

Package ‘lbreg’

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Type Package

Title Log-Binomial Regression with Constrained Optimization

Description Maximum likelihood estimation of log-binomial regression with special functionality when the MLE is on the boundary of the parameter space.

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 lbreg-package

Log-Binomial Regression with Constrained Optimization

Description

Maximum likelihood estimation of log-binomial regression with special functionality when the MLE is on the boundary of the parameter space.

Package lbreg performs maximum likelihood estimation of Log-Binomial Regression. The main functions are `lbreg` which provides a shortcut to `constrOptim` to estimate LBR coefficients and `relrisk` which takes lbreg results to produce estimated relative risks and associated confidence intervals and prediction. Results differ from `glm` when the MLE is on the boundary of the parameter space as explained in the reference below (Andrade, Andrade (submitted)).

Details

The DESCRIPTION file:

```
Package:      lbreg
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Title:        Log-Binomial Regression with Constrained Optimization
Description:  Maximum likelihood estimation of log-binomial regression with special functionality when the MLE is on the
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```

Index of help topics:

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HL_test	Hosmer-Lemeshow Goodness of Fit Test
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PCS	PCS Dataset
lbreg	Log-Binomial regression
lbreg-package	Log-Binomial Regression with Constrained Optimization
predict.lbreg	Predict method for Log-Binomial regression.
relrisk	Regression Adjusted Relative Risks

Author(s)

Bernardo B. Andrade

Maintainer: Bernardo Andrade <bbandrade@unb.br>

References

Andrade, BB; Andrade JML (submitted) Some results for Maximum Likelihood Estimation of Adjusted Relative Risks. Communications in Statistics - Theory and Methods.

Birth

Birth Weight Data

Description

Data used by Wacholder (1986) to illustrate the use of log binomial regression for estimating adjusted relative risks of a low-birthweight baby.

Usage

```
data("Birth")
```

Format

A data frame with 900 observations on the following 5 variables.

lowbw low birth weight delivery (1=yes)

alc mother's alcohol drinking frequency (1=Light, 2=Moderate, 3=Heavy)

smo mother smoked (1=no)

soc mother's social status (1=I and II (lower), 2=III (middle), 3=IV and V (upper))

Source

Stata's online manual <http://www.stata.com/manuals13/rbinreg.pdf>

References

Wright JT, Waterson EJ, Barrison PJ, et al. (1983). Alcohol consumption, pregnancy and low birthweight. Lancet 1:663-665.

Examples

```
data(Birth)
dim(Birth)
names(Birth)
```

Caesarian

Caesarian Infection Dataset

Description

Adapted dataset from Fahrmeir et al (2013): grouped data on infections of 251 mothers after a C-section collected at the clinical center of the University of Munich.

Usage

```
data("Caesarian")
```

Format

A data frame with 7 rows and 5 variables.

n1 Caesarians with infections.

n0 Caesarians without infections.

NPLAN = 1 if C-section was not planned.

RISK = 1 if risk factors existed.

ANTIB = 1 if antibiotics were administered as prophylaxis.

Source

<http://www.uni-goettingen.de/de/551625.html>

References

Fahrmeir, L., Kneib, Th., Lang, S., Marx, B. (2013) Regression - Models, Methods and Applications. Springer.

Examples

```
data(Caesarian)
Caesarian
# no observations for case (RISK=0, NPLAN=1, ANTIB=1)
y = Caesarian[,1:2]
cbind(Caesarian[,3:5], total=rowSums(y))
colSums(y)
```

Death

Death Penalty Data

Description

See references.

Usage

```
data("Death")
```

Format

A data frame with 147 observations on the following 6 variables.

death death = 1, life in prison = 0

blackd black defendant = 1

whitvic white victim = 1

serious a measure of crime seriousness

culp a measure of culpability

serious2 another measure of crime seriousness

Source

SAS Institute Inc. (2006). Logistic regression using the SAS system: Theory and application. SAS Publishing, Cary, NC: SAS Institute Inc; <http://ftp.sas.com/~samples/A55770>

References

Petersen MR, Deddens JA (2010). Maximum Likelihood Estimation of the Log-Binomial Model. Communications in Statistics: Theory and Methods, 39, 874-883.

Examples

```
data(Death)
dim(Death)
names(Death)
```

Evans

Evans County dataset

Description

Data from cohort study in which white males in Evans County were followed for 7 years, with coronary heart disease as the outcome of interest.

Usage

```
data("Evans")
```

Format

A data frame with 609 observations on the following 9 variables.

CDH outcome variable; 1 = coronary heart disease

CAT 1 = high, 0 = normal catecholamine level

AGE age (in years)

CHL cholesterol, mg/dl

SMK 1 = subject has ever smoked

ECG 1 = presence of electrocardiogram abnormality

DBP diastolic blood pressure, mmHg

SBP systolic blood pressure, mmHg

HPT 1 = SBP greater than or equal to 160 or DBP greater than or equal to 95

Source

<http://web1.sph.emory.edu/dkleinb/logreg3.htm#data>

References

D. Kleinbaum and M. Klein (2010) *Survival Analysis: A Self-Learning Text*. 3rd ed. Springer.

Examples

