Package ‘ordinal’

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Description Implementation of cumulative link (mixed) models also known as ordered regression models, proportional odds models, proportional hazards models for grouped survival times and ordered logit/probit/... models. Estimation is via maximum likelihood and mixed models are fitted with the Laplace approximation and adaptive Gauss-Hermite quadrature. Multiple random effect terms are allowed and they may be nested, crossed or partially nested/crossed. Restrictions of symmetry and equidistance can be imposed on the thresholds (cut-points/intercepts). Standard model methods are available (summary, anova, drop-methods, step, confint, predict etc.) in addition to profile methods and slice methods for visualizing the likelihood function and checking convergence.
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| ordinal-package | Regression Models for Ordinal Data via Cumulative Link (Mixed) Models |

Description

This package facilitates analysis of ordinal (ordered categorical data) via cumulative link models (CLMs) and cumulative link mixed models (CLMMs). Robust and efficient computational methods gives speedy and accurate estimation. A wide range of methods for model fits aids the data analysis.

Details

Package: ordinal
Type: Package
License: GPL (>= 2)
LazyLoad: yes
This package implements cumulative link models and cumulative link models with normally distributed random effects, denoted cumulative link mixed (effects) models. Cumulative link models are also known as ordered regression models, proportional odds models, proportional hazards models for grouped survival times and ordered logit/probit/... models.

Cumulative link models are fitted with `clm` and the main features are:

- A range of standard link functions are available.
- In addition to the standard location (additive) effects, scale (multiplicative) effects are also allowed.
- Nominal effects are allowed for any subset of the predictors — these effects are also known as partial proportional odds effects when using the logit link.
- Restrictions can be imposed on the thresholds/cut-points, e.g., symmetry or equidistance.
- A (modified) Newton-Raphson algorithm provides the maximum likelihood estimates of the parameters. The estimation scheme is robust, fast and accurate.
- Rank-deficient designs are identified and unidentified coefficients exposed in `print` and `summary` methods as with `glm`.
- A suite of standard methods are available including `anova`, `add/drop-methods`, `step`, `profile`, `confint`.
- A `slice` method facilitates illustration of the likelihood function and a convergence method summarizes the accuracy of the model estimation.
- The `predict` method can predict probabilities, response class-predictions and cumulative probabilities, and it provides standard errors and confidence intervals for the predictions.

Cumulative link mixed models are fitted with `clmm` and the main features are:

- Any number of random effect terms can be included.
- The syntax for the model formula resembles that of `lmer` from the `lme4` package.
- Nested random effects, crossed random effects and partially nested/crossed random effects are allowed.
- Estimation is via maximum likelihood using the Laplace approximation or adaptive Gauss-Hermite quadrature (one random effect).
- Vector-valued and correlated random effects such as random slopes (random coefficient models) are fitted with the Laplace approximation.
- Estimation employs sparse matrix methods from the `Matrix` package.
- During model fitting a Newton-Raphson algorithm updates the conditional modes of the random effects a large number of times. The likelihood function is optimized with a general purpose optimizer.

A major update of the package in August 2011 introduced new and improved implementations of `clm` and `clmm`. The old implementations are available with `clm2` and `clmm2`. At the time of writing there is functionality in `clm2` and `clmm2` not yet available in `clm` and `clmm`. This includes flexible link functions (log-gamma and Aranda-Ordaz links) and a profile method for random effect variance parameters in CLMMs. The new implementations are expected to take over the old implementations at some point, hence the latter will eventually be deprecated and defunct.
Author(s)

Rune Haubo B Christensen
Maintainer: Rune Haubo B Christensen <rune.haubo@gmail.com>

Examples

```r
## A simple cumulative link model:
fm1 <- clm(rating ~ contact + temp, data=wine)
summary(fm1)

## A simple cumulative link mixed model:
fmml <- clmm(rating ~ contact + temp + (1|judge), data=wine)
summary(fmml)
```

Description

Type I, II, and III analysis of deviance (ANODE) tables for cumulative link models and comparison of cumulative link models with likelihood ratio tests. Models may differ by terms in location, scale and nominal formulae, in link, threshold function.

Usage

```r
## S3 method for class 'clm'
anova(object, ..., type = c("I", "II", "III", "1", "2", "3"))
```

Arguments

- `object`: a `clm` object.
- `...`: optionally one or more additional `clm` objects.
- `type`: the type of hypothesis test if `anova` is called with a single model; ignored if more than one model is passed to the method.

Details

The ANODE table returned when `anova` is called with a single model apply only to terms in `formula`, that is, terms in `nominal` and `scale` are ignored.

Value

An analysis of deviance table based on Wald chi-square test if called with a single model and a comparison of models with likelihood ratio tests if called with more than one model.
Author(s)

Rune Haubo B Christensen

See Also

clm

Examples

```r
## Analysis of deviance tables with Wald chi-square tests:
fm <- clm(rating ~ temp * contact, scale=~contact, data=wine)
anova(fm, type="I")
anova(fm, type="II")
anova(fm, type="III")

options(contrasts = c("contr.treatment", "contr.poly"))
m1 <- clm2(SURENESS ~ PROD, scale = ~PROD, data = soup,
           link = "logistic")

## anova
anova(m1, update(m1, scale = ~.-PROD))
mN1 <- clm2(SURENESS ~ 1, nominal = ~PROD, data = soup,
           link = "logistic")
anova(m1, mN1)
anova(m1, update(m1, scale = ~.-PROD), mN1)

## Fit model from polr example:
if(require(MASS)) {
  fm1 <- clm2(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
anova(fm1, update(fm1, scale =~ Cont))
}
```

---

### clm

**Cumulative Link Models**

**Description**

Fits cumulative link models (CLMs) such as the proportional odds model. The model allows for various link functions and structured thresholds that restricts the thresholds or cut-points to be e.g., equidistant or symmetrically arranged around the central threshold(s). Nominal effects (partial proportional odds with the logit link) are also allowed. A modified Newton algorithm is used to optimize the likelihood function.
Usage

clm(formula, scale, nominal, data, weights, start, subset, doFit = TRUE, 
na.action, contrasts, model = TRUE, control=list(), 
link = c("logit", "probit", "cloglog", "loglog", "cauchit", 
"Aranda-Ordaz", "log-gamma"), 
threshold = c("flexible", "symmetric", "symmetric2", "equidistant"), ...)

