Package ‘ProfileLikelihood’

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Description Provides profile likelihoods for a parameter of interest in commonly used statistical models. The models include linear models, generalized linear models, proportional odds models, linear mixed-effects models, and linear models for longitudinal responses fitted by generalized least squares. The package also provides plots for normalized profile likelihoods as well as the maximum profile likelihood estimates and the kth likelihood support intervals.
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Description

This package provides profile likelihoods for a parameter of interest in commonly used statistical models. The models include linear models, generalized linear models, proportional odds models, linear mixed-effects models, and linear models for longitudinal responses fitted by generalized least squares. The package also provides plots for normalized profile likelihoods as well as the maximum profile likelihood estimates and the kth likelihood support intervals (Royall, 1997).

Details

| Package:     | ProfileLikelihood |
| Type:        | Package           |
| Version:     | 1.0               |
| Date:        | 2011-01-25        |
| License:     | GPL (>=3)         |
| LazyLoad:    | yes               |

Use `profilelike.lm, profilelike.glm, profilelike.polr, profilelike.gls` and `profilelike.lme` to obtain profile likelihoods and normalized profile likelihoods, and plot the normalized profile likelihoods using `profilelike.plot`. Use `profilelike.summary` to obtain the maximum profile likelihood estimate and the kth likelihood support intervals.

Author(s)

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References


See Also

`profilelike.lm, profilelike.glm, profilelike.polr, profilelike.gls, profilelike.lme, profilelike.plot, profilelike.summary`
Examples

```r
c <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
t <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- c(rep(0, 10), rep(1, 10))
weight <- c(c, t)
xx <- profilelike.lm(formula = weight ~ 1, data=dd, profile.theta="group",
  lo.theta=-2, hi.thet=1, length=500)
  profilelike.plot(theta=xx$theta, profile.lik.norm=xx$profile.lik.norm, round=2)
```

---

**dataglm**  
*Example Data for a Profile Likelihood in Generalized Linear Models*

**Description**  
This data is used to illustrate how to obtain values for a profile likelihood of a parameter of interest in a generalized linear model.

**Usage**  
`data(dataglm)`

**Format**  
A data frame with 100 observations on the following 5 variables.

- `id`: a numeric vector; unique identification number
- `y`: a numeric vector; binary outcome variable
- `x1`: a numeric vector; covariate
- `x2`: a numeric vector; covariate
- `group`: a numeric vector; covariate and a parameter of interest

**Details**  
This data is used to illustrate how to obtain values for a profile likelihood of a parameter of interest in a logistic regression model. A parameter of interest is `group` indicator variable, `y` is a binary outcome, and `x1` and `x2` are covariates in a logistic regression model.

**Examples**  
```r
data(dataglm)
xx <- profilelike.glm(y ~ x1 + x2, data=dataglm, profile.theta="group",
  family=binomial(link="logit"), length=500, round=2)
  profilelike.plot(theta=xx$theta, profile.lik.norm=xx$profile.lik.norm, round=2)
```
Data for a Profile Likelihood in Proportional Odds Models

Description

This data is used to illustrate how to obtain values for a profile likelihood of a parameter of interest in a proportional odds model.

Usage

data(datapolr)

Format

A data frame with 66 observations on the following 5 variables.

- id: a numeric vector; unique identification number
- y: a numeric vector; ordinal outcome variable; should be defined as a factor
- x1: a numeric vector; covariate
- x2: a numeric vector; covariate
- group: a numeric vector; covariate and a parameter of interest

Details

This data is used to illustrate how to obtain values for a profile likelihood of a parameter of interest in a proportional odds model. A parameter of interest is group indicator variable, y is an ordinal outcome, and x1 and x2 are covariates in a proportional odds model.