```
data(Evans)
dim(Evans)
names(Evans)
```

Heart

Heart Dataset

Description

Heart attack data from the ASSENT-2 study.

Usage

```
data("Heart")
```

Format

A data frame with 16,949 observations on the following 5 variables.

Heart binary response; 1 = death

age categorized into <65, 65-75 or >75 years

severity Killip class I, II, or III/IV

region code for three USA regions

onset treatment delay categorized into <2, 2-4 or >4 hours

Source

<http://biostatistics.oxfordjournals.org/content/13/1/179/suppl/DC1>

References

ASSENT-2 INVESTIGATORS (1999). Single-bolus tenecteplase compared with front-loaded alteplase in acute myocardial infarction: the ASSENT-2 double-blind randomised trial. *Lancet* 354, 716-722.

Ian C. Marschner and Alexandra C. Gillett (2012) Relative risk regression: reliable and flexible methods for log-binomial models. *Biostatistics* 13, 179-192

Examples

```
data(Heart)
dim(Heart)
names(Heart)
```

`HL_test`*Hosmer-Lemeshow Goodness of Fit Test*

Description

The HL decile-of-risk test. Validity of the test assumes that the number of covariate patterns is close to the number of observations which is violated when many observations have the same covariate pattern and several ties will impact the required ordering and grouping (by deciles) of observations. This is less likely when there is at least one continuous covariate. Not valid for grouped data.

Usage

```
HL_test(object, g = 10)
```

Arguments

<code>object</code>	object of class 'lbgreg'.
<code>g</code>	number of groups

Value

A list with elements

<code>X2</code>	HL statistic
<code>pvalue</code>	p-value for the test from Chi Squared with $df = g-2$

Author(s)

Bernardo B. Andrade

References

Hosmer D W, Lemeshow S 2000. Applied Logistic Regression. New York, USA: John Wiley and Sons.

See Also

[lbgreg](#)

Examples

```
require(lbgreg)

# data preparation
data(PCS)
w <- PCS
w <- w[, -1]
w$race <- factor(w$race)
```



```
w$dpros <- factor(w$dpros)
w$dcaps <- factor(w$dcaps)

fm <- lbreg(tumor ~ ., data=w)

HL_test(fm)
```

lbreg	<i>Log-Binomial regression</i>
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Description

Fitting a Log-Binomial Regression Model

Usage

```
lbreg(formula, data, start.beta, tol=0.9999, delta=1, ...)
```

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.
data	an optional 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 lbreg is called.
start.beta	starting values for the parameters in the linear predictor. If missing, the default value explained in Andrade and Andrade (2018) is used according to the choice of delta.
tol	defaults to 0.9999; threshold for declaring a probability on the boundary ($p = 1$).
delta	defaults to 1. See reference below.
...	not used.

Details

This function uses `constrOptim` with the BFGS method in order to perform maximum likelihood estimation of the log-binomial regression model as described in the reference below. When the MLE is the interior of the parameter space results should agree with `glm(..., family=binomial(link='log'))`. `lbreg` uses the adaptive logarithmic barrier algorithm rather than iteratively weighted least squares (`glm`).

Value

Active	matrix of active constraints.
barrier.value	same as in <code>constrOptim</code> .
coefficients	named vector of estimated regression coefficients.
convergence	same as in <code>constrOptim</code> .

call	the matched call.
cook.distance	Cook's distance.
data	the data argument.
deviance	residual deviance.
dev.resid	deviance residuals.
fitted.values	fitted probabilities.
formula	the formula supplied.
hat.matrix	hat matrix for GLMs (whose diagonal contains leverage values).
loglik	maximized loglikelihood.
outer.iterations	same as in constrOptim.
residuals	Pearson residuals.
se	standard errors of estimated coefficients.
start.beta	starting values used by constrOptim.
vcov	variance-covariance matrix of estimates.
vcov0	inverse of observed Fisher information; should be equal to vcov if there are no active constraints (Active = NULL).
X2	sum of squared residuals (variance-inflation estimate (dispersion) = X2/df).

Author(s)

Bernardo B. Andrade

References

Andrade, BB; Andrade JML (forthcoming) Some results for Maximum Likelihood Estimation of Adjusted Relative Risks. Communications in Statistics - Theory and Methods.

See Also

`glm` (family=binomial(link='log')), [relrisk](#)

Examples

```
require(lbreg)

# data preparation
data(PCS) # ungrouped data
w <- PCS
w <- w[, -1]
w$race <- factor(w$race)
w$dpros <- factor(w$dpros)
w$dcaps <- factor(w$dcaps)