Arguments

formula a formula expression as for regression models, of the form response ~ predictors. 
The response should be a factor (preferably an ordered factor), which will be inter- 
terpreted as an ordinal response with levels ordered as in the factor. The model 
must have an intercept: attempts to remove one will lead to a warning and will 
be ignored. An offset may be used. See the documentation of formula for other 
details.

scale an optional formula expression, of the form ~ predictors, i.e. with an empty 
left hand side. An offset may be used. Variables included here will have multi- 
plicative effects and can be interpreted as effects on the scale (or dispersion) of 
a latent distribution.

nominal an optional formula of the form ~ predictors, i.e. with an empty left hand side. 
The effects of the predictors in this formula are assumed to be nominal rather 
than ordinal - this corresponds to the so-called partial proportional odds (with 
the logit link).

data an optional data frame in which to interpret the variables occurring in the for- 
mulas.

weights optional case weights in fitting. Defaults to 1. Negative weights are not allowed.

start initial values for the parameters in the format c(alpha,beta,zeta), where 
alpha are the threshold parameters (adjusted for potential nominal effects), 
beta are the regression parameters and zeta are the scale parameters.

subset expression saying which subset of the rows of the data should be used in the fit. 
All observations are included by default.

doFit logical for whether the model should be fitted or the model environment should 
be returned.

na.action a function to filter missing data. Applies to terms in all three formulae.

contrasts a list of contrasts to be used for some or all of the factors appearing as variables 
in the model formula.

model logical for whether the model frame should be part of the returned object.

control a list of control parameters passed on to clm.control.

link link function, i.e., the type of location-scale distribution assumed for the latent 
distribution. The default "logit" link gives the proportional odds model.

threshold specifies a potential structure for the thresholds (cut-points). "flexible" pro- 
vides the standard unstructured thresholds, "symmetric" restricts the distance 
between the thresholds to be symmetric around the central one or two thresholds 
for odd or equal numbers or thresholds respectively, "symmetric2" restricts the
latent mean in the reference group to zero; this means that the central threshold (even no. response levels) is zero or that the two central thresholds are equal apart from their sign (uneven no. response levels), and “equidistant” restricts the distance between consecutive thresholds to be of the same size.

... additional arguments are passed on to \texttt{clm.control}.

\textbf{Details}

This is a new (as of August 2011) improved implementation of CLMs. The old implementation is available in \texttt{clm2}, but will probably be removed at some point.

There are methods for the standard model-fitting functions, including \texttt{summary}, \texttt{anova}, \texttt{model.frame}, \texttt{model.matrix}, \texttt{drop1}, \texttt{dropterm}, \texttt{step}, \texttt{stepAIC}, \texttt{extractAIC}, \texttt{AIC}, \texttt{coef}, \texttt{nobs}, \texttt{profile}, \texttt{confint}, \texttt{vcov} and \texttt{slice}.

\textbf{Value}

If \texttt{doFit = FALSE} the result is an environment representing the model ready to be optimized. If \texttt{doFit = TRUE} the result is an object of class “clm” with the components listed below.

Note that some components are only present if \texttt{scale} and \texttt{nominal} are used.

- \texttt{aliased} list of length 3 or less with components \texttt{alpha}, \texttt{beta} and \texttt{zeta} each being logical vectors containing alias information for the parameters of the same names.
- \texttt{alpha} a vector of threshold parameters.
- \texttt{alpha.mat} (where relevant) a table (\texttt{data.frame}) of threshold parameters where each row corresponds to an effect in the nominal formula.
- \texttt{beta} (where relevant) a vector of regression parameters.
- \texttt{call} the mathed call.
- \texttt{coefficients} a vector of coefficients of the form \texttt{c(alpha, beta, zeta)}
- \texttt{cond.H} condition number of the Hessian matrix at the optimum (i.e. the ratio of the largest to the smallest eigenvalue).
- \texttt{contrasts} (where relevant) the contrasts used for the \texttt{formula} part of the model.
- \texttt{control} list of control parameters as generated by \texttt{clm.control}.
- \texttt{convergence} convergence code where 0 indicates successful convergence and negative values indicate convergence failure; 1 indicates successful convergence to a non-unique optimum.
- \texttt{edf} the estimated degrees of freedom, i.e., the number of parameters in the model fit.
- \texttt{fitted.values} the fitted probabilities.
- \texttt{gradient} a vector of gradients for the coefficients at the estimated optimum.
- \texttt{Hessian} the Hessian matrix for the parameters at the estimated optimum.
- \texttt{info} a table of basic model information for printing.
- \texttt{link} character, the link function used.
- \texttt{logLik} the value of the log-likelihood at the estimated optimum.
maxGradient  the maximum absolute gradient, i.e., max(abs(gradient)).
model      if requested (the default), the model.frame containing variables from formula, scale and nominal parts.
n                      the number of observations counted as nrow(X), where X is the design matrix.
na.action   (where relevant) information returned by model.frame on the special handling of NAs.
nobs        the number of observations counted as sum(weights).
nom.contrasts (where relevant) the contrasts used for the nominal part of the model.
nom.terms   (where relevant) the terms object for the nominal part.
nom.xlevels (where relevant) a record of the levels of the factors used in fitting for the nominal part.
start      the parameter values at which the optimization has started. An attribute start.iter gives the number of iterations to obtain starting values for models where scale is specified or where the cauchit link is chosen.
S.contrasts (where relevant) the contrasts used for the scale part of the model.
S.terms    (where relevant) the terms object for the scale part.
S.xlevels  (where relevant) a record of the levels of the factors used in fitting for the scale part.
terms      the terms object for the formula part.
Theta       (where relevant) a table (data.frame) of thresholds for all combinations of levels of factors in the nominal formula.
threshold   character, the threshold structure used.
tJac        the transpose of the Jacobian for the threshold structure.
xlevels     (where relevant) a record of the levels of the factors used in fitting for the formula part.
y.levels   the levels of the response variable after removing levels for which all weights are zero.
zeta       (where relevant) a vector of scale regression parameters.

Author(s)
Rune Haubo B Christensen

Examples

fm1 <- clm(rating ~ temp * contact, data = wine)
fm1 ## print method
summary(fm1)
fm2 <- update(fm1, .~-.temp:contact)
anova(fm1, fm2)
drop1(fm1, test = "Chi")
add1(fm1, .~+.judge, test = "Chi")
\begin{verbatim}

fm2 <- step(fm1)
summary(fm2)

coef(fm1)
vcov(fm1)
AIC(fm1)
extractAIC(fm1)
logLik(fm1)
fitted(fm1)

confint(fm1) ## type = "profile"
confint(fm1, type = "Wald")
pr1 <- profile(fm1)
confint(pr1)

## plotting the profiles:
par(mfrow = c(2, 2))
plot(pr1, root = TRUE) ## check for linearity
par(mfrow = c(2, 2))
plot(pr1)
par(mfrow = c(2, 2))
plot(pr1, approx = TRUE)
par(mfrow = c(2, 2))
plot(pr1, Log = TRUE)
par(mfrow = c(2, 2))
plot(pr1, Log = TRUE, relative = FALSE)

