

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.

License GPL (>= 3)

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R topics documented:

ProfileLikelihood-package	2
dataglm	3
datapolr	4
LR.pvalue	5
profilelike.glm	6
profilelike.gls	8
profilelike.lm	10
profilelike.lme	11
profilelike.plot	13
profilelike.polr	14
profilelike.summary	16

ProfileLikelihood-package

Profile Likelihood for a Parameter in Commonly Used Statistical Models

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 k th likelihood support intervals (Royall, 1997).

Details

Package:	ProfileLikelihood
Type:	Package
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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 k th likelihood support intervals.

Author(s)

Leena Choi <naturechoi@gmail.com>

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References

Royall, Richard M. (1997). *Statistical Evidence: A Likelihood Paradigm*. Chapman & Hall/CRC.

Pawitan, Yudi (2001). In *All Likelihood: Statistical Modelling and Inference Using Likelihood*. Oxford University Press.

See Also

[profilelike.lm](#), [profilelike.glm](#), [profilelike.polr](#), [profilelike.gls](#), [profilelike.lme](#), [profilelike.plot](#), [profilelike.summary](#)

Examples

```

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)

```

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

```

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)

```

`datapolr`*Example 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

```
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 ($y_1=0$ or $y_2=0$) in 2×2 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)

Leena Choi <naturechoi@gmail.com>

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.

Author(s)

Leena Choi <naturechoi@gmail.com>

See Also

[profilelike.plot](#), [profilelike.summary](#), [profilelike.lm](#), [profilelike.polr](#), [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	<i>Profile Likelihood for Linear Models for Longitudinal Responses Fitted by Generalized Least Squares</i>
-----------------	--

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 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 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)
```

`profilelike.lm`*Profile Likelihood for Linear Models*

Description

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

Usage

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

Arguments

<code>formula</code>	see corresponding documentation in lm .
<code>data</code>	a data frame. See corresponding documentation in lm .
<code>profile.theta</code>	a parameter of interest, theta; must be a numeric variable.
<code>lo.theta</code>	lower bound for a parameter of interest to obtain values for a profile likelihood.
<code>hi.theta</code>	upper bound for a parameter of interest to obtain values for a profile likelihood.
<code>length</code>	length of numerical grid values for a parameter of interest to obtain values for a profile likelihood.
<code>round</code>	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 <code>lo.theta</code> and <code>hi.theta</code> .
<code>subset</code>	should not be provided.
<code>weights</code>	should not be provided.
<code>offset</code>	should not be provided.
<code>...</code>	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.

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 `lm` function are not comparable.
Missing values should be removed.

Author(s)

Leena Choi <naturechoi@gmail.com>

See Also

[profilelike.plot](#), [profilelike.summary](#), [profilelike.glm](#), [profilelike.polr](#), [profilelike.gls](#),
[profilelike.lme](#), [lm](#)

Examples

```
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)
```

profilelike.lme

Profile Likelihood for Linear Mixed-Effects Models

Description

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

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

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)
```

profilelike.plot *Profile Likelihood Plot*

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 k th likelihood support intervals.

Author(s)

Leena Choi <naturechoi@gmail.com>

References

Royall, Richard M. (1997). *Statistical Evidence: A Likelihood Paradigm*. Chapman & Hall/CRC.
 Pawitan, Yudi (2001). In *All Likelihood: Statistical Modelling and Inference Using Likelihood*. Oxford University Press.

See Also

[profilelike.summary](#), [profilelike.lm](#), [profilelike.glm](#), [profilelike.polr](#), [profilelike.gls](#), [profilelike.lme](#)

Examples

```
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)
profilelike.summary(k=8, theta=xx$theta, profile.lik.norm=xx$profile.lik.norm, round=3)
```

profilelike.polr

Profile Likelihood for Proportional Odds Models

Description

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

Usage

```
profilelike.polr(formula, data, profile.theta, method = "logistic",
  lo.theta = NULL, hi.theta = NULL, length = 300, round = 2,
  subset = NULL, weights = NULL, offset = NULL, ...)
```

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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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	<i>Summary for the Maximum Profile Likelihood Estimate and Likelihood Support Intervals</i>
---------------------	---

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.

Value

k	strength of evidence for the kth likelihood support interval.
mle	the maximum profile likelihood estimate.
LI.k	the kth likelihood support interval.
LI.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

- Royall, Richard M. (1997). *Statistical Evidence: A Likelihood Paradigm*. Chapman & Hall/CRC.
- Pawitan, Yudi (2001). In *All Likelihood: Statistical Modelling and Inference Using Likelihood*. Oxford University Press.

See Also

[profilelike.plot](#), [profilelike.lm](#), [profilelike.glm](#), [profilelike.polr](#), [profilelike.gls](#),
[profilelike.lme](#)

Examples

```
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)
profilelike.summary(k=8, theta=xx$theta, profile.lik.norm=xx$profile.lik.norm, round=3)
```

Index

- * **2-by-2 table**
 - LR.pvalue, 5
 - * **LR p-value**
 - LR.pvalue, 5
 - * **datasets**
 - dataglm, 3
 - datapolr, 4
 - * **likelihood support interval**
 - ProfileLikelihood-package, 2
 - * **profile likelihood plot**
 - ProfileLikelihood-package, 2
 - * **profile likelihood**
 - ProfileLikelihood-package, 2
- chisq.test, 6
- dataglm, 3
- datapolr, 4
- fisher.test, 6
- glm, 7, 8
- gls, 8, 9
- lm, 10, 11
- lme, 12, 13
- LR.pvalue, 5
- polr, 15, 16
- profilelike.glm, 2, 6, 6, 9, 11, 13, 14, 16, 17
- profilelike.gls, 2, 8, 8, 11, 13, 14, 16, 17
- profilelike.lm, 2, 8, 9, 10, 13, 14, 16, 17
- profilelike.lme, 2, 8, 9, 11, 11, 13, 14, 16, 17
- profilelike.plot, 2, 6, 8, 9, 11, 13, 13, 16, 17
- profilelike.polr, 2, 8, 9, 11, 13, 14, 14, 16, 17
- profilelike.summary, 2, 6, 8, 9, 11, 13, 14, 16, 16
- ProfileLikelihood
(ProfileLikelihood-package), 2
- ProfileLikelihood-package, 2
- round, 7, 8, 10, 12, 13, 15, 16