 <- glm(y4~group, family=binomial,na.action=na.omit,data=mn6.9)  
amtest(list(model1,model2,model3,model4),"group2",vcov.="model-based")  
amtest(list(model1,model2,model3,model4),"group2")
```

```
##Multiple testing in case of perfectly correlated outcomes
```

```
amtest(list(model2,model2),"group2",vcov.="model-based")  
amtest(list(model2,model2),"group2")
```

```
## Multiple testing in a subgroup analysis and overall analysis
```

```
subgroup<-mn6.9  
set.seed(2982)  
subgroup[sample(1:2982,1500),]<-NA  
model1<- glm(y2~group, family=binomial,na.action=na.omit,data=mn6.9)  
model2<- glm(y2~group, family=binomial,na.action=na.omit,data=subgroup)
```

```
amtest(list(model1,model2),"group2",vcov.="model-based")
amtest(list(model1,model2),"group2")
```

amtest.efron

Adjusted p-values for multiple tests

Description

Provides adjusted p-values for multiple z-tests utilizing correlation between pairs of z-tests

Usage

```
amtest.efron(modelList, varName, sig.level = 0.05, display = TRUE)
```

Arguments

modelList	list of model fits. The fits may be obtained using <code>lm</code> , <code>glm</code> , or <code>coxph</code> . The fits should all be based on exactly the same dataset (data frame) and missing values should be handled using <code>na.omit</code> . All models should contain the explanatory variable of interest.
varName	string specifying the name of the explanatory variable for which the effect is to be assessed.
sig.level	numeric specifying the nominal significance level or type I error rate (default is 0.05).
display	logical indicating whether or not the results should be shown at the command line.

Details

The function calculates adjusted p-values based on an approximation provided in Efron (1997) to bound the type I error. An algorithm described in Jensen et al (2011) is utilized to pair the test statistics so as to ensure an optimal bound based on this approximation. Correlation between test statistics is obtained by means of the i.i.d. decomposition as detailed in Pipper et al (2011). If test statistics are correlated the implemented method is less conservative than the Bonferroni correction. The function is designed to be applicable to large scale multiple testing.

Value

Efron adjusted p-values, Sleipan adjusted p-values, original p-values.
 These values are also returned invisibly in a list.

Author(s)

Signe Marie Jensen, Christian Ritz, and Christian Pipper

References

- Efron, B. (1997). The Length Heuristic for Simultaneous Hypothesis Tests. *Biometrika*, 84, 143-157.
- Jensen, S.M., Ritz, C., Pipper, C.B. (2011). An efficient single-step adjustment in large-scale multiple testing problems. *Submitted*.
- Pipper, C. B., Ritz, C., Bisgaard, H. (2011). A versatile method for confirmatory evaluation of the effects of a covariate in multiple models. *To appear in JRSSC*.

Examples

```
##Example from: McCullagh, P. and Nelder, J.A. (1989,p. 239). Generalized Linear Models.
##Second Edition. Chapman & Hall/CRC.
```

```
model <- glm(y2~group, family=binomial,na.action=na.omit,data=mn6.9)
```

```
##Multiple testing in case of perfectly correlated test statistics
```

```
amtest.efron(list(model,model),"group2")
```

mn6.9

I.Q. and attitude towards science

Description

Responses given by 2982 New Jersey high-school seniors on 4 questions concerning attitude towards science. Also recorded was whether students had a high or low I.Q.

Usage

```
data(mn6.9)
```

Format

A data frame with 2982 observations on the following 5 variables.

- y1 Agree=1/disagree=0 to "The development of new ideas is the scientist's greatest source of satisfaction"
 - y2 Agree=1/disagree=0 to "Scientists and engineers should be eliminated form the military draft"
 - y3 Agree=1/disagree=0 to "The scientist will make his maximum contribution to society when he has freedom to work on problems that interest him"
 - y4 Agree=1/disagree=0 to "The monetary compensation of a Nobel Prize-winner in physics should be at least equal to that given to popular entertainers"
- group I.Q. levels: 1=low, 2=high

Source

McCullagh, P. and Nelder, J.A. (1989, p. 239). *Generalized Linear Models*. Second Edition. Chapman & Hall/CRC.

Examples

```
##Marginal assessment of effect of I.Q. group on response probability  
model1 <- glm(y1~group, family=binomial,data=mn6.9)  
model2 <- glm(y2~group, family=binomial,data=mn6.9)  
model3 <- glm(y3~group, family=binomial,data=mn6.9)  
model4 <- glm(y4~group, family=binomial,data=mn6.9)
```

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