## other link functions:
fm4.lgt <- update(fm1, link = "logit") ## default
fm4.prt <- update(fm1, link = "probit")
fm4.ll <- update(fm1, link = "loglog")
fm4.cll <- update(fm1, link = "cloglog")
fm4.cct <- update(fm1, link = "cauchit")
anova(fm4.lgt, fm4.prt, fm4.ll, fm4.cll, fm4.cct)

## structured thresholds:
fm5 <- update(fm1, threshold = "symmetric")
fm6 <- update(fm1, threshold = "equidistant")
anova(fm1, fm5, fm6)

## the slice methods:
slice.fm1 <- slice(fm1)
par(mfrow = c(3, 3))
plot(slice.fm1)
## see more at '?slice.clm'

## Another example:
fm.soup <- clm(SURENESS ~ PRODID, data = soup)
summary(fm.soup)

if(require(MASS)) { ## dropterm, addterm, stepAIC, housing
  fm1 <- clm(rating ~ temp * contact, data = wine)
}
\end{verbatim}
clm.control

Set control parameters for cumulative link models

Description

Set control parameters for cumulative link models

Usage

clm.control(method = c("Newton", "model.frame", "design", "ucminf", "nlminb", "optim"),
    sign.location = c("negative", "positive"),
    sign.nominal = c("positive", "negative"),
    ..., trace = 0L,
    maxIter = 100L, gradTol = 1e-06, maxLineIter = 15L, relTol = 1e-6,
    tol = sqrt(.Machine$double.eps), maxModIter = 5L,
    convergence = c("warn", "silent", "stop", "message"))

Arguments

method "Newton" fits the model by maximum likelihood and "model.frame" cause clm to return the model.frame, "design" causes clm to return a list of design matrices etc. that can be used with clm.fit. ucminf, nlminb and optim refer to general purpose optimizers.

sign.location change sign of the location part of the model.

sign.nominal change sign of the nominal part of the model.

trace numerical, if > 0 information is printed about and during the optimization process. Defaults to 0.

maxIter the maximum number of Newton-Raphson iterations. Defaults to 100.

gradTol the maximum absolute gradient; defaults to 1e-6.

maxLineIter the maximum number of step halfings allowed if a Newton(-Raphson) step over shoots. Defaults to 15.

relTol relative convergence tolerance: relative change in the parameter estimates between Newton iterations. Defaults to 1e-6.
clm.fit   

**tol**  
numerical tolerance on eigenvalues to determine negative-definiteness of Hessian. If the Hessian of a model fit is negative definite, the fitting algorithm did not converge. If the Hessian is singular, the fitting algorithm did converge albeit not to a unique optimum, so one or more parameters are not uniquely determined even though the log-likelihood value is.

**maxModIter**  
the maximum allowable number of consecutive iterations where the Newton step needs to be modified to be a decent direction. Defaults to 5.

**convergence**  
action to take if the fitting algorithm did not converge.

### Control Arguments

...  
control arguments parsed on to `ucminf`, `nlminb` or `optim`.

### Value

a list of control parameters.

### Author(s)

Rune Haubo B Christensen

### See Also

- `clm`

---

**clm.fit**  

*Fit Cumulative Link Models*

---

**Description**

A direct fitter of cumulative link models.

**Usage**

```r
clm.fit(y, ...)  
```

## Default S3 method:
```r
clm.fit(y, ...)  
```

## S3 method for class 'factor'
```r
clm.fit(y, X, S, N, weights = rep(1, nrow(X)),  
       offset = rep(0, nrow(X)), S.offset = rep(0, nrow(X)),  
       control = list(), start, doFit=TRUE,  
       link = c("logit", "probit", "cloglog", "loglog", "cauchit",  
               "Aranda-Ordaz", "log-gamma"),  
       threshold = c("flexible", "symmetric", "symmetric2", "equidistant"),  
       ...)  
```
Arguments

- **y**: for the default method a list of model components. For the factor method the response variable; a factor, preferably and ordered factor.
- **X, S, N**: optional design matrices for the regression parameters, scale parameters and nominal parameters respectively.
- **weights**: optional case weights.
- **offset**: an optional offset.
- **S.offset**: an optional offset for the scale part of the model.
- **control**: a list of control parameters, optionally a call to `clm.control`.
- **start**: an optional list of starting values of the form `c(alpha, beta, zeta)` for the thresholds and nominal effects (`alpha`), regression parameters (`beta`) and scale parameters (`zeta`).
- **doFit**: logical for whether the model should be fit or the model environment should be returned.
- **link**: the link function.
- **threshold**: the threshold structure, see further at `clm`.
- **...**: currently not used.

Details

This function does almost the same thing that `clm` does: it fits a cumulative link model. The main differences are that `clm.fit` does not setup design matrices from formulae and only does minimal post processing after parameter estimation.

Compared to `clm`, `clm.fit` does little to warn the user of any problems with data or model. However, `clm.fit` will attempt to identify column rank deficient designs. Any unidentified parameters are indicated in the `aliased` component of the fit.

`clm.fit.factor` is not able to check if all thresholds are increasing when nominal effects are specified since it needs access to the terms object for the nominal model. If the terms object for the nominal model (`nom.terms`) is included in `y`, the default method is able to check if all thresholds are increasing.

Value

A list with the following components: `aliased`, `alpha`, `coefficients`, `cond.H`, `convergence`, `df.residual`, `edf`, `fitted.values`, `gradient`, `Hessian`, `logLik`, `maxGradient`, `message`, `n`, `niter`, `nobs`, `tJac`, `vcov` and optionally `beta`, `zeta`. These components are documented in `clm`.

Author(s)

Rune Haubo B Christensen

See Also

`clm`
Examples

```r
## A simple example:
fm1 <- clm(rating ~ contact + temp, data=wine)
summary(fm1)
## get the model frame containing y and X:
mf1 <- update(fm1, method="design")
names(mf1)
res <- clm.fit(mf1$y, mf1$X) ## invoking the factor method
stopifnot(all.equal(coef(res), coef(fm1)))
names(res)

## Fitting with the default method:
mf1$control$method <- "Newton"
res2 <- clm.fit(mf1)
stopifnot(all.equal(coef(res2), coef(fm1)))
```

---

clm2  

Cumulative link models

Description

A new improved implementation of CLMs is available in *clm*.

Fits cumulative link models with an additive model for the location and a multiplicative model for the scale. The function allows for structured thresholds. A popular special case of a CLM is the proportional odds model. In addition to the standard link functions, two flexible link functions, "Arandar-Ordaz" and "log-gamma" are available, where an extra link function parameter provides additional flexibility. A subset of the predictors can be allowed to have nominal rather than ordinal effects. This has been termed "partial proportional odds" when the link is the logistic.

