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 boundary of the parameter space.

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Contents

lbreg-package 2
Birth 3
Caesarian 4
Death 5
Evans 6
Heart 7
HL_test 8
lbreg 9
PCS 11
predict.lbreg 12
relrisk 13

Index **15**

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 (2018)).

Details

The DESCRIPTION file:

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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
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Index of help topics:

Birth	Birth Weight Data
Caesarian	Caesarian Infection Dataset
Death	Death Penalty Data
Evans	Evans County dataset
HL_test	Hosmer-Lemeshow Goodness of Fit Test
Heart	Heart Dataset
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 (2018) 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

object	object of class 'lbreg'.
g	number of groups

Value

A list with elements

X2	HL statistic
pvalue	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

lbreg

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)

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

HL_test(fm)
```

`lbreg` *Log-Binomial regression*

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 logarithimic barrier algorithm rather than iteratively weighted least squares (`glm`).

Value

`Active`	matrix of active constraints.
`barrier.value`	same as in `constrOptim`.
`coefficients`	named vector of estimated regression coefficients.
`convergence`	same as in `constrOptim`.

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 (2018) 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` *Predict method for Log-Binomial regression.*

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 (2018) 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 condifidence intervals.

Author(s)

Bernardo B. Andrade

References

Andrade, BB; Andrade JML (2018) 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)
```

Index

∗ **datasets**
Birth, 3
Caesarian, 4
Death, 5
Evans, 6
Heart, 7
PCS, 11

Birth, 3

Caesarian, 4
constrOptim, *2*, *9*

Death, 5

Evans, 6

glm, *2*, *10*

Heart, 7
HL_test, 8

lbreg, *2*, *8*, 9, *14*
lbreg-package, 2

PCS, 11
predict.lbreg, 12

relrisk, *2*, *10*, 13