Package ‘mdscore’

February 16, 2017

Type Package
Title Improved Score Tests for Generalized Linear Models
Version 0.1-3
Date 2017-02-16
Depends R (>= 3.3.2), MASS, stats
Suggests Sleuth3
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Description A set of functions to obtain modified score test for generalized linear models.
License GPL (>= 2)
LazyLoad yes
LazyData yes
NeedsCompilation no
Repository CRAN
Date/Publication 2017-02-16 17:27:45

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lr.test

Likelihood ratio test for generalized linear models

Description

Computes the likelihood ratio test for the coefficients of a generalized linear model.

Usage

lr.test(fit1, fit2)

Arguments

fit1 an object that stores the results of glm fit of the model under the null hypothesis.
fit2 an object that stores the results of glm fit of the model under the alternative hypothesis.

Details

The objects fit1 and fit2 are obtained using the usual options passed to the glm function.

Value

The function lr.test() returns the following list of values:

LR the value of the likelihood ratio statistic.
pvalue the p value of test under null hypothesis chi-square distribution.

Note

Both fit1 and fit2 must have the same family and link function.

Author(s)

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References


See Also

mdscore
wald.test
Examples

```r
data(strength)
fitf <- glm(y ~ cut * lot, data = strength,family = inverse.gaussian("inverse"))
fit0 <- glm(y ~ cut + lot, data = strength, family = inverse.gaussian("inverse"))
lr.test(fit0,fitf)
```

Description

Computes the modified score test based for the coefficients of a generalized linear model.

Usage

```r
mdscore(model = model, X1 = X1, phi = NULL)
```

Arguments

- `model`: an object that stores the results of `glm` fit of the model under the null hypothesis.
- `X1`: the matrix with the columns of the model matrix X that correspond to the coefficients being specified in the null hypothesis.
- `phi`: the precision parameter.

Details

The object `fit.model` is obtained using the usual options passed to the `glm` function.

Value

The function `mdscore()` returns the following list of values:

- `sr`: the value of the score statistic.
- `srcor`: the value of the modified score statistic.
- `coef`: a vector with the coefficients A1, A2 and A3.
- `n`: the total sample size.
- `df`: the number of degrees of freedom of the chi–squared approximations for the tests.
- `phi`: the precision parameter used in the computations

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### References


### See Also

summary.mdscore

### Examples

```r
data(strength)
fitf <- glm(y ~ cut * lot, data = strength,family = inverse.gaussian("inverse"))
summary(fitf)
X <- model.matrix(fitf, data = strength)
fit0 <- glm(y ~ cut + lot, data = strength, family = inverse.gaussian("inverse"))
mdscore(fit0, X=X[, 7:10])
```

<table>
<thead>
<tr>
<th>strength</th>
<th>Impact Strength an Insulating Material</th>
</tr>
</thead>
</table>

### Description

The dataset is a subsample of the 5 x 2 factorial experiment given by Ostle and Mensing (1963).

### Usage

```r
data(strength)
```

### Format

A data frame with 30 observations on the following 3 variables.

- **cut**: type of specimen cut.
- **lot**: lof of the material – I, II, III, IV and V.
- **y**: observations of the impact strength.

### Source

summary.mdscore

Examples

```r
data(strength)
fitf <- glm(y ~ cut * lot, data = strength, family = inverse.gaussian("inverse"))
summary(fitf)
X <- model.matrix(fitf, data = strength)
fit0 <- glm(y ~ cut + lot, data = strength, family = inverse.gaussian("inverse"))
test <- mdscore(fit0, X[1:10])
summary(test)
```

summary.mdscore  Summary methods for mdscore objects

Description

summary methods for the mdscore objects

Usage

```r
## S3 method for class 'mdscore'
summary(object, ...)  
```

Arguments

- `object` object resulting from a run of the `mdscore` function.
- `...` not currently used

Author(s)

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References

[http://www.jstatsoft.org/v61/c02/](http://www.jstatsoft.org/v61/c02/)

See Also

- `mdscore`

Examples

```r
library(Sleuth3)
d <- transform(case1102, TLrat = Brain/Liver, Ltime = log(Time),
               Lwrat = log((Weight + Loss)/Weight),
               Treat = factor(Treatment == "BD",
               labels=c("NS", "BD")))
```
wald.test <- glm(TLrat ~ Ltime * Treat + Days + Sex + Lwrat + Tumor + Treat*Lwrat, data = d, family = Gamma("log")
)
X <- model.matrix(fitf)
fit0 <- glm(TLrat ~ Ltime * Treat + Sex + Lwrat + Tumor + Days, data=d, family=Gamma("log"))
test <- mdscore(fit0, X1=X[9], phi=NULL)
summary(test)

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**wald.test**

_Wald test for generalized linear models_

**Description**

Computes the Wald score test for the coefficients of a generalized linear model.

**Usage**

wald.test(model = model, terms)

**Arguments**

- **model**: an object that stores the results of glm fit of the model under the null hypothesis.
- **terms**: number of coefficients to be tested under null hypothesis

**Details**

The object model is obtained using the usual options passed to the glm function.

**Value**

The function wald.test() returns the following list of values:

- **w**: the value of the Wald statistic.
- **pvalue**: the p value of test under null hypothesis chi-square distribution.

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**References**

wald.test

See Also

   lr.test
   mdscore

Examples

data(strength)
fitf <- glm(y ~ cut * lot, data = strength,family = inverse.gaussian("inverse"))
wald.test(fitf,term=9)
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