Usage

```r
clm2(location, scale, nominal, data, weights, start, subset,  
     na.action, contrasts, Hess = TRUE, model,  
     link = c("logistic", "probit", "cloglog", "loglog",  
              "cauchit", "Aranda-Ordaz", "log-gamma"), lambda,  
     doFit = TRUE, control,  
     threshold = c("flexible", "symmetric", "equidistant"), ...)
```

Arguments

- **location**: a formula expression as for regression models, of the form `response ~ predictors`. The response should be a factor (preferably an ordered factor), which will be interpreted as an ordinal response with levels ordered as in the factor. The model must have an intercept: attempts to remove one will lead to a warning and will be ignored. An offset may be used. See the documentation of `formula` for other details.
scale

a optional formula expression as for the location part, of the form ~ predictors, i.e. with an empty left hand side. An offset may be used. See the documentation of formula for other details.

nominal

an optional formula of the form ~ predictors, i.e. with an empty left hand side. The effects of the predictors in this formula are assumed to nominal.

data

an optional data frame in which to interpret the variables occurring in the formulas.

weights

optional case weights in fitting. Defaults to 1.

start

initial values for the parameters in the format c(alpha, beta, log(zeta), lambda).

subset

expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.

na.action

a function to filter missing data. Applies to terms in all three formulae.

contrasts

a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.

Hess

logical for whether the Hessian (the inverse of the observed information matrix) should be computed. Use Hess = TRUE if you intend to call summary or vcov on the fit and Hess = FALSE in all other instances to save computing time. The argument is ignored if method = "Newton" where the Hessian is always computed and returned. Defaults to TRUE.

model

logical for whether the model frames should be part of the returned object.

link

link function, i.e. the type of location-scale distribution assumed for the latent distribution. The Aranda-Ordaz and log-gamma links add additional flexibility with a link function parameter, lambda. The Aranda-Ordaz link (Aranda-Ordaz, 1983) equals the logistic link, when lambda = 1 and approaches the loglog link when lambda approaches zero. The log-gamma link (Genter and Farewell, 1985) equals the loglog link when lambda = 1, the probit link when lambda = 0 and the cloglog link when lambda = -1.

lambda

numerical scalar: the link function parameter. Used in combination with link Aranda-Ordaz or log-gamma and otherwise ignored. If lambda is specified, the model is estimated with lambda fixed at this value and otherwise lambda is estimated by ML. For Aranda-Ordaz lambda has to be positive; > 1e-5 for numerical reasons.

doFit

logical for whether the model should be fit or the model environment should be returned.

control

a call to clm2.control.

threshold

specifies a potential structure for the thresholds (cut-points). "flexible" provides the standard unstructured thresholds, "symmetric" restricts the distance between the thresholds to be symmetric around the central one or two thresholds for odd or equal numbers or thresholds respectively, and "equidistant" restricts the distance between consecutive thresholds to the same value.

... additional arguments are passed on to clm2.control and possibly further on to the optimizer, which can lead to surprising error or warning messages when mistyping arguments etc.
Details

There are methods for the standard model-fitting functions, including `summary`, `vcov`, `predict`, `anova`, `logLik`, `profile`, `plot.profile`, `confint`, `update`, `dropterm`, `addterm`, and an `extractAIC` method.

The design of the implementation is inspired by an idea proposed by Douglas Bates in the talk "Exploiting sparsity in model matrices" presented at the DSC conference in Copenhagen, July 14 2009. Basically an environment is set up with all the information needed to optimize the likelihood function. Extractor functions are then used to get the value of likelihood at current or given parameter values and to extract current values of the parameters. All computations are performed inside the environment and relevant variables are updated during the fitting process. After optimizer termination relevant variables are extracted from the environment and the remaining are discarded.

Some aspects of `clm2`, for instance, how starting values are obtained, and of the associated methods are inspired by `polr` from package `MASS`.

Value

If `doFit = FALSE` the result is an environment representing the model ready to be optimized. If `doFit = TRUE` the result is an object of class "clm2" with the following components:

- `beta`: the parameter estimates of the location part.
- `zeta`: the parameter estimates of the scale part on the log scale; the scale parameter estimates on the original scale are given by \( \exp(zeta) \).
- `Alpha`: vector or matrix of the threshold parameters.
- `Theta`: vector or matrix of the thresholds.
- `xi`: vector of threshold parameters, which, given a threshold function (e.g. "equidistant"), and possible nominal effects define the class boundaries, Theta.
- `lambda`: the value of lambda if lambda is supplied or estimated, otherwise missing.
- `coefficients`: the coefficients of the intercepts (theta), the location (beta), the scale (zeta), and the link function parameter (lambda).
- `df.residual`: the number of residual degrees of freedoms, calculated using the weights.
- `fitted.values`: vector of fitted values for each observation. An observation here is each of the scalar elements of the multinomial table and not a multinomial vector.
- `convergence`: TRUE if the gradient based convergence criterion is met and FALSE otherwise.
- `gradient`: vector of gradients for all the parameters at termination of the optimizer.
- `optRes`: list with results from the optimizer. The contents of the list depends on the choice of optimizer.
- `logLik`: the log likelihood of the model at optimizer termination.
- `Hessian`: if the model was fitted with `Hess = TRUE`, this is the Hessian matrix of the parameters at the optimum.
- `scale`: `model.frame` for the scale model.
- `location`: `model.frame` for the location model.
- `nominal`: `model.frame` for the nominal model.
edf  
the (effective) number of degrees of freedom used by the model.

start  
the starting values.

convTol  
convergence tolerance for the maximum absolute gradient of the parameters at termination of the optimizer.

method  
character, the optimizer.

y  
the response variable.

lev  
the names of the levels of the response variable.

nobs  
the (effective) number of observations, calculated as the sum of the weights.

threshold  
character, the threshold function used in the model.

estimLambda  
1 if lambda is estimated in one of the flexible link functions and 0 otherwise.

link  
character, the link function used in the model.

call  
the matched call.

contrasts  
contrasts applied to terms in location and scale models.

na.action  
the function used to filter missing data.

