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Function to compute asymptotic likelihood ratio test of two models.

Description

This function computes the asymptotic likelihood ratio test of two models by comparing twice the difference in the log-likelihoods of the models with the Chi-squared distribution with degrees of freedom equal to the difference in the degrees of freedom of the models.

Usage

alrt(x1, x2, boundary = FALSE)

Arguments

x1 A fitted model as an object that logLik will work for.
x2 A fitted model as an object that logLik will work for.
boundary A flag that reports whether a boundary correction should be made.

Value

out.tab A data frame that summarizes the test.
jl. diff The difference between the log-likelihoods.
df. diff The difference between the degrees of freedom.
p. value The p-value of the statistical test of the null hypothesis that there is no difference between the fit of the models.

Note

The function does not provide any checks for nesting, data equivalence, etc.

Author(s)

Andrew Robinson and Joe Hilbe.

References

See Also

`ml_glm, ml_glm2`

Examples

data(medpar)

ml.poi.1 <- ml_glm(loss ~ hmo + white,
                   family = "poisson",
                   link = "log",
                   data = medpar)

ml.poi.2 <- ml_glm(loss ~ hmo,
                   family = "poisson",
                   link = "log",
                   data = medpar)

alrt(ml.poi.1, ml.poi.2)

doll

Physician smoking and mortality count data

Description

The data are a record of physician smoking habits and the frequency of death by myocardial infarction, or heart attack.

Usage

data(doll)

Format

A data frame with 10 observations on the following variables.

- **age** Ordinal age group
- **smokes** smoking status
- **deaths** count of deaths in category
- **pyears** number of physician years in scope of data
- **a1** Dummy variable for age level 1
- **a2** Dummy variable for age level 2
- **a3** Dummy variable for age level 3
- **a4** Dummy variable for age level 4
- **a5** Dummy variable for age level 5
Details

The physicians were divided into five age divisions, with deaths as the response, person years (pyears) as the binomial denominator, and both smoking behavior (smokes) and agegroup (a1–a5) as predictors.

Source


References


Examples

data(doll)

i.glog <- irls(deaths ~ smokes + ordered(age),
               family = "binomial",
               link = "logit",
               data = doll,
               m = doll$pyears)
summary(i.glog)

glm.glog <- glm(cbind(deaths, pyears - deaths) ~
               smokes + ordered(age),
               data = doll,
               family = binomial)
coef(summary(glm.glog))

hatvalues.msme Function to return the hat matrix of a msme-class model.

Description

This function uses QR decomposition to determine the hat matrix of a model given its design matrix X. It is specific to objects of class msme.

Usage

## S3 method for class 'msme'
hatvalues(model, ...)

hatvalues.msme
Arguments

model  A fitted model of class msme.
...  other arguments, retained for compatibility with generic method.

Value

An n*n matrix of hat values, where n is the number of observations used to fit the model. Needed to standardize the residuals.

Note

Leverages can be obtained as the diagonal of the output. See the examples.

Author(s)

Andrew Robinson and Joe Hilbe.

References


See Also

hatvalues

Examples

data(medpar)

ml.poi <- ml_glm(los ~ hmo + white,
    family = "poisson",
    link = "log",
    data = medpar)

str(diag(hatvalues(ml.poi)))

heart  Heart surgery outcomes for Canadian patients

Description

The data consists of Canadian patients who have either a Coronary Artery Bypass Graft surgery (CABG) or Percutaneous Transluminal Coronary Angioplasty (PTCA) heart procedure.

Usage

data(heart)
Format

A grouped binomial data frame with 15 observations.

- **death**: number of patients that died within 48 hours of hospital admission
- **cases**: number of patients monitored
- **anterior**: 1: anterior site damage heart attack; 0: other site damage
- **hcabg**: 1: previous CABG procedure; 0: previous PTCA procedure;
- **killip**: 1: normal heart; 2: angina; 3: minor heart blockage; 4: heart attack or myocardial infarction;

Details

The data are presented as a grouped binomial dataset, with each row representing a different combination of the predictor variables.