Examples

data(datapolr)
datapolr$y <- as.factor(datapolr$y)
xx <- profilelike.polr(y ~ x1 + x2, data=datapolr, profile.theta="group",
method="logistic", lo.theta=-2, hi.theta=2.5, length=500)
profilelike.plot(theta=xx$theta, profile.lik.norm=xx$profile.lik.norm, round=2)
**LR.pvalue**

---

**P-values based on LR statistics for 2 x 2 Tables**

**Description**

This function provides p-values based on likelihood ratio (LR) statistics for 2 x 2 tables.

**Usage**

```r
LR.pvalue(y1, y2, n1, n2, interval=0.01)
```

**Arguments**

- `y1`: the number of success for treatment 1.
- `y2`: the number of success for treatment 2.
- `n1`: the sample size for treatment 1.
- `n2`: the sample size for treatment 2.
- `interval`: grid for evaluating a parameter of interest to obtain values for likelihoods. The default is 0.01.

**Details**

This function provides p-values based on the profile and conditional likelihood ratio (LR) statistics for 2 x 2 tables. The function also provides the profile and conditional likelihood support intervals \((k=6.8)\) corresponding to a 95% confidence interval based on a normal approximation. For comparison purpose, p-values from Pearson’s Chi-squared test, Fisher’s exact test and Pearson’s Chi-squared test with continuity correction are also provided.

**Value**

- `mle.lor.uncond`: the maximum likelihood estimate for log odds ratio.
- `mle.lor.cond`: the maximum conditional likelihood estimate for log odds ratio.
- `LI.norm.profile`: profile likelihood support interval \((k=6.8)\) corresponding to a 95% confidence interval based on a normal approximation.
- `LI.norm.cond`: conditional likelihood support interval \((k=6.8)\) corresponding to a 95% confidence interval based on a normal approximation.
- `LR.profile`: profile likelihood ratio.
- `LR.cond`: conditional likelihood ratio.
- `Pvalue.LR.profile`: p-value based on the profile LR statistic.
- `Pvalue.LR.cond`: p-value based on the conditional LR statistic.
Pvalue.chisq.test
p-value from Pearson’s Chi-squared test.

Pvalue.fisher.test
p-value from Fisher’s exact test.

Pvalue.chisq.cont.correction
p-value from Pearson’s Chi-squared test with continuity correction.

Warning

Likelihood intervals, LRs and the corresponding p-values are not reliable with empty cells (y1=0 or y2=0) in 2 x 2 tables.

P-values from Pearson’s Chi-squared test, Fisher’s exact test and Pearson’s Chi-squared test with continuity correction are provided only for comparison purpose. For more options, use chisq.test and fisher.test for these tests.

Author(s)

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See Also

profilelike.plot, profilelike.summary, profilelike.glm

Examples

(fit <- LR.pvalue(y1=20, y2=30, n1=50, n2=50, interval=0.01))

profilelike.glm Profile Likelihood for Generalized Linear Models

Description

This function provides values for a profile likelihood and a normalized profile likelihood for a parameter of interest in a generalized linear model.

Usage

profilelike.glm(formula, data, profile.theta, family = stats::gaussian, offset.glm = NULL, lo.theta = NULL, hi.theta = NULL, length = 300, round = 2, subset = NULL, weights = NULL, offset = NULL, ...)
Arguments

- `formula`: see corresponding documentation in `glm`.
- `data`: a data frame. See corresponding documentation in `glm`.
- `profile.theta`: a parameter of interest, theta; must be a numeric variable.
- `family`: see corresponding documentation in `glm`.
- `offset.glm`: same usage as offset in `glm`. See corresponding documentation for offset in `glm`.
- `lo.theta`: lower bound for a parameter of interest to obtain values for a profile likelihood.
- `hi.theta`: upper bound for a parameter of interest to obtain values for a profile likelihood.
- `length`: length of numerical grid values for a parameter of interest to obtain values for a profile likelihood.
- `round`: the number of decimal places for `round` function to automatically define lower and upper bounds of numerical grid for a parameter of interest. If an automatically defined parameter range is not appropriate, increase the number or specify `lo.theta` and `hi.theta`.
- `subset`: should not be provided.
- `weights`: should not be provided.
- `offset`: should not be provided. Instead use offset.glm.
- `...`: further arguments passed to or from other methods.