Author(s)

Rune Haubo B Christensen

References


Examples

```r
options(contrasts = c("contr.treatment", "contr.poly"))

## A tabular data set:
(tab26 <- with(soup, table("Product" = PROD, "Response" = SURENESS)))
dimnames(tab26)[[2]] <- c("Sure", "Not Sure", "Guess", "Guess", "Not Sure", "Sure")
dat26 <- expand.grid(sureness = as.factor(1:6), prod = c("Ref", "Test"))
dat26$wghts <- c(t(tab26))

m1 <- clm2(sureness ~ prod, scale = ~prod, data = dat26, weights = wghts, link = "logistic")

## print, summary, vcov, logLik, AIC:

m1
summary(m1)
vcov(m1)
```
logLik(m1)
AIC(m1)
coef(m1)
coef(summary(m1))

## link functions:

m2 <- update(m1, link = "probit")
m3 <- update(m1, link = "cloglog")
m4 <- update(m1, link = "loglog")
m5 <- update(m1, link = "cauchit", start = coef(m1))
m6 <- update(m1, link = "Aranda-Ordaz", lambda = 1)
m7 <- update(m1, link = "Aranda-Ordaz")
m8 <- update(m1, link = "log-gamma", lambda = 1)
m9 <- update(m1, link = "log-gamma")

## nominal effects:

mN1 <- clm2(sureness ~ 1, nominal = ~ prod, data = dat26,
weights = wghts, link = "logistic")
anova(m1, mN1)

## optimizer / method:

update(m1, scale = ~ 1, method = "Newton")
update(m1, scale = ~ 1, method = "nlminb")
update(m1, scale = ~ 1, method = "optim")

## threshold functions

mT1 <- update(m1, threshold = "symmetric")
mT2 <- update(m1, threshold = "equidistant")
anova(m1, mT1, mT2)

## Extend example from polr in package MASS:

## Fit model from polr example:
if(require(MASS)) {
  fm1 <- clm2(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
  fm1
  summary(fm1)
  ## With probit link:
  summary(update(fm1, link = "probit"))
  ## Allow scale to depend on Cont-variable
  summary(fm2 <- update(fm1, scale = ~ Cont))
  anova(fm1, fm2)
  ## which seems to improve the fit
}

# It is possible to fit multinomial models (i.e. with nominal
## effects) as the following example shows:
if(require(nnet)) {
  (hous1.mu <- multinom(Sat ~ 1, weights = Freq, data = housing))
  (hous1.clm <- clm2(Sat ~ 1, weights = Freq, data = housing))

  ## It is the same likelihood:
all.equal(logLik(hous1.mu), logLik(hous1.clm))

## and the same fitted values:
fitHous.mu <-
t(fitted(hous1.mu))[t(col(fitted(hous1.mu)) == unclass(housing$Sat))]
all.equal(fitted(hous1.clm), fitHous.mu)

## The coefficients of multinom can be retrieved from the clm2-object
## by:
Pi <- diff(c(0, plogis(hous1.clm$xi), 1))
log(Pi[2:3]/Pi[1])

## A larger model with explanatory variables:
(hous.mu <- multinom(Sat ~ Infl + Type + Cont, weights = Freq, data = housing))
(hous.clm <- clm2(Sat ~ 1, nominal = ~ Infl + Type + Cont, weights = Freq,
data = housing))

## Almost the same likelihood:
all.equal(logLik(hous.mu), logLik(hous.clm))

## And almost the same fitted values:
fitHous.mu <-
t(fitted(hous.mu))[t(col(fitted(hous.mu)) == unclass(housing$Sat))]
all.equal(fitted(hous.clm), fitHous.mu)
all.equal(round(fitted(hous.clm), 5), round(fitHous.mu), 5)

---
clm2.control

Set control parameters for cumulative link models

description
Set control parameters for cumulative link models

usage
clm2.control(method = c("ucminf", "Newton", "nlminb", "optim",
"model.frame"), ..., convTol = 1e-4,
trace = 0, maxIter = 100, gradTol = 1e-5,
maxLineIter = 10)

arguments
method the optimizer used to maximize the likelihood function. "Newton" only works
for models without scale, structured thresholds and flexible link functions, but
is considerably faster than the other optimizers when applicable. model.frame
simply returns a list of model frames with the location, scale and nominal model
frames. "optim" uses the "BFGS" method.
... control arguments passed on to the chosen optimizer; see `ucminf`, `optim`, and `nlminb` for details.

`convTol` convergence criterion on the size of the maximum absolute gradient.

`trace` numerical, if > 0 information is printed about and during the optimization process. Defaults to 0.

`maxIter` the maximum number of Newton-Raphson iterations. Defaults to 100.

`gradTol` the maximum absolute gradient. This is the termination criterion and defaults to 1e-5.

`maxLineIter` the maximum number of step halvings allowed if a Newton(-Raphson) step over shoots. Defaults to 10.

Value

a list of control parameters.

Author(s)

Rune Haubo B Christensen

See Also

`clm2`

---

**clmm**

*Cumulative Link Mixed Models*

Description

Fits Cumulative Link Mixed Models with one or more random effects via the Laplace approximation or quadrature methods.

Usage

```r
clmm(formula, data, weights, start, subset, na.action, contrasts, Hess = TRUE, model = TRUE, link = c("logit", "probit", "cloglog", "loglog", "cauchit"), doFit = TRUE, control = list(), nAGQ = 1L, threshold = c("flexible", "symmetric", "symmetric2", "equidistant"), ...)
```
Arguments

**formula**

A two-sided linear formula object describing the fixed-effects part of the model, with the response on the left of a `~` operator and the terms, separated by `+` operators, on the right. The vertical bar character `|` separates an expression for a model matrix and a grouping factor.

**data**

An optional data frame in which to interpret the variables occurring in the formula.

**weights**

Optional case weights in fitting. Defaults to 1.

**start**

Optional initial values for the parameters in the format `c(alpha, beta, tau)`, where `alpha` are the threshold parameters, `beta` are the fixed regression parameters and `tau` are variance parameters for the random effects on the log scale.

**subset**

Expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.

**na.action**

A function to filter missing data.

**contrasts**

A list of contrasts to be used for some or all of the factors appearing as variables in the model formula.

**Hess**

Logical for whether the Hessian (the inverse of the observed information matrix) should be computed. Use `Hess = TRUE` if you intend to call `summary` or `vcov` on the fit and `Hess = FALSE` in all other instances to save computing time.

**model**

Logical for whether the model frames should be part of the returned object.

**link**

Link function, i.e. the type of location-scale distribution assumed for the latent distribution. The default "logit" link gives the proportional odds mixed model.

**doFit**

Logical for whether the model should be fit or the model environment should be returned.

**control**

A call to `clmm.control`.

**nAGQ**

Integer; the number of quadrature points to use in the adaptive Gauss-Hermite quadrature approximation to the likelihood function. The default (1) gives the Laplace approximation. Higher values generally provide higher precision at the expense of longer computation times, and values between 5 and 10 generally provide accurate maximum likelihood estimates. Negative values give the non-adaptive Gauss-Hermite quadrature approximation, which is generally faster but less accurate than the adaptive version. See the references for further details. Quadrature methods are only available with a single random effects term; the Laplace approximation is always available.

