Package ‘chantrics’

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adj_loglik

Loglikelihood adjustments for fitted models

Description

This function adjusts the loglikelihood of fitted model objects based on Chandler and Bate (2007). It is a generic function for different types of models, which are listed in Supported models. This section also contains links to function-specific help pages.

Usage

adj_loglik(x, cluster = NULL, use_vcov = TRUE, use_mle = TRUE, ...)

Arguments

x A supported fitted model object, see Supported models

cluster A vector or factor indicating the cluster the corresponding loglikelihood contribution belongs to. It is required to have the same length as the vector returned by logLik_vec(). If cluster is not supplied or NULL, then it is assumed that each observation forms its own cluster.

use_vcov A logical scalar. By default, the vcov() method for x is used to estimate the Hessian of the independence loglikelihood, if the function exists. Otherwise, or if use_vcov = FALSE, H is estimated using stats::optimHess() inside chandwich::adjust_loglik().

use_mle A logical scalar. By default, the MLE from x is taken as given, and is not reestimated. By setting use_mle to FALSE, the parameters are reestimated in the function chandwich::adjust_loglik() using stats::optim(). This feature is currently for development purposes only, may return misleading/false results and may be removed without notice.

... Further arguments to be passed to sandwich::meatCL() if cluster is defined, if cluster = NULL, they are passed into sandwich::meat().
**Details**

If `use_vcov = TRUE`, the current default, the function will test whether a vcov S3 method exists for `x`, and will take the variance-covariance matrix from there. Otherwise, or if `use_vcov = FALSE` the variance-covariance matrix of the MLE is estimated inside `chandwich::adjust_loglik()` using `stats::optimHess()`.

**Value**

An object of class "chantrics" inheriting from class "chandwich". See the documentation provided with `chandwich::adjust_loglik()`.

**Supported models**

- glm
- glm.nb

**Available methods**

"chantrics" objects have the following methods available to them:

- AIC
- anova
- alrtest - Adjusted Likelihood ratio tests
- coef
- lmtest::coeftest - \(z\) tests for all coefficients
- confint and plot.confint - confidence intervals for all coefficients, and diagnostics plots for `confint()`.
- conf_intervals - enhanced confidence interval reports
- conf_region - two-dimensional confidence regions
- df.residual
- fitted
- logLik
- logLik_vec
- nobs
- plot
- predict
- print
- residuals
- summary
- terms
- vcov
Examples

See the model-specific pages in the supported models section.

References


See Also

lax::alogLik() supports adjustment for user-supplied objects.

---

alrtest  Adjusted Likelihood Ratio Test of Nested Models

Description

alrtest is a helper function to simulate the functions lmtest::waldtest() and lmtest::lrtest() for adjusted chantrics objects. The method can be employed to compare nested models (see details).

Usage

alrtest(object, ...)

Arguments

object  a chantrics object as returned from adj_loglik().

...  further object specifications (see details), as well as named parameters that will be passed to sandwich::compare_models(). The type of adjustment, out of "vertical", "cholesky", "spectral", "none", as specified in the parameter type, can also be specified here.

Details

This function is a helper function that creates an interface to anova.chantrics() that is similar to lmtest::waldtest() and lmtest::lrtest().

The standard method is to compare the fitted model object object with the models in .... Instead of passing the fitted models into .... other specifications are possible. Note that the types of specifications cannot be mixed, except between numerics/characters. The type of the second object supplied determines the algorithm used.

• "chantrics" objects: When supplying two or more "chantrics" objects, they will be sorted as in anova.chantrics(). Then, the ALRTS will be computed consecutively between the two neighbouring models. Note that all models must be nested. For details refer to anova.chantrics().
• "numeric": If the second object is "numeric" or "character", then "numeric" objects corresponding element in attr(terms(object1),"term.labels") will be turned into their corresponding "character" element and will be handled as in "character" below.

• "character": If the second object is "numeric" or "character", then the "character" objects are consecutively included in an update formula like update(object1,. ~ . -object2)

• "formula": If the second object is a "formula", then the second model will be computed as update(object1,object2).

Then, the adjusted likelihood ratio test statistic (ALRTS), as described in Section 3.5 of Chandler and Bate (2007), is computed by anova.chantrics().

If a single unnamed object is passed in ..., sequential ANOVA is performed on object.