Source

National Canadian Registry of Cardiovascular Disease

References


Examples

```r
data(heart)

heart.nb <- irls(death ~ anterior + hcabg + factor(killip),
                 a = 0.0001,
                 offset = log(heart$cases),
                 family = "negBinomial", link = "log",
                 data = heart)
```

---

**irls**

*Function to fit generalized linear models using IRLS.*

Description

This function fits a wide range of generalized linear models using the iteratively reweighted least squares algorithm. The intended benefit of this function is for teaching. Its scope is similar to that of R’s glm function, which should be preferred for operational use.

Usage

```r
irls(formula, data, family, link, tol = 1e-06, offset = 0, m = 1, a = 1, verbose = 0)
```
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. (See the help for `glm` for more details).
- **data**: a data frame containing the variables in the model.
- **family**: a description of the error distribution to be used in the model. This must be a character string naming a family.
- **link**: a description of the link function to be used in the model. This must be a character string naming a link function.
- **tol**: an optional quantity to use as the convergence criterion for the change in deviance.
- **offset**: this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be 0 or a numeric vector of length equal to the number of cases.
- **m**: the number of cases per observation for binomial regression.
- **a**: the scale for negative binomial regression.
- **verbose**: a flag to control the amount of output printed by the function.

Details

The containing package, msme, provides the needed functions to use the irls function to fit the Poisson, negative binomial (2), Bernoulli, and binomial families, and supports the use of the identity, log, logit, probit, complementary log-log, inverse, inverse^2, and negative binomial link functions. All statistics are computed at the final iteration of the IRLS algorithm. The convergence criterion is the magnitude of the change in deviance. The object returned by the function is designed to be reported by the print.glm function.

Value

- **coefficients**: parameter estimates.
- **se.beta.hat**: standard errors of parameter estimates.
- **model**: the final, weighted linear model.
- **call**: the function call used to create the object.
- **nobs**: the number of observations.
- **eta**: the linear predictor at the final iteration.
- **mu**: the estimated mean at the final iteration.
- **df.residual**: the residual degrees of freedom.
- **df.null**: the degrees of freedom for the null model.
- **deviance**: the residual deviance.
- **null.deviance**: a place-holder for the null deviance - returned as NA.
- **p.dispersion**: Pearson's Chi-squared statistic.
- **pearson**: Pearson's deviance.
loglik  the maximized log-likelihood.
family  the chosen family.
X       the design matrix.
i       the number of iterations required for convergence.
residuals  the deviance residuals.
aic    Akaike’s Information Criterion.

Author(s)

Andrew Robinson and Joe Hilbe.

References


See Also

glm, ml_glm

Examples

data(medpar)

irls.poi <- irls(los ~ hmo + white,
  family = "poisson",
  link = "log",
  data = medpar)
summary(irls.poi)

irls.probit <- irls(died ~ hmo + white,
  family = "binomial",
  link = "probit",
  data = medpar)
summary(irls.probit)

medpar  US national Medicare inpatient hospital database for Arizona patients.

Description

hospital database is referred to as the Medpar data, which is prepared yearly from hospital filing records. Medpar files for each state are also prepared. The full Medpar data consists of 115 variables. The national Medpar has some 14 million records, with one record for each hospitalization. The data in the medpar file comes from 1991 Medicare files for the state of Arizona. The data are limited to only one diagnostic group (DRG 112). Patient data have been randomly selected from the original data.
Usage

data(medpar)

Format

A data frame with 1495 observations on the following 10 variables.

los length of hospital stay
hmo Patient belongs to a Health Maintenance Organization, binary
white Patient identifies themselves as Caucasian, binary
died Patient died, binary
age80 Patient age 80 and over, binary
type Type of admission, categorical
type1 Elective admission, binary
type2 Urgent admission, binary
type3 Elective admission, binary
provnum Provider ID

Details

Medpar is saved as a data frame. Count models use los as response variable. 0 counts are structurally excluded

Source


References


Examples

data(medpar)
glmp <- glm(los ~ hmo + white + factor(type),
            family = poisson, data = medpar)
summary(glmp)
exp(coef(glmp))

ml.p <- ml_glm(los ~ hmo + white + factor(type),
               family = “poisson”,
               link = “log”,
               data = medpar)

summary(ml.p)
ml_g

Function to fit linear regression using maximum likelihood.