Details

This function provides values for a profile likelihood and a normalized profile likelihood for a parameter of interest in a generalized linear model. Users must define a parameter of interest in a generalized linear model. This function can be used for generalized linear models comparable with the `glm` function. However, arguments weights, subset, and offset should not be provided. An argument offset in `glm` function can be provided using offset.glm. A normalized profile likelihood is obtained by a profile likelihood being divided by the maximum value of the profile likelihood so that a normalized profile likelihood ranges from 0 to 1.

Value

- `theta`: numerical grid values for a parameter of interest in a specified range (between lower and upper bounds).
- `profile.lik`: numerical values for a profile likelihood corresponding to theta in a specified range (between lower and upper bounds).
- `profile.lik.norm`: numerical values for a normalized profile likelihood ranging from 0 to 1.

Warning

Arguments weights, subset, and offset in the `glm` function are not comparable.

Missing values should be removed.
profilelike.gls

Author(s)
Leena Choi <naturechoi@gmail.com>

See Also
profilelike.plot, profilelike.summary, profilelike.lm, profilelike.polv, profilelike.gls, profilelike.lme, glm

Examples
data(dataglm)
xx <- profilelike.glm(y ~ x1 + x2, data=dataglm, profile.theta="group", family=binomial(link="logit"), length=500, round=2)
profilelike.plot(theta=xx$theta, profile.lik.norm=xx$profile.lik.norm, round=2)

profilelike.gls
Profile Likelihood for Linear Models for Longitudinal Responses Fitted by Generalized Least Squares

Description
This function provides values for a profile likelihood and a normalized profile likelihood for a parameter of interest in a linear model for longitudinal responses fitted by generalized least squares.

Usage
profilelike.gls(formula, data, correlation = NULL, subject, profile.theta, method = "ML", lo.theta, hi.theta, length = 300, round = 2, subset = NULL, weights = NULL, ...)

Arguments
formula see corresponding documentation in gls.
data a data frame. See corresponding documentation in gls.
correlation see corresponding documentation in gls.
subject see corresponding documentation in gls.
profile.theta a parameter of interest, theta; must be a numeric variable.
method see corresponding documentation in gls.
lo.theta lower bound for a parameter of interest to obtain values for a profile likelihood.
hi.theta upper bound for a parameter of interest to obtain values for a profile likelihood.
length length of numerical grid values for a parameter of interest to obtain values for a profile likelihood.
round the number of decimal places for \texttt{round} function to automatically define lower and upper bounds of numerical grid for a parameter of interest. If an automatically defined parameter range is not appropriate, increase the number or specify \texttt{lo.theta} and \texttt{hi.theta}.


Details

This function provides values for a profile likelihood and a normalized profile likelihood for a parameter of interest in a linear model for longitudinal responses fitted by generalized least squares. Users must define a parameter of interest in the model. This function can be used for models for longitudinal responses comparable with the `gls` function. However, arguments weights and subset should not be provided. A normalized profile likelihood is obtained by a profile likelihood being divided by the maximum value of the profile likelihood so that a normalized profile likelihood ranges from 0 to 1.

Value

`theta` numerical grid values for a parameter of interest in a specified range (between lower and upper bounds).

`profile.lik` numerical values for a profile likelihood corresponding to `theta` in a specified range (between lower and upper bounds).

`profile.lik.norm` numerical values for a normalized profile likelihood ranging from 0 to 1.

Warning

Arguments weights and subset in the `gls` function are not comparable.

Missing values should be removed.

