Package ‘metaLik’

June 22, 2015

Version 0.42.0

Priority optional

Title Likelihood Inference in Meta-Analysis and Meta-Regression Models

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Depends R (>= 3.0.0)

Description First- and higher-order likelihood inference in meta-analysis and meta-regression models.

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NeedsCompilation no

Repository CRAN

Date/Publication 2015-06-22 01:40:57

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**albumin**  
*Albumin data.*

**Description**
Data from four experiments about the percentage of albumin in the plasma protein of the normal human subjects.

**Usage**
data(albumin)

**Format**
y mean albumin percentage.
sigma2 estimated within-study variance.

**Source**

**Examples**
data(albumin)

---

**cholesterol**  
*Serum cholesterol data.*

**Description**
Data from 28 randomized trials about the effect of serum cholesterol reduction on the risk of ischaemic heart disease.

**Usage**
data(cholesterol)

**Format**
heart_disease log odds ratio of ischaemic heart disease.
cholesterol_reduction average serum cholesterol reduction measured in mmol/l.
sigma2 estimated within-study variance.
Diuretics data.

### Description
Data from nine randomized trials on prevention of pre-eclampsia with diuretics.

### Usage
```r
data(diuretics)
```

### Format
- `y` logarithm of the risk ratio in each study.
- `sigma2` estimated within-study variance.

### Source
education

Open education data.

Description

Data from eleven studies on the effect of open versus traditional education on student attitude toward schools.

Usage

data(education)

Format

y  standardized estimated mean difference in attitude according to the type of education.
sigma2  estimated within-study variance.

Source


Examples

data(education)

metaLik

First- and higher-order likelihood inference in meta-analysis and meta-regression models

Description

Implements first-order and higher-order likelihood methods for inference in meta-analysis and meta-regression models, as described in Guolo (2012). Higher-order asymptotics refer to the higher-order adjustment to the log-likelihood ratio statistic for inference on a scalar component of interest as proposed by Skovgaard (1996). See Guolo and Varin (2012) for illustrative examples about the usage of metaLik package.

Usage

metaLik(formula, data, subset, contrasts = NULL, offset, sigma2, weights=1/sigma2)
Arguments

- **formula**: an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under `Details`.

- **data**: an optional data frame, list or environment (or object coercible by `as.data.frame` to a data frame) containing the variables in the model. If not found in data, the variables are taken from `environment(formula)`, typically the environment from which `metaLik` is called.

- **subset**: an optional vector specifying a subset of observations to be used in the fitting process.

- **contrasts**: an optional list. See the contrasts.arg of `model.frame.default`.

- **offset**: this can be used to specify an a priori known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one are specified their sum is used. See `model.offset`.

- **sigma2**: a vector of within-study estimated variances. The length of the vector must be the same of the number of studies.

- **weights**: a vector of the inverse of within-study estimated variances. The length of the vector must be the same of the number of studies. If `sigma2` is supplied, the value of `weights` is discarded.

Details

Models for `metaLik.fit` are specified symbolically. A typical model has the form \( y \sim x_1 + \ldots + x_J \), where \( y \) is the continuous response term and \( x_j \) is the j-th covariate available at the aggregated meta-analysis level for each study. The case of no covariates corresponds to the classical meta-analysis model specified as \( y \sim 1 \).

Within-study variances are specified through `sigma2`: the rare case of equal within-study variances implies Skovgaard's adjustment reaching a third-order accuracy.

DerSimonian and Laird estimates (DerSimonian and Laird, 1986) are also supplied.

Value

An object of class "metaLik" with the following components:

- \( y \) the y vector used.
- \( X \) the model matrix used.
- `fitted.values` the fitted values.
- `sigma2` the within-study variances used.
- \( K \) the number of studies.
- `mle` the vector of the maximum likelihood parameter estimates.
- `vcov` the variance-covariance matrix of the parameter estimates.
- `max.lik` the maximum log-likelihood value.
beta.mle the vector of fixed-effects parameters estimated according to maximum likelihood.

tau2.mle the maximum likelihood estimate of $\tau^2$.

DL the vector of fixed-effects parameters estimated according to DerSimonian and Laird’s approach.

tau2.DL the method of moments estimate of the heterogeneity parameter $\tau^2$.

vcov.DL the variance-covariance matrix of the DL parameter estimates.

call the matched call.

formula the formula used.

terms the terms object used.

offset the offset used.

contrasts (only where relevant) the contrasts specified.

xlevels (only where relevant) a record of the levels of the factors used in fitting.

model the model frame used.

Generic functions coefficients, vcov, logLik, fitted, residuals can be used to extract fitted model quantities.

Author(s)

Annamaria Guolo and Cristiano Varin.

References


See Also

Function summary.metaLik for summaries.

Function test.metaLik for hypothesis testing.

Examples

```r
## meta-analysis
data(education)
m <- metaLik(y~1, data=education, sigma2=sigma2)
summary(m)
## meta-analysis
data(albumin)
```
m <- metaLik(y-1, data=albumin, sigma2=sigma2)
summary(m)
## meta-regression
data(vaccine)
m <- metaLik(y-latitude, data=vaccine, sigma2=sigma2)
summary(m)
## meta-regression
data(cholesterol)
m <- metaLik(heart_disease-chol_reduction, data=cholesterol, weights=1/sigma2)
summary(m)

simulate.metaLik

Simulate meta-analysis outcomes

Description

Simulate one or more meta-analysis outcomes from a fitted metaLik object.