Description
This function demonstrates the use of maximum likelihood to fit ordinary least-squares regression models, by maximizing the likelihood as a function of the parameters. Only conditional normal errors are supported.

Usage
ml_g(formula, data)

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. (See the help for 'lm' for more details).
data a data frame containing the variables in the model.

Details
This function has limited functionality compared with R’s internal lm function, which should be preferred in general.

Value
fit the output of optim.
X the design matrix.
y the response variable.
call the call used for the function.
beta.hat the parameter estimates.
se.beta.hat estimated standard errors of the parameter estimates.
sigma.hat the estimated conditional standard deviation of the response variable.

Note
We use least squares to get initial estimates, which is a pretty barbaric hack. But the purpose of this function is as a starting point, not to replace existing functions.
**ml_glm**

**Author(s)**

Andrew Robinson and Joe Hilbe.

**References**


**See Also**

*lm*

**Examples**

```r
data(ufc)
ufc <- na.omit(ufc)

ufc.g.reg <- ml_glm(height.m ~ dbh.cm, data = ufc)

summary(ufc.g.reg)
```

---

**ml_glm**

*A function to fit generalized linear models using maximum likelihood.*

**Description**

This function fits generalized linear models by maximizing the joint log-likelihood, which is set in a separate function. Only single-parameter members of the exponential family are covered. The post-estimation output is designed to work with existing reporting functions.

**Usage**

```r
ml_glm(formula, data, family, link, offset = 0, start = NULL, verbose = FALSE, ...)
```

**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. (See the help for ’glm’ for more details).
- `data` a data frame containing the variables in the model.
- `family` a description of the error distribution be used in the model. This must be a character string naming a family.
- `link` a description of the link function be used in the model. This must be a character string naming a link function.
offset  this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be 0 or a numeric vector of length equal to the number of cases.

start  optional starting points for the parameter estimation.

verbose  logical flag affecting the detail of printing. Defaults to FALSE.

...  optional arguments to pass within the function.

**Details**

The containing package, msme, provides the needed functions to use the ml_glm function to fit the Poisson and Bernoulli families, and supports the use of the identity, log, logit, probit, and complementary log-log link functions. The object returned by the function is designed to be reported by the print.glm function.

**Value**

- **fit**  the output of optim.
- **x**  the design matrix.
- **y**  the response variable.
- **call**  the call used for the function.
- **obs**  the number of observations.
- **df.null**  the degrees of freedom for the null model.
- **df.residual**  the residual degrees of freedom.
- **deviance**  the residual deviance.
- **null.deviance**  the residual deviance for the null model.
- **residuals**  the deviance residuals.
- **coefficients**  parameter estimates.
- **se.beta.hat**  standard errors of parameter estimates.
- **aic**  Akaike's Information Criterion.
- **i**  the number of iterations required for convergence.

**Note**

This function is neither as comprehensive nor as stable as the inbuilt glm function. It is a lot easier to read, however.

**Author(s)**

Andrew Robinson and Joe Hilbe.

**References**

ml_glm2

See Also

irls, glm, ml_glm2

Examples

data(medpar)

ml.poi <- ml_glm(los ~ hmo + white,
                family = "poisson",
                link = "log",
                data = medpar)

ml.poi
summary(ml.poi)

ml_glm2

A function to fit generalized linear models using maximum likelihood.

Description

This function fits generalized linear models by maximizing the joint log-likelihood, which is set in a separate function. Two-parameter members of the exponential family are covered. The post-estimation output is designed to work with existing reporting functions.

Usage

ml_glm2(formula1, formula2 = ~1, data, family, mean.link, scale.link,
         offset = 0, start = NULL, verbose = FALSE)

Arguments

formula1 an object of class "formula" (or one that can be coerced to that class): a symbolic description of the mean function for the model to be fitted. (See the help for 'glm' for more details).

formula2 an object of class "formula" (or one that can be coerced to that class): a symbolic description of the scale function for the model to be fitted. (See the help for 'glm' for more details).

data a data frame containing the variables in the model.

family a description of the error distribution be used in the model. This must be a character string naming a family.

mean.link a description of the link function be used for the mean in the model. This must be a character string naming a link function.

scale.link a description of the link function be used for the scale in the model. This must be a character string naming a link function.
offset
this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be 0 or a numeric vector of length equal to the number of cases.

start
optional starting points for the parameter estimation.

verbose
logical flag affecting the detail of printing. Defaults to FALSE.