**threshold**

Specifies a potential structure for the thresholds (cut-points). "flexible" provides the standard unstructured thresholds, "symmetric" restricts the distance between the thresholds to be symmetric around the central one or two thresholds for odd or equal numbers or thresholds respectively, "symmetric2" restricts the latent mean in the reference group to zero; this means that the central threshold (even no. response levels) is zero or that the two central thresholds are equal apart from their sign (uneven no. response levels), and "equidistant" restricts the distance between consecutive thresholds to be of the same size.

... Additional arguments are passed on to `clm.control`. 

---

*clmm*
Details
This is a new (as of August 2011) improved implementation of CLMMs. The old implementation is available in clmm2. Some features are not yet available in clmm: for instance scale effects, nominal effects and flexible link functions are currently only available in clmm2. clmm is expected to take over clmm2 at some point.

There are standard print, summary and anova methods implemented for "clmm" objects.

Value
a list containing

alpha  threshold parameters.
beta   fixed effect regression parameters.
stDev  standard deviation of the random effect terms.
tau    log(stDev) - the scale at which the log-likelihood function is optimized.
coefficients the estimated model parameters = c(alpha, beta, tau).
control List of control parameters as generated by clm.control.
Hessian Hessian of the model coefficients.
edf    the estimated degrees of freedom used by the model = length(coefficients).
nobs   sum(weights).
n      length(y).
fitted.values fitted values evaluated with the random effects at their conditional modes.
df.residual residual degrees of freedom; length(y) - sum(weights)
tJac    Jacobian of the threshold function corresponding to the mapping from standard flexible thresholds to those used in the model.
terms  the terms object for the fixed effects.
contrasts contrasts applied to the fixed model terms.
na.action the function used to filter missing data.
call   the matched call.
logLik  value of the log-likelihood function for the model at the optimum.
Niter   number of Newton iterations in the inner loop update of the conditional modes of the random effects.
optRes  list of results from the optimizer.
ranef   list of the conditional modes of the random effects.
condVar list of the conditional variance of the random effects at their conditional modes.

Author(s)
Rune Haubo B Christensen
### Examples

```r
## Cumulative link model with one random term:
# fmm1 <- clmm(rating ~ temp + contact + (1|judge), data = wine)
# summary(fmm1)

## Not run:
## May take a couple of seconds to run this.

## Cumulative link mixed model with two random terms:
# mm1 <- clmm(SURENESS ~ PROD + (1|RESP) + (1|RESP:PROD), data = soup,
#              link = "probit", threshold = "equidistant")
# mm1
# summary(mm1)

## test random effect:
# mm2 <- clmm(SURENESS ~ PROD + (1|RESP), data = soup,
#              link = "probit", threshold = "equidistant")
# anova(mm1, mm2)

## End(Not run)
```

---

### clmm.control

Set control parameters for cumulative link mixed models

#### Description

Set control parameters for cumulative link mixed models

#### Usage

```r
clmm.control(method = c("nlminb", "ucminf", "model.frame"), ..., trace = 0,
              maxIter = 50, gradTol = 1e-4, maxLineIter = 50, useMatrix = FALSE,
              innerCtrl = c("warnOnly", "noWarn", "giveError"),
              checkRanef = c("warn", "error", "message"))
```

#### Arguments

- `method`: the optimizer used to maximize the marginal likelihood function.
- `...`: control arguments passed on to the optimizer; see `ucminf` for details. `ucminf` for details.
- `trace`: numerical, if > 0 information is printed about and during the outer optimization process, if < 0 information is also printed about the inner optimization process. Defaults to 0.
- `maxIter`: the maximum number of Newton updates of the inner optimization. 50.
- `gradTol`: the maximum absolute gradient of the inner optimization.
maxLineIter  the maximum number of step halfings allowed if a Newton(-Raphson) step over
shoots during the inner optimization.

useMatrix if TRUE, a general implementation of the Laplace approximation using the Matrix
package is used, while if FALSE (default), a C implementation of the Laplace
approximation valid only for models with a single random effects term is used
when possible. TRUE is not valid for models fitted with quadrature methods.

innerCtrl the use of warnings/errors if the inner optimization fails to converge.

checkRanef the use of message/warning/error if there are more random effects than observa-
tions.

Value
a list of control parameters

Author(s)
Rune Haubo B Christensen

See Also

clmm

clmm2  Cumulative link mixed models

Description
Fits cumulative link mixed models, i.e. cumulative link models with random effects via the Laplace
approximation or the standard and the adaptive Gauss-Hermite quadrature approximation. The
functionality in clm2 is also implemented here. Currently only a single random term is allowed in
the location-part of the model.

A new implementation is available in clmm that allows for more than one random effect.

Usage

clmm2(location, scale, nominal, random, data, weights, start, subset,
na.action, contrasts, Hess = FALSE, model = TRUE, sdFixed,
link = c(“logistic”, “probit”, “cloglog”, “loglog”,
"cauchit", "Aranda-Ordaz", "log-gamma"), lambda,
doFit = TRUE, control, nAGQ = 1,
threshold = c(“flexible", "symmetric", “equidistant"), ...)

Arguments

location as in clm2.
scale as in clm2.
nominal as in clm2.
random a factor for the random effects in the location-part of the model.
data as in clm2.
weights as in clm2.
start initial values for the parameters in the format \(c(\alpha, \beta, \log(zeta), \lambda, \log(stDev))\) where stDev is the standard deviation of the random effects.
subset as in clm2.
na.action as in clm2.
contrasts as in clm2.
Hess logical for whether the Hessian (the inverse of the observed information matrix) should be computed. Use Hess = TRUE if you intend to call summary or vcov on the fit and Hess = FALSE in all other instances to save computing time.
model as in clm2.
sdFixed If sdFixed is specified (a positive scalar), a model is fitted where the standard deviation for the random term is fixed at the value of sdFixed. If sdFixed is left unspecified, the standard deviation of the random term is estimated from data.
link as in clm2.
lambda as in clm2.
doFit as in clm2 although it can also be one of c("no", "R", "C"), where "R" use the R-implementation for fitting, "C" (default) use C-implementation for fitting and "no" behaves as FALSE and returns the environment.
control a call to clmm2.control.
threshold as in clm2.
nAGQ the number of quadrature points to be used in the adaptive Gauss-Hermite quadrature approximation to the marginal likelihood. Defaults to 1 which leads to the Laplace approximation. An odd number of quadrature points is encouraged and 3, 5 or 7 are usually enough to achieve high precision. Negative values give the standard, i.e. non-adaptive Gauss-Hermite quadrature.

