Package ‘mdscore’

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Title Improved Score Tests for Generalized Linear Models
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Description A set of functions to obtain modified score test for generalized linear models.
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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.

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References

See Also
mdscore
wald.test
### mdscore

#### Examples
```
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
```
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


http://www.jstatsoft.org/v61/c02/

See Also

*summary.mdscore*

Examples

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[, 1:10])

---

**strength**  
*Impact Strength an Insulating Material*

Description

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

Usage

data(strength)

Format

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

cut  type of specimen cut.
lot  lot 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[, 7:10])
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"))
)
```
fitf <- 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, X=X[,9], phi=NULL)
summary(test)

---

**wald.test**

**Wald test for generalized linear models**

**Description**

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

**Usage**

```r
call: 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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