Details
The containing package, msme, provides the needed functions to use the ml_glm2 function to fit the normal and negative binomial (2), families, and supports the use of the identity and log link functions.

The object returned by the function is designed to be reported by the print.glm function.

Value

<table>
<thead>
<tr>
<th>fit</th>
<th>the output of optim.</th>
</tr>
</thead>
<tbody>
<tr>
<td>loglike</td>
<td>the maximized log-likelihood.</td>
</tr>
<tr>
<td>x</td>
<td>the design matrix.</td>
</tr>
<tr>
<td>y</td>
<td>the response variable.</td>
</tr>
<tr>
<td>p</td>
<td>the number of parameters estimated.</td>
</tr>
<tr>
<td>call</td>
<td>the call used for the function.</td>
</tr>
<tr>
<td>obs</td>
<td>the number of observations.</td>
</tr>
<tr>
<td>df.null</td>
<td>the degrees of freedom for the null model.</td>
</tr>
<tr>
<td>df.residual</td>
<td>the residual degrees of freedom.</td>
</tr>
<tr>
<td>deviance</td>
<td>the residual deviance.</td>
</tr>
<tr>
<td>null.deviance</td>
<td>the residual deviance for the null model.</td>
</tr>
<tr>
<td>residuals</td>
<td>the deviance residuals.</td>
</tr>
<tr>
<td>coefficients</td>
<td>parameter estimates.</td>
</tr>
<tr>
<td>se.beta.hat</td>
<td>standard errors of parameter estimates.</td>
</tr>
<tr>
<td>aic</td>
<td>Akaike’s Information Criterion.</td>
</tr>
<tr>
<td>offset</td>
<td>the offset used.</td>
</tr>
<tr>
<td>i</td>
<td>the number of iterations required for convergence.</td>
</tr>
</tbody>
</table>

Author(s)
Andrew Robinson and Joe Hilbe.

References
See Also

glm, irls, ml_glm.

Examples

data(medpar)
ml.nb2 <- ml_glm2(loss ~ hmo + white,
    formula2 = ~ 1,
    data = medpar,
    family = "negBinomial",
    mean.link = "log",
    scale.link = "inverse_s")
data(ufc)
ufc <- na.omit(ufc)
ml.g <- ml_glm2(height.m ~ dbh.cm,
    formula2 = ~ dbh.cm,
    data = ufc,
    family = "normal",
    mean.link = "identity",
    scale.link = "log_s")

summary(ml.g)

---

ml_glm3

A reduced maximum likelihood fitting function that omits null models.

Description

This function fits generalized linear models by maximizing the joint log-likelihood, which is set in a separate function. Null models are omitted from the fit. The post-estimation output is designed to work with existing reporting functions.

Usage

ml_glm3(formula, data, family, link, offset = 0, start = NULL, verbose = FALSE, ...)

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. (See the help for 'glm' for more details).
data a data frame containing the variables in the model.
family a description of the error distribution be used in the model. This must be a character string naming a family.
link  a description of the link function be used in the model. This must be a character string naming a link function.

offset  this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be 0 or a numeric vector of length equal to the number of cases.

start  optional starting points for the parameter estimation.

verbose  logical flag affecting the detail of printing. Defaults to FALSE.

...  other arguments to pass to the likelihood function, e.g. group structure.

Details
This function is essentially the same as ml_glm, but includes the dots argument to allow a richer set of model likelihoods to be fit, and omits computation of the null deviance. The function is presently set up to only fit the conditional fixed-effects negative binomial model.

Value
fit  the output of optim.
X  the design matrix.
y  the response variable.
call  the call used for the function.
obs  the number of observations.
df.null  the degrees of freedom for the null model.
df.residual  the residual degrees of freedom.
deviance  the residual deviance.
null.deviance  the residual deviance for the null model, set to NA.
residuals  the deviance residuals.
coefficients  parameter estimates.
se.beta.hat  standard errors of parameter estimates.
aic  Akaike’s Information Criterion.
i  the number of iterations required for convergence.

Author(s)
Andrew Robinson and Joe Hilbe.