Usage

```r
## S3 method for class 'metaLik'
simulate(object, nsim=1, seed=NULL, DL=FALSE, ...)
```

Arguments

- `object` an object of class "metaLik".
- `nsim` number of outcome vectors to simulate. Default is 1.
- `seed` an object specifying if and how the random number generator should be initialized, see simulate for details.
- `DL` logical, whether simulation is based on DerSimonian and Laird estimate (DerSimonian and Laird, 1986). Default is FALSE, corresponding to simulation from maximum likelihood estimate.
- `...` additional optional arguments.

Value

A dataframe containing the simulated meta-analysis outcomes.

Author(s)

Annamaria Guolo and Cristiano Varin.

References

Examples

data(vaccine)
m <- metalik(y~latitude, data=vaccine, sigma2=sigma2)
sim <- simulate(m, nsim=2)
sim

summary.metaLik  Summarizing meta-analysis and meta-regression model fits

Description

Summary method for class "metaLik".

Usage

## S3 method for class 'metaLik'
summary(object, ...)

Arguments

object  an object of class "metaLik", usually a result of a call to "metaLik".
...
additional arguments

Details

summary.metaLik prints summary information about within-study heterogeneity, parameter estimates, standard errors, first- and higher-order log-likelihood ratio statistics. See test.metaLik for more details about the first- and higher-order statistics.

Value

The function summary.metaLik returns the metaLik object from which summary.metaLik is called.

See Also

The generic functions coefficients, confint and vcov.
Function test.metaLik allows for hypothesis testing.

Examples

## meta-analysis
data(education)
m <- metalik(y~1, data=education, sigma2=sigma2)
summary(m)
## meta-analysis
data(albumin)
m <- metalik(y~1, data=albumin, sigma2=sigma2)
summary(m)
## meta-regression

data(vaccine)
m <- metalik(y~latitudeL data=vaccineL sigmaR=sigmaR)
summary(m)

## meta-regression

data(cholesterol)
m <- metalik(heart_disease~chol_reduction, data=cholesterol, weights=1/sigma2)
summary(m)

test.metaLik

Hypothesis testing on a scalar fixed-effect component in meta-analysis
and meta-regression models

Description

Performs hypothesis testing on a scalar component of the fixed-effects vector in meta-analysis and
meta-regression models, using the signed profile log-likelihood ratio test and its higher-order Skov-
gaard’s adjustment (Skovgaard, 1996), as described in Guolo (2012). See Guolo and Varin (2012)
for illustrative examples about the usage of metaLik package.

Usage

test.metaLik(object, param=1, value=0, alternative=c("two.sided", "less", "greater"),
print=TRUE)

Arguments

object an object of class "metaLik".
param a specification of which parameter is to be given confidence interval, either a
number or a name. Default is 1 corresponding to the intercept.
value a single number indicating the value of the fixed-effect parameter under the null
hypothesis. Default is 0.
alternative a character string specifying the alternative hypothesis, must be one of "two.sided"
(default), "greater" or "less". Just the initial letter can be specified.
print logical, whether output information should be printed or not; default is TRUE.

Details

test.metaLik allows hypothesis testing on a scalar component of interest in the fixed-effects vec-
tor. The signed profile log-likelihood ratio statistic for inference on scalar component $\beta$ of $\theta$ is

$$r(\beta) = \text{sign}(\hat{\beta} - \beta) \sqrt{2\{l(\hat{\theta}) - l(\theta)\}},$$

where $l$ is the log-likelihood function and $\hat{\theta}$ is the maximum likelihood estimate of $\theta$. The Skov-
gaard’s adjustment is defined as

$$T(\beta) = r(\beta) + \frac{1}{r(\beta)} \log \frac{u(\beta)}{r(\beta)},$$

where $u(\beta)$ is the profile log-likelihood. The Skovgaard’s adjustment is used to improve the
accuracy of the test statistic.
where \( u(\beta) \) is a correction term involving the observed and the expected information matrix and covariances of likelihood quantities, as described in Guolo (2012). Skovgaard’s statistic has a second-order accuracy in approximating the standard normal distribution. In the rare case of equal within-study variances, Skovgaard’s statistic reaches third-order accuracy.

**Value**

A list with the following components:

- \( r \): the value of the signed profile log-likelihood ratio statistic.
- \( pvalue.r \): the p-value of the signed profile log-likelihood ratio test.
- \( rskov \): the value of the Skovgaard’s statistic.
- \( pvalue.rskov \): the p-value of the Skovgaard’s test.

**Author(s)**

Annamaria Guolo and Cristiano Varin.

**References**


**See Also**

Function `metalik` for fitting meta-analysis and meta-regression models. Function `summary.metalik` for summaries.

**Examples**

data(vaccine)
m <- metalik(y~latitude, data=vaccine, sigma2=sigma2)
## significance test for the intercept coefficient
  test.metalik(m)
## significance test for the 'latitude' coefficient
  test.metalik(m, param=2)
## testing for the 'latitude' coefficient less than 0
  test.metalik(m, param=2, value=0, alternative='less')
Data for Bacillus Calmette-Guerin (BCG) vaccine studies.

**Description**

Data from thirteen clinical studies evaluating the efficacy of the BCG vaccine for the prevention of tuberculosis.

**Usage**

data(vaccine)

**Format**

- `y` log odds ratio in each study.
- `latitude` latitude, distance of each study from the equator, surrogate for the presence of environmental mycobacteria providing a level of natural immunity against tuberculosis.
- `year` year of the study.
- `sigma2` estimated within-study variance.

**Source**


**Examples**

data(vaccine)
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