Details

There are methods for the standard model-fitting functions, including summary, vcov, profile, plot.profile, confint, anova, logLik, predict and an extractAIC method.

A Newton scheme is used to obtain the conditional modes of the random effects for Laplace and AGQ approximations, and a non-linear optimization is performed over the fixed parameter set to
get the maximum likelihood estimates. The Newton scheme uses the observed Hessian rather than the expected as is done in e.g. \texttt{glmer}, so results from the Laplace approximation for binomial fits should in general be more precise - particularly for other links than the "logistic".

Core parts of the function are implemented in C-code for speed.

The function calls \texttt{clm2} to set up an environment and to get starting values.

\textbf{Value}

If \texttt{doFit = FALSE} the result is an environment representing the model ready to be optimized. If \texttt{doFit = TRUE} the result is an object of class "clmm2" with the following components:

- \texttt{stDev}: the standard deviation of the random effects.
- \texttt{Niter}: the total number of iterations in the Newton updates of the conditional modes of the random effects.
- \texttt{grFac}: the grouping factor defining the random effects.
- \texttt{nAGQ}: the number of quadrature points used in the adaptive Gauss-Hermite Quadrature approximation to the marginal likelihood.
- \texttt{ranef}: the conditional modes of the random effects, sometimes referred to as "random effect estimates".
- \texttt{condVar}: the conditional variances of the random effects at their conditional modes.
- \texttt{beta}: the parameter estimates of the location part.
- \texttt{zeta}: the parameter estimates of the scale part on the log scale; the scale parameter estimates on the original scale are given by \(\exp(zeta)\).
- \texttt{Alpha}: vector or matrix of the threshold parameters.
- \texttt{Theta}: vector or matrix of the thresholds.
- \texttt{xi}: vector of threshold parameters, which, given a threshold function (e.g. "equidistant"), and possible nominal effects define the class boundaries, \texttt{Theta}.
- \texttt{lambda}: the value of lambda if lambda is supplied or estimated, otherwise missing.
- \texttt{coefficients}: the coefficients of the intercepts (\texttt{theta}), the location (\texttt{beta}), the scale (\texttt{zeta}), and the link function parameter (\texttt{lambda}).
- \texttt{df.residual}: the number of residual degrees of freedoms, calculated using the weights.
- \texttt{fitted.values}: vector of fitted values conditional on the values of the random effects. Use \texttt{predict} to get the fitted values for a random effect of zero. An observation here is taken to be each of the scalar elements of the multinomial table and not a multinomial vector.
- \texttt{convergence}: \texttt{TRUE} if the optimizer terminates without error and \texttt{FALSE} otherwise.
- \texttt{gradient}: vector of gradients for the unit-variance random effects at their conditional modes.
- \texttt{optRes}: list with results from the optimizer. The contents of the list depends on the choice of optimizer.
- \texttt{logLik}: the log likelihood of the model at optimizer termination.
- \texttt{Hessian}: if the model was fitted with \texttt{Hess = TRUE}, this is the Hessian matrix of the parameters at the optimum.
scale model.frame for the scale model.
location model.frame for the location model.
nominal model.frame for the nominal model.
edf the (effective) number of degrees of freedom used by the model.
start the starting values.
method character, the optimizer.
y the response variable.
lev the names of the levels of the response variable.
nobs the (effective) number of observations, calculated as the sum of the weights.
threshold character, the threshold function used in the model.
estimLambda 1 if lambda is estimated in one of the flexible link functions and 0 otherwise.
link character, the link function used in the model.
call the matched call.
contrasts contrasts applied to terms in location and scale models.
na.action the function used to filter missing data.

Author(s)
Rune Haubo B Christensen

References

Examples

```r
options(contrasts = c("contr.treatment", "contr.poly"))

## More manageable data set:
dat <- subset(soup, as.numeric(as.character(RESP)) <= 24)
dat$RESP <- dat$RESP[drop=TRUE]

m1 <- clmm2(SURENESS ~ PROD, random = RESP, data = dat, link="probit",
             Hess = TRUE, method="ucminf", threshold = "symmetric")

m1
summary(m1)
logLik(m1)
vcov(m1)
extractAIC(m1)
anova(m1, update(m1, location = SURENESS ~ 1, Hess = FALSE))
anova(m1, update(m1, random = NULL))

## Use adaptive Gauss-Hermite quadrature rather than the Laplace approximation:
update(m1, Hess = FALSE, nAGQ = 3)
```
## Use standard Gauss-Hermite quadrature:
update(m1, Hess = FALSE, nAGQ = -7)

### Binomial example with the cbpp data from the lme4-package:
if(require(lme4)) {
  cbpp2 <- rbind(cbpp[,-(2:3)], cbpp[,-(2:3)])
  cbpp2 <- within(cbpp2, {
    incidence <- as.factor(rep(0:1, each=nrow(cbpp)))
    freq <- with(cbpp, c(incidence, size - incidence))
  })

  ## Fit with Laplace approximation:
  fm1 <- clmm2(incidence ~ period, random = herd, weights = freq,
                data = cbpp2, Hess = 1)
  summary(fm1)

  ## Fit with adaptive Gauss-Hermite quadrature approximation:
  fm2 <- clmm2(incidence ~ period, random = herd, weights = freq,
                data = cbpp2, Hess = 1, nAGQ = 7)
  summary(fm2)
}

---

**clmm2.control**

**Set control parameters for cumulative link mixed models**

**Description**

Set control parameters for cumulative link mixed models

**Usage**

clmm2.control(method = c("ucminf", "nlminb", "model.frame"), ...,
               trace = 0, maxIter = 50, gradTol = 1e-4,
               maxLineIter = 50,
               innerCtrl = c("warnOnly", "noWarn", "giveError"))

**Arguments**

- **method**: the optimizer used to maximize the marginal likelihood function.
- **...**: control arguments passed on to the chosen optimizer; see `ucminf`, `optim`, and `nlminb` for details.
- **trace**: numerical, if > 0 information is printed about and during the outer optimization process, if < 0 information is also printed about the inner optimization process. Defaults to 0.
- **maxIter**: the maximum number of Newton updates of the inner optimization. 50.
- **gradTol**: the maximum absolute gradient of the inner optimization.
condVar

maxLineIter the maximum number of step halfings allowed if a Newton(-Raphson) step over shoots during the inner optimization.

innerCtrl the use of warnings/errors if the inner optimization fails to converge.

Details

When the default optimizer, ucminf is used, the default values of that optimizers control options are changed to grtol = 1e-5 and grad = "central".

Value

a list of control parameters.

Author(s)

Rune Haubo B Christensen

See Also

clmm2

condVar

condVar(object, ...)