References

See Also
irls, glm, ml_glm
nbinomial

Examples

data(medpar)
med.nb.g <- ml_glm3(los ~ hmo + white,
  family = "gNegBinomial",
  link = "log",
  group = medpar$provnum,
  data = medpar)
summary(med.nb.g)

nbinomial

A function to fit negative binomial generalized linear models using maximum likelihood.

Description

This function fits generalized linear models by maximizing the joint log-likelihood, which is set in a separate function. Two-parameter members of the negative binomial family are covered. The post-estimation output is designed to work with existing reporting functions.

Usage

nbinomial(formula1, formula2 = ~1, data, family="nb2", mean.link="log",
  scale.link="inverse_s", offset=0, start= NULL, verbose=FALSE)

Arguments

formula1 an object of class "formula" (or one that can be coerced to that class): a symbolic description of the mean function for the model to be fitted. (See the help for glm for more details).

formula2 an object of class "formula" (or one that can be coerced to that class): a symbolic description of the scale function for the model to be fitted. (See the help for glm for more details).

data a data frame containing the variables in the model.

family a description of the error distribution be used in the model. This must be a character string naming a family.

mean.link a description of the link function be used for the mean in the model. This must be a character string naming a link function.

scale.link a description of the link function be used for the scale in the model. This must be a character string naming a link function.

offset this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be 0 or a numeric vector of length equal to the number of cases.

start optional starting points for the parameter estimation.

verbose logical flag affecting the detail of printing. Defaults to FALSE.
Details

The containing package, msme, provides the needed functions to use the nbinomial function to fit the negative binomial (2), families, and supports the use of the identity and log link functions.

The object returned by the function is designed to be reported by the print.glm function.

Value

- fit: the output of optim.
- loglike: the maximized log-likelihood.
- X: the design matrix.
- y: the response variable.
- p: the number of parameters estimated.
- call: the call used for the function.
- obs: the number of observations.
- fitted.values: estimated response variable.
- linear.predictor: linear predictor.
- df.null: the degrees of freedom for the null model.
- df.residual: the residual degrees of freedom.
- pearson: the Pearson Chi2.
- null.pearson: the Pearson Chi2 for the null model.
- dispersion: the dispersion.
- deviance: the residual deviance.
- null.deviance: the residual deviance for the null model.
- residuals: the deviance residuals.
- presiduals: the Pearson residuals.
- coefficients: parameter estimates.
- se.beta.hat: standard errors of parameter estimates.
- aic: Akaike’s Information Criterion.
- offset: the offset used.
- i: the number of iterations required for convergence.

Author(s)

Andrew Robinson and Joe Hilbe.

References

See Also

glm, irls, ml_glm2.

Examples

data(medpar)

# TRADITIONAL NB REGRESSION WITH ALPHA

mynb1 <- nbinomial(los ~ hmo + white, data=medpar)
summary(mynb1)

# TRADITIONAL NB -- SHOWING ALL OPTIONS

mynb2 <- nbinomial(los ~ hmo + white,
    formula2 = ~ 1,
    data = medpar,
    family = "nb2",
    mean.link = "log",
    scale.link = "inverse_s")
summary(mynb2)

# R GLM.NB - LIKE INVERTED DISPERSION BASED M

mynb3 <- nbinomial(los ~ hmo + white,
    formula2 = ~ 1,
    data = medpar,
    family = "negBinomial",
    mean.link = "log",
    scale.link = "inverse_s")
summary(mynb3)

# R GLM.NB-TYPE INVERTED DISPERSON --THETA ; WITH DEFAULTS

mynb4 <- nbinomial(los ~ hmo + white, family="negBinomial", data =medpar)
summary(mynb4)

# HETEROGENEOUS NB; DISPERSION PARAMETERIZED

mynb5 <- nbinomial(los ~ hmo + white,
    formula2 = ~ hmo + white,
    data = medpar,
    family = "negBinomial",
    mean.link = "log",
    scale.link = "log_s")
summary(mynb5)
plot.ml_g_fit  A plot method for objects of class ml_g_fit.

Description

This function provides a four-way plot for fitted models.

Usage

```r
## S3 method for class 'ml_g_fit'
plot(x, ...)
```

Arguments

- `x`  the fitted model.
- `...`  other arguments, retained for compatibility with generic method.