Author(s)

Leena Choi <naturechoi@gmail.com>

See Also

`profilelike.plot`, `profilelike.summary`, `profilelike.lm`, `profilelike.glm`, `profilelike.polr`, `profilelike.lme`, `gls`

Examples

data(Gasoline, package = "nlme")
xx <- profilelike.gls(formula=yield ~ endpoint, correlation=nlme::corAR1(form = ~ 1 | id),
  data=Gasoline, subject="Sample", profile.theta="vapor", method="ML",
  lo.theta=1, hi.theta=5, length=500, round=2)
profilelike.plot(theta=xx$theta, profile.lik.norm=xx$profile.lik.norm, round=4)
Description

This function provides values for a profile likelihood and a normalized profile likelihood for a parameter of interest in a linear model.

Usage

```r
profilelike.lm(formula, data, profile.theta, lo.theta = NULL, hi.theta = NULL, length = 300, round = 2, subset = NULL, weights = NULL, offset = NULL, ...)
```

Arguments

- `formula`: see corresponding documentation in `lm`.
- `data`: a data frame. See corresponding documentation in `lm`.
- `profile.theta`: a parameter of interest, theta; must be a numeric variable.
- `lo.theta`: lower bound for a parameter of interest to obtain values for a profile likelihood.
- `hi.theta`: upper bound for a parameter of interest to obtain values for a profile likelihood.
- `length`: length of numerical grid values for a parameter of interest to obtain values for a profile likelihood.
- `round`: the number of decimal places for `round` function to automatically define lower and upper bounds of numerical grid for a parameter of interest. If an automatically defined parameter range is not appropriate, increase the number or specify `lo.theta` and `hi.theta`.
- `subset`: should not be provided.
- `weights`: should not be provided.
- `offset`: should not be provided.
- `...`: further arguments passed to or from other methods.

Details

This function provides values for a profile likelihood and a normalized profile likelihood for a parameter of interest in a linear model. Users must define a parameter of interest in a linear model. This function can be used for linear models comparable with the `lm` function. However, arguments weights, subset, and offset should not be provided. A normalized profile likelihood is obtained by a profile likelihood being divided by the maximum value of the profile likelihood so that a normalized profile likelihood ranges from 0 to 1.
Profile Likelihood for Linear Mixed-Effects Models

This function provides values for a profile likelihood and a normalized profile likelihood for a parameter of interest in a linear mixed-effects model.

Usage

```r
profilelike.lme(formula, data, subject, random, correlation = NULL, profile.theta, method = "ML", lo.theta, hi.theta, length = 300, round = 2, subset = NULL, weights = NULL, ...)
```

Examples

```r
ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- c(rep(0, 10), rep(1, 10))
weight <- c(ctl, trt)

dd <- data.frame(group = group, weight = weight)

xx <- profilelike.lm(formula = weight ~ 1, data = dd, profile.theta = "group", lo.theta = -2, hi.theta = 1, length = 500)
profilelike.plot(theta = xx$theta, profile.lik.norm = xx$profile.lik.norm, round = 2)
```
Arguments

- **formula**: see corresponding documentation in `lme`.
- **data**: a data frame. See corresponding documentation in `lme`.
- **subject**: see corresponding documentation in `lme`.
- **random**: see corresponding documentation in `lme`.
- **correlation**: see corresponding documentation in `lme`.
- **profile.theta**: a parameter of interest, theta; must be a numeric variable.
- **method**: see corresponding documentation in `lme`.
- **lo.theta**: lower bound for a parameter of interest to obtain values for a profile likelihood.
- **hi.theta**: upper bound for a parameter of interest to obtain values for a profile likelihood.
- **length**: length of numerical grid values for a parameter of interest to obtain values for a profile likelihood.
- **round**: the number of decimal places for `round` function to automatically define lower and upper bounds of numerical grid for a parameter of interest. If an automatically defined parameter range is not appropriate, increase the number or specify lo.theta and hi.theta.
- **subset**: should not be provided.
- **weights**: should not be provided.
- **...**: further arguments passed to or from other methods.