# log-binomial regression
fm <- lbreg(tumor ~ ., data=w)
```

```

fm
coef(fm)
summary(fm)

# grouped data
require(lbreg)
data(Caesarian)
m1 <- lbreg( cbind(n1, n0) ~ RISK + NPLAN + ANTIB, data=Caesarian)
summary(m1)

# dispersion estimate based on deviance residuals
sum(m1$dev.res^2)
# dispersion estimate based on Pearson residuals (reported in the summary above)
sum(m1$residuals^2)/(8-4)

predict(m1, newdata=data.frame(RISK=0, NPLAN=1, ANTIB=1))

# m0 <- glm( cbind(n1, n0) ~ RISK + NPLAN + ANTIB, data=Dat, family=binomial(link='log'))
# summary(m0)

```

PCS

PCS Dataset

Description

Prostate Cancer Study

Usage

```
data("PCS")
```

Format

A data frame with 380 observations on the following 9 variables.

id Identification Code; 1 - 380
tumor Tumor Penetration of Prostatic Capsule, 0 = No Penetration
age in years
race Race; 1= White, 2 = Black
dpros Results of the Digital Rectal Exam, 4 levels
dcaps Detection of Capsular Involvement in Rectal Exam; 1 = No, 2 = Yes
psa antigen mg/ml
vol Tumor Volume Obtained from Ultrasound, cm3
gleason Total Gleason Score; 0 - 10

Source

<https://www.umass.edu/statdata/statdata/data/pros.txt>

References

Hosmer and Lemeshow (2000) Applied Logistic Regression, Wiley.

Examples

```
data(PCS)
## View(PCS)
## str(PCS) ; plot(PCS) ...
```

predict.lbreg	<i>Predict method for Log-Binomial regression.</i>
---------------	--

Description

Predicted values based on 'lbreg' object.

Usage

```
## S3 method for class 'lbreg'
predict(object, newdata, ...)
```

Arguments

object	Object of class inheriting from "lbreg"
newdata	a data frame with covariate values with which to predict. If omitted, the fitted probabilities are returned.
...	not used

Details

If newdata is omitted the predictions are simply the fitted values stored in the object supplied.

Value

Active	active restrictions (taking newdata into account).
coef.pred	regression coefficients re-estimated to satisfy possibly new restrictions imposed by newdata. See reference below.
convergence	same as in the object supplied.
se.pred	estimated standard errors of predictions.
tol	same as in the object supplied.
ypred	predicted probabilities for newdata.

Author(s)

Bernardo B. Andrade

References

Andrade, BB; Andrade JML (forthcoming) Some results for Maximum Likelihood Estimation of Adjusted Relative Risks. Communications in Statistics - Theory and Methods.

Examples

```
require(lbreg)

# data preparation
data(PCS)
w <- PCS
w <- w[,-1]
w$race <- factor(w$race)
w$dpros <- factor(w$dpros)
w$dcaps <- factor(w$dcaps)

# log-binomial regression
fm <- lbreg(tumor ~ ., data=w)
novo <- data.frame(age=c(41, 32), race=c(1,2), dpros=c(2,4),
                  dcaps=c(1,1), psa=c(7.24,3.25), vol=c(4.3,5.6),
                  gleason=c(2,8))
predict(fm, newdata=novo)
```

relrisk

*Regression Adjusted Relative Risks***Description**

This function calculates the relative risks RR adjusted for covariates (acting on a previous log-binomial regression fit) and confidence intervals (by default 95 percent) for the estimated RR. The confidence interval is calculated from the log(RR) and backtransformed.

Usage

```
relrisk(object, alpha = 0.05, dispersion = FALSE)
```

Arguments

object	object of class 'lbreg'.
alpha	1 - desired confidence level.
dispersion	logical. TRUE if standard errors should be adjusted for dispersion estimate based on Pearson residuals.

Value

value table with estimated relative risks, lower and upper bounds of confidence intervals.

Author(s)

Bernardo B. Andrade

References

Andrade, BB; Andrade JML (forthcoming) Some results for Maximum Likelihood Estimation of Adjusted Relative Risks. Communications in Statistics - Theory and Methods.

See Also

[lbreg](#)

Examples

```
require(lbreg)

# ungrouped data
# data preparation
data(PCS)
w <- PCS
w <- w[,-1]
w$race <- factor(w$race)
w$dpros <- factor(w$dpros)
w$dcaps <- factor(w$dcaps)

# log-binomial regression
fm <- lbreg(tumor ~ ., data=w)

# relative risks
relrisk(fm)
relrisk(fm, alpha=.10)

# grouped data
require(lbreg)
data(Caesarian)
m1 <- lbreg( cbind(n1, n0) ~ RISK + NPLAN + ANTIB, data=Caesarian)
relrisk(m1)
relrisk(m1, dispersion=TRUE)
```

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