Details

The function plots a summary. The output is structured to broadly match the default options of the `plot.lm` function.

Value

Run for its side effect of producing a plot object.

Author(s)

Andrew Robinson and Joe Hilbe.

References


See Also

- `ml_g`

Examples

```r
data(ufc)
ufc <- na.omit(ufc)

ufc.g.reg <- ml_g(height.m ~ dbh.cm, data = ufc)
plot(ufc.g.reg)
```
**P__disp**

A function to calculate Pearson Chi2 and its dispersion statistic following glm and glm.nb.

---

**Description**

This function calculates Pearson Chi2 statistic and the Pearson-based dispersion statistic. Values of the dispersion greater than 1 indicate model overdispersion. Values under 1 indicate underdispersion.

**Usage**

```r
P__disp(x)
```

**Arguments**

- `x`: the fitted model.

**Details**

To be used following glm and glm.nb functions.

**Value**

- `pearson.chi2`: Pearson Chi2 value.

**Author(s)**

Joseph Hilbe and Andrew Robinson

**References**


**See Also**

- `glm`, `glm.nb`

**Examples**

```r
data(medpar)
mymod <- glm(los ~ hmo + white + factor(type),
             family = poisson,
             data = medpar)
P__disp(mymod)
```
Function to produce residuals from a model of class msme.

Description

Function to produce deviance and standardized deviance residuals from a model of class msme.

Usage

```r
## S3 method for class 'msme'
residuals(object, type = c("deviance", "standard"), ...)
```

Arguments

- `object`: a model of class msme.
- `type`: the type of residual requested. Defaults to deviance.
- `...`: arguments to pass on. Retained for compatibility with generic method.

Details

Presently only deviance or standardized deviance residuals are computed.

Value

A vector of residuals.

Author(s)

Andrew Robinson and Joe Hilbe.

References


Examples

```r
data(medpar)

ml.poi <- ml_glm(los ~ hmo + white,
                 family = "poisson",
                 link = "log",
                 data = medpar)

str(residuals(ml.poi))
```
Description

German health registry for the years 1984-1988. Health information for years immediately prior to health reform.

Usage

data(rwm5yr)

Format

A data frame with 19,609 observations on the following 17 variables.

- id: patient ID (1=7028)
- docvis: number of visits to doctor during year (0-121)
- hospvis: number of days in hospital during year (0-51)
- edlevel: educational level (categorical: 1-4)
- age: age: 25-64
- outwork: out of work=1; 0=working
- female: female=1; 0=male
- married: married=1; 0=not married
- kids: have children=1; no children=0
- hhinc: household yearly income in marks (in Marks)
- educ: years of formal education (7-18)
- self: self-employed=1; not self employed=0
- edlevel1: (1/0) not high school graduate
- edlevel2: (1/0) high school graduate
- edlevel3: (1/0) university/college
- edlevel4: (1/0) graduate school

Details

rwm5yr is saved as a data frame. Count models typically use docvis as response variable. 0 counts are included

Source

German Health Reform Registry, years pre-reform 1984-1988,
References


Examples

```r
data(rwm5yr)

glmrp <- glm(docvis ~ outwork + female + age + factor(edlevel),
              family = poisson, data = rwm5yr)
summary(glmrp)
exp(coef(glmrp))

ml_p <- ml_glm(docvis ~ outwork + female + age + factor(edlevel),
                family = "poisson",
                link = "log",
                data = rwm5yr)
summary(ml_p)
exp(coef(ml_p))

library(MASS)
glmnb <- glm.nb(docvis ~ outwork + female + age + factor(edlevel),
                data = rwm5yr)
summary(glmnb)
exp(coef(glmnb))
## Not run:
library(gee)
mygee <- gee(docvis ~ outwork + age + factor(edlevel), id=id,
             corstr = "exchangeable", family=poisson, data=rwm5yr)
summary(mygee)
exp(coef(mygee))
## End(Not run)
```

summary.ml_g_fit

A summary method for objects of class ml_g_fit.

Description

This function provides a compact summary for fitted models.