Details

This function provides values for a profile likelihood and a normalized profile likelihood for a parameter of interest in a linear mixed-effects model. Users must define a parameter of interest in a linear mixed-effects model. This function can be used for models comparable with the `lme` function. However, arguments weights and subset should not be provided. A normalized profile likelihood is obtained by a profile likelihood being divided by the maximum value of the profile likelihood so that a normalized profile likelihood ranges from 0 to 1.

Value

- **theta**: numerical grid values for a parameter of interest in a specified range (between lower and upper bounds).
- **profile.lik**: numerical values for a profile likelihood corresponding to theta in a specified range (between lower and upper bounds).
- **profile.lik.norm**: numerical values for a normalized profile likelihood ranging from 0 to 1.

Warning

Arguments weights and subset in the `lme` function are not comparable.

Missing values should be removed.
Author(s)
Leena Choi <naturechoi@gmail.com>

See Also
profilelike.plot, profilelike.summary, profilelike.lm, profilelike glm, profilelike.polr, profilelike.gls, lme

Examples
## Not run:
xx <- profilelike.lme(formula = yield ~ endpoint, random = ~ 1 | id, correlation=corAR1(form = ~ 1 | id), data=Gasoline, subject="Sample", profile.theta="vapor", method="ML", lo.theta=1, hi.theta=5, length=500, round=2)
profilelike.plot(theta=xx$theta, profile.lik.norm=xx$profile.lik.norm, round=4)
## End(Not run)

Description
The function provides a plot for a normalized profile likelihood as well as the maximum profile likelihood estimate and the kth likelihood support intervals (Royall, 1997).

Usage
profilelike.plot(theta = theta, profile.lik.norm = profile.lik.norm, round = 2)

Arguments
theta numerical grid values for a parameter of interest in a specified range.
profile.lik.norm numerical values for a normalized profile likelihood ranging from 0 to 1.
round the number of decimal places for round function for presentation of the maximum profile likelihood estimate and the kth likelihood support intervals.

Details
The function provides a plot for a normalized profile likelihood obtained from profilelike.lm, profilelike glm, profilelike.polr, profilelike.gls and profilelike.lme. The maximum profile likelihood estimate, the kth likelihood support interval (k=8, k=20, and k=32), and the likelihood support interval (k=6.8) corresponding to a 95% confidence interval based on a normal approximation are also presented.
Value

A normalized profile likelihood plot with the maximum profile likelihood estimate and the kth likelihood support intervals.

Author(s)

Leena Choi <naturechoi@gmail.com>

References


See Also

profilelike.summary, profilelike.lm, profilelike.glm, profilelike.polr, profilelike.gls, profilelike.lme

Examples

c <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- c(rep(0, 10), rep(1, 10))
weight <- c(ctl, trt)

data <- data.frame(group = group, weight = weight)
xx <- profilelike.lm(formula = weight ~ 1, data = data, profile.theta = "group",
  lo.theta = -2, hi.theta = 1, length = 500)
profilelike.plot(theta = xx$theta, profile.lik.norm = xx$profile.lik.norm, round = 2)
profilelike.summary(k = 8, theta = xx$theta, profile.lik.norm = xx$profile.lik.norm, round = 3)
Arguments

- **formula**: see corresponding documentation in `polr`.
- **data**: a data frame. See corresponding documentation in `polr`.
- **profile.theta**: a parameter of interest, theta; must be a numeric variable.
- **method**: see corresponding documentation in `polr`.
- **lo.theta**: lower bound for a parameter of interest to obtain values for a profile likelihood.
- **hi.theta**: upper bound for a parameter of interest to obtain values for a profile likelihood.
- **length**: length of numerical grid values for a parameter of interest to obtain values for a profile likelihood.
- **round**: the number of decimal places for `round` function to automatically define lower and upper bounds of numerical grid for a parameter of interest. If an automatically defined parameter range is not appropriate, increase the number or specify `lo.theta` and `hi.theta`.
- **subset**: should not be provided.
- **weights**: should not be provided.
- **offset**: should not be provided.
- **...**: further arguments passed to or from other methods.