Value
An object of class "anova" inheriting from class "data.frame". The columns are as follows:

- Resid.df: The residual number of degrees of freedom in the model.
- df: The increase in residual degrees of freedom with respect to the model in the row above.
- ALRTS: The adjusted likelihood ratio statistic.
- Pr(>ALRTS): The p-value of the test that the model above is a "significantly better" model as the one in the current row.

References

See Also
anova.chantrics() for the implementation of the computations of the test statistics.
lmtest::waldtest() and lmtest::lrtest() for syntax.
Arguments

object Object of class chantrics, as returned by adj_loglik().

... Further objects of class chantrics, as returned by adj_loglik(), and named parameters that should be passed to chandwich::compare_models(). The type of adjustment, out of "vertical", "cholesky", "spectral", "none", as specified in the parameter type, can also be specified here.

Details

Create an analysis of adjusted deviance table for one object (sequential), or two or more nested models that have been adjusted using the adj_loglik() method. It uses the adjusted likelihood ratio test statistic (ALRTS), as described in Section 3.5 of Chandler and Bate (2007).

Each line represents the model as given above the table, with each line (except for the first line) showing the residual degrees of freedom of that model, the change in degrees of freedom, the ALRTS and the associated p-value in comparison to the model in the line above.

When a single model is specified, the function returns a sequential analysis of deviance table, where, iteratively, one term is being removed from the right of the full formula. This process is continued until the "intercept only" model is left. The row names are the names of the dropped term in comparison to the model in the line above.

If more than one model is specified, the function sorts the models by their number of variables as returned by adj_loglik() in attr(x,"p_current").

Details of the ALRT can be found in chandwich::compare_models() and in Chandler and Bate (2007).

Value

An object of class "anova" inheriting from class "data.frame". The columns are as follows:

Resid.df The residual number of degrees of freedom in the model.
df The increase in residual degrees of freedom with respect to the model in the row above.
ALRTS The adjusted likelihood ratio statistic.
Pr(>ALRTS) The p-value of the test that the model above is a "significantly better" model as the one in the current row.

References


See Also

chandwich::compare_models: implementation of the comparison mechanism
Examples

```r
# from Introducing Chandwich.
set.seed(123)
x <- rnorm(250)
y <- rnbinom(250, mu = exp(1 + x), size = 1)
fm_pois <- glm(y ~ x + I(x^2), family = poisson)
fm_pois_adj <- adj_loglik(fm_pois)
fm_pois_small_adj <- update(fm_pois_adj, formula = . ~ . - I(x^2))
fm_pois_smallest_adj <- update(fm_pois_adj, formula = . ~ 1)

anova(fm_pois_adj, fm_pois_small_adj, fm_pois_smallest_adj)
# use different types of adjustment with type, default is "vertical"
anova(fm_pois_adj, fm_pois_small_adj, fm_pois_smallest_adj, type = "cholesky")

# sequential anova
anova(fm_pois_adj)
```

Description

chantrics adjusts the loglikelihood of common econometric models for clustered data based on
the estimation process suggested in Chandler and Bate (2007), using the chandwich package, and
provides convenience functions for inference on the adjusted models. adj_loglik() adjusts the
model’s parameter covariance matrix to incorporate clustered data, and can mitigate model mis-
specification by wrapping chandwich::adjust_loglik for the supported models.

Details

The returned model of class chantrics can be plugged into standard model evaluation and model
comparison methods, for example, summary(), confint() and anova(), and a hypothesis test
framework provided by alrtest().

See vignette("chantrics-vignette",package = "chantrics") for an overview of the pack-
age.

References

R. E. Chandler and S. Bate, Inference for clustered data using the independence loglikelihood,
glm

Loglikelihood adjustments for glm fits

Description

In a generalised linear model (glm), the user can choose between a range of distributions of a
response $y$, and can allow for non-linear relations between the mean outcome for a particular com-
bination of covariates $x$, $E(y_i \mid x_i) = \mu_i$, and the linear predictor, $\eta_i = x_i^T \beta$, which is the link
function $g(\mu_i) = \eta_i$. it is required to be monotonic. (For a quick introduction, see Kleiber and
Zeileis (2008, Ch. 5.1), for more complete coverage of the topic, see, for example, Davison (2003,
Ch. 10.3))

Details

For more usage examples and more information on glm models, see the Introducing chantrics vignette by running vignette("chantrics-vignette",package = "chantrics")

Supported families (within each family, any link function should work)

- gaussian
- poisson
- binomial
- MASS::negative.binomial

Also works for MASS::glm.nb(), note that the standard errors of the theta are not adjusted.