Usage

```r
## S3 method for class 'ml_g_fit'
summary(object, dig = 3, ...)
Arguments

- **object**: the fitted model.
- **dig**: an optional integer detailing the number of significant digits for printing.
- **...**: other arguments, retained for compatibility with generic method.

Details

The function prints out a summary and returns an invisible list with useful objects. The output is structured to match the print.summary.lm function.

Value

- **call**: the call used to fit the model.
- **coefficients**: a dataframe of estimates, standard errors, etc.
- **residuals**: deviance residuals from the model.
- **aliased**: included to match the print.summary.lm function. Lazily set to FALSE for all parameters.
- **sigma**: the estimate of the conditional standard deviation of the response variable.

Author(s)

Andrew Robinson and Joe Hilbe.

References


See Also

- **ml_g**

Examples

```r
data(ufc)
ufc <- na.omit(ufc)

ufc.g.reg <- ml_g(height.m ~ dbh.cm, data = ufc)

summary(ufc.g.reg)
```
A summary method for objects of class `msme`.

### Description

This function provides a compact summary for fitted models.

### Usage

```r
## S3 method for class 'msme'
summary(object, ...)
```

### Arguments

- **object**: the fitted model.
- **...**: optional arguments to be passed through.

### Details

The function prints out a summary and returns an invisible list with useful objects.

### Value

- **call**: the call used to fit the model.
- **coefficients**: a dataframe of estimates, standard errors, etc.
- **deviance**: deviance from the model fit.
- **null.deviance**: deviance from the null model fit.
- **df.residual**: residual degrees of freedom from the model fit.
- **df.null**: residual degrees of freedom from the null model fit.

### Author(s)

Andrew Robinson and Joe Hilbe.

### References

Examples

data(medpar)

ml.poi <- ml_glm(los ~ hmo + white,
family = "poisson",
link = "log",
data = medpar)

summary(ml.poi)

---

titanic Titanic passenger survival data

Description

Passenger survival data from 1912 Titanic shipping accident.

Usage

data(titanic)

Format

A data frame with 1316 observations on the following 4 variables.

survived 1=survived; 0=died
age 1=adult; 0=child
sex 1=Male; 0=female
class ticket class 1= 1st class; 2= second class; 3= third class

Details

Titanic is saved as a data frame. Used to assess risk ratio; not standard count model; good binary response model.

Source

Found in many other texts

References

Examples

```r
data(titanic)

glm.lr <- glm(survived ~ age + sex + factor(class),
              family=binomial, data=titanic)
summary(glm.lr)
exp(coef(glm.lr))

glm.irls <- irls(survived ~ age + sex + factor(class),
                 family = "binomial",
                 link = "cloglog",
                 data = titanic)
summary(glm.irls)
exp(coef(glm.irls))

glm.ml <- ml_glm(survived ~ age + sex + factor(class),
                 family = "bernoulli",
                 link = "cloglog",
                 data = titanic)
summary(glm.ml)
exp(coef(glm.ml))
```

---

### ufc

**Upper Flat Creek forest cruise tree data**

**Description**

These are a subset of the tree measurement data from the Upper Flat Creek unit of the University of Idaho Experimental Forest, which was measured in 1991.

**Usage**

```r
data(ufc)
```

**Format**

A data frame with 336 observations on the following 5 variables.

- **plot** plot label
- **tree** tree label
- **species** species kbd with levels DF, GF, WC, WL
- **dbh.cm** tree diameter at 1.37 m. from the ground, measured in centimetres.
- **height.m** tree height measured in metres
Details

The inventory was based on variable radius plots with 6.43 sq. m. per ha. BAF (Basal Area Factor). The forest stand was 121.5 ha. This version of the data omits errors, trees with missing heights, and uncommon species. The four species are Douglas-fir, grand fir, western red cedar, and western larch.

Source

The data are provided courtesy of Harold Osborne and Ross Appelgren of the University of Idaho Experimental Forest.

References


Examples

data(ufc)

ufc <- na.omit(ufc)
ml.g <- ml_glm2(height.m ~ dbh.cm,
              formula2 = ~1,
              data = ufc,
              family = "normal",
              mean.link = "identity",
              scale.link = "log_s")

lm.g <- lm(height.m ~ dbh.cm,
           data = ufc)

ml.g
lm.g

summary(ml.g)
summary(lm.g)
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