Details

This function provides values for a profile likelihood and a normalized profile likelihood for a parameter of interest in a proportional odds model. Users must define a parameter of interest in a proportional odds model. This function can be used for proportional odds models comparable with the `polr` function. However, arguments weights, subset, and offset should not be provided. A normalized profile likelihood is obtained by a profile likelihood being divided by the maximum value of the profile likelihood so that a normalized profile likelihood ranges from 0 to 1.

Value

- **theta**: numerical grid values for a parameter of interest in a specified range (between lower and upper bounds).
- **profile.lik**: numerical values for a profile likelihood corresponding to theta in a specified range (between lower and upper bounds).
- **profile.lik.norm**: numerical values for a normalized profile likelihood ranging from 0 to 1.

Warning

Arguments weights, subset, and offset in the `polr` function are not comparable. Missing values should be removed.

Author(s)

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profilelike.summary

See Also

profilelike.plot, profilelike.summary, profilelike.lm, profilelike.glm, profilelike.gls, profilelike.lme, polr

Examples

data(datapolr)
datapolr$y <- as.factor(datapolr$y)
xx <- profilelike.polr(y ~ x1 + x2, data=datapolr, profile.theta="group",
method="logistic", lo.theta=-2, hi.theta=2.5, length=500)
profilelike.plot(theta=xx$theta, profile.lik.norm=xx$profile.lik.norm, round=2)

profilelike.summary

Summary for the Maximum Profile Likelihood Estimate and Likelihood Support Intervals

Description

The function provides the maximum profile likelihood estimate and likelihood support intervals
(Royall, 1997).

Usage

profilelike.summary(k, theta = theta, profile.lik.norm = profile.lik.norm, round = 2)

Arguments

- **k**: strength of evidence for the kth likelihood support interval.
- **theta**: numerical grid values for a parameter of interest in a specified range.
- **profile.lik.norm**: numerical values for a normalized profile likelihood ranging from 0 to 1.
- **round**: the number of decimal places for round function for presentation of the maximum profile likelihood estimate and the kth likelihood support intervals.

Details

The function provides the maximum profile likelihood estimate and likelihood support intervals
for a profile likelihood obtained from profilelike.lm, profilelike.glm, profilelike.polr, profilelike.gls and profilelike.lme. The kth likelihood support interval and the likelihood support interval (k=6.8) corresponding to a 95% confidence interval based on a normal approximation are provided.
profilelike.summary

Value

- \( k \): strength of evidence for the \( k \)th likelihood support interval.
- \( \text{mle} \): the maximum profile likelihood estimate.
- \( \text{LI}.k \): the \( k \)th likelihood support interval.
- \( \text{LI}.\text{norm} \): likelihood support interval \((k=6.8)\) corresponding to a 95\% confidence interval based on a normal approximation.

Author(s)

Leena Choi <naturechoi@gmail.com>

References


See Also

profilelike.plot, profilelike.lm, profilelike.glm, profilelike.polr, profilelike.gls, profilelike.lme

Examples

c1 <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
c2 <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
group <- c(rep(0,10), rep(1,10))
weight <- c(c1, c2)

dd <- data.frame(group=group, weight=weight)

xx <- profilelike.lm(formula = weight ~ 1, data=dd, profile.theta="group",
lo.theta=-2, hi.theta=1, length=500)
profilelike.plot(theta=xx$theta, profile.lik.norm=xx$profile.lik.norm, round=2)
profilelike.summary(k=8, theta=xx$theta, profile.lik.norm=xx$profile.lik.norm, round=3)
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