References


Gentleman, Kurt Hornik, and Giovanni Parmigiani. Use r! New York: Springer-Verlag.

Examples

# binomial example from Applied Econometrics in R, Kleiber/Zeileis (2008)
# == probit ==
data("SwissLabor", package = "AER")
swiss_probit <- glm(participation ~ . + I(age^2),
                   data = SwissLabor,
                   family = binomial(link = "probit")
)
summary(swiss_probit)
swiss_probit_adj <- adj_loglik(swiss_probit)
summary(swiss_probit_adj)

# == logit ==
swiss_logit <- glm(participation ~ . + I(age^2),
                   data = SwissLabor,
                   family = binomial(link = "logit")
)
summary(swiss_logit)
logLik_vec

```r
data = SwissLabor,
      family = binomial(link = "logit")
)
summary(swiss_logit)
swiss_logit_adj <- adj_loglik(swiss_logit)
summary(swiss_logit_adj)
```

---

**logLik_vec**

*Evaluate loglikelihood contributions from specific observations*

**Description**

Generic function for calculating the loglikelihood contributions from individual observations for a fitted model.

**Usage**

```r
logLik_vec(object, ...)
```

**Arguments**

- `object` A fitted model object.
- `...` Further arguments.

**Value**

An object of class "logLik_vec", which is a numeric vector of length `nobs(object)` (i.e. the number of observations in `object`) of the loglikelihood of each observation. Additionally, it contains the attributes `df` (model degrees of freedom) and `nobs` (number of observations).

The methods `stats::logLik()`, and `stats::nobs()` are available.

**See Also**

- `stats::logLik()`

---

**predict.chantrics**

*Predict Method for chantrics fits*

**Description**

Obtains predictions from chantrics objects. The function can currently only supply predictions of the link and the response values of the data used for the fit.

**Usage**

```r
## S3 method for class 'chantrics'
predict(object, newdata = NULL, type = c("response", "link"), ...)
```
Arguments

object Object of class chantrics, as returned by \texttt{adj_loglik()}

newdata optionally, a data frame in which to look for variables with which to predict. If omitted, the fitted linear predictors are used. Supplying new data is currently not supported.

type the type of prediction required. The default "response" is on the scale of the response variables. The alternative "link" is on the scale of the linear predictors, if applicable. Otherwise, an error is returned.

... unused.

Details

If \texttt{newdata} is omitted, the predictions are based on the data used for the fit. Any instances of \texttt{NA} will return \texttt{NA}.

Value

A vector of predictions.

residuals.chantrics \hspace{1cm} Residuals of chantrics model fits

Description

\texttt{residuals()} returns the residuals specified in \texttt{type} from a "chantrics" object.

Usage

\begin{verbatim}
## S3 method for class 'chantrics'
residuals(object, type = c("response", "working", "pearson"), ...)\end{verbatim}

Arguments

object an object of class "chantrics", returned by \texttt{adj_loglik()}.

type the type of residuals which should be returned. The alternatives are: "response" (default), "working", and "pearson" (for glm fits).

... further arguments passed to or from other methods

Details

The different types of residuals are as in \texttt{stats::residuals.glm()}. 

Value

A vector of residuals.
References


See Also

adj_loglik() for model fitting, stats::residuals.glm(), and stats::residuals().

update.chantrics

Description

update.chantrics() will update a model that has been adjusted by adj_loglik(). It passes all arguments to the standard stats::update() function.

Usage

## S3 method for class 'chantrics'
update(object, ...)

Arguments

object A "chantrics" returned by adj_loglik().
...

Additional arguments to the call, passed to stats::update() to update the original model specification.

Details

The function cannot change any arguments passed to the adj_loglik() function. To change any of these arguments, re-run adj_loglik().

Passing evaluate = FALSE is not supported, if this is required, run stats::update() on the unadjusted object.

Value

The fitted, adjusted "chantrics" object.

See Also

stats::update()
stats::update.formula()
Examples

# from Introducing Chandwich.
set.seed(123)
x <- rnorm(250)
y <- rnbinom(250, mu = exp(1 + x), size = 1)
fm_pois <- glm(y ~ x + I(x^2), family = poisson)
fm_pois_adj <- adj_loglik(fm_pois)
fm_pois_small_adj <- update(fm_pois_adj, formula = . ~ . - I(x^2))
summary(fm_pois_small_adj)
fm_pois_smallest_adj <- update(fm_pois_adj, formula = . ~ 1)
summary(fm_pois_smallest_adj)
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