Extract conditional modes and conditional variances from clmm objects

Description

The ranef function extracts the conditional modes of the random effects from a clmm object. That is, the modes of the distributions for the random effects given the observed data and estimated model parameters. In a Bayesian language they are posterior modes.

The conditional variances are computed from the second order derivatives of the conditional distribution of the random effects. Note that these variances are computed at a fixed value of the model parameters and thus do not take the uncertainty of the latter into account.

Usage

condVar(object, ...)

## S3 method for class 'clmm'
ranef(object, condVar=FALSE, ...)

## S3 method for class 'clmm'
condVar(object, ...)

condVar

Arguments

object a clmm object.

condVar an optional logical argument indicating of conditional variances should be added as attributes to the conditional modes.

... currently not used by the clmm methods.

Details

The ranef method returns a list of data.frames; one for each distinct grouping factor. Each data.frame has as many rows as there are levels for that grouping factor and as many columns as there are random effects for each level. For example a model can contain a random intercept (one column) or a random intercept and a random slope (two columns) for the same grouping factor.

If conditional variances are requested, they are returned in the same structure as the conditional modes (random effect estimates/predictions).

Value

The ranef method returns a list of data.frames with the random effects predictions/estimates computed as conditional modes. If condVar = TRUE a data.frame with the conditional variances is stored as an attribute on each data.frame with conditional modes.

The condVar method returns a list of data.frames with the conditional variances. It is a convenience function that simply computes the conditional modes and variances, then extracts and returns only the latter.

Author(s)

Rune Haubo B Christensen

Examples

fm1 <- clmm(rating ~ contact + temp + (1|judge), data=wine)

## Extract random effect estimates/conditional modes:
re <- ranef(fm1, condVar=TRUE)

## Get conditional variances:
attr(re$judge, "condVar")
## Alternatively:
condVar(fm1)
### Description

Computes confidence intervals from the profiled likelihood for one or more parameters in a cumulative link model, or plots the profile likelihood.

### Usage

```r
## S3 method for class 'clm'
confint(object, parm, level = 0.95,
    type = c("profile", "Wald"), trace = FALSE, ...)

## S3 method for class 'profile.clm'
confint(object, parm = seq_len(nprofiles),
    level = 0.95, ...)

## S3 method for class 'clm'
profile(fitted, which.beta = seq_len(nbeta),
    which.zeta = seq_len(nzeta), alpha = 0.001,
    max.steps = 50, nsteps = 8, trace = FALSE, step.warn = 5,
    control = list(), ...)

## S3 method for class 'profile.clm'
plot(x, which.par = seq_len(nprofiles),
    level = c(0.95, 0.99), Log = FALSE, relative = TRUE, root =
    FALSE, fig = FALSE, approx = root, n = 1e3,
    ask = prod(par("mfcol")) < length(which.par) && dev.interactive(),
    ..., ylim = NULL)
```

### Arguments

- `object, fitted, x`  
  a fitted `clm` object or a `profile.clm` object.
- `parm, which.par, which.beta, which.zeta`  
  a numeric or character vector indicating which regression coefficients should be profiled. By default all coefficients are profiled. Ignored for `confint.clm` where all parameters are considered.
- `level`  
  the confidence level. For the `plot` method a vector of levels for which horizontal lines should be drawn.
- `type`  
  the type of confidence interval.
- `trace`  
  if `trace` is `TRUE` or positive, information about progress is printed.
- `Log`  
  should the profile likelihood be plotted on the log-scale?
relative should the relative or the absolute likelihood be plotted?
root should the (approximately linear) likelihood root statistic be plotted?
approx should the Gaussian or quadratic approximation to the (log) likelihood be included?
fig should the profile likelihood be plotted?
ask logical; if TRUE, the user is asked before each plot, see par(ask=.).
n the no. points used in the spline interpolation of the profile likelihood.
ylim overrules default y-limits on the plot of the profile likelihood.
apro alpha the likelihood is profiled in the 100*(1-alpha)% confidence region as determined by the profile likelihood.
control a list of control parameters for clm. Possibly use clm.control to set these.
max.steps the maximum number of profiling steps in each direction for each parameter.
nsteps the (approximate) number of steps to take in each direction of the profile for each parameter. The step length is determined accordingly assuming a quadratic approximation to the log-likelihood function. The actual number of steps will often be close to nsteps, but will deviate when the log-likelihood functions is irregular.
step.warn a warning is issued if the number of steps in each direction (up or down) for a parameter is less than step.warn. If few steps are taken, the profile will be unreliable and derived confidence intervals will be inaccurate.
... additional arguments to be parsed on to methods.

Details

These confint methods call the appropriate profile method, then finds the confidence intervals by interpolation of the profile traces. If the profile object is already available, this should be used as the main argument rather than the fitted model object itself.

Value

confint: A matrix with columns giving lower and upper confidence limits for each parameter. These will be labelled as (1-level)/2 and 1 - (1-level)/2 in % (by default 2.5% and 97.5%).
plot.profile.clm invisibly returns the profile object, i.e., a list of data.frames with an lroot component for the likelihood root statistic and a matrix par.vals with values of the parameters.

Author(s)

Rune Haubo B Christensen

See Also

profile and confint
## Examples

```r
## Accurate profile likelihood confidence intervals compared to the
## conventional Wald intervals:
fm1 <- clm(rating ~ temp * contact, data = wine)
confint(fm1) ## type = "profile"
confint(fm1, type = "Wald")
pr1 <- profile(fm1)
confint(pr1)

## plotting the profiles:
par(mfrow = c(2, 2))
plot(pr1, root = TRUE) ## check for linearity
par(mfrow = c(2, 2))
plot(pr1)
par(mfrow = c(2, 2))
plot(pr1, approx = TRUE)
par(mfrow = c(2, 2))
plot(pr1, Log = TRUE)
par(mfrow = c(2, 2))
plot(pr1, Log = TRUE, relative = FALSE)
## Not likely to be useful but allowed for completeness:
par(mfrow = c(2, 2))
plot(pr1, Log = FALSE, relative = FALSE)

## Example from polr in package MASS:
## Fit model from polr example:
if(require(MASS)) {
  fm1 <- clm(Sat ~ Infl + Type + Cont, weights = Freq,
              data = housing)
  pr1 <- profile(fm1)
  confint(pr1)
  par(mfrow=c(2,2))
  plot(pr1)
}
```

---

### convergence

**convergence**

**Check convergence of cumulative link models**

### Description

Check the accuracy of the parameter estimates of cumulative link models. The number of correct decimals and number of significant digits is given for the maximum likelihood estimates of the parameters in a cumulative link model fitted with \texttt{clm}.

### Usage
convergence(object, ...)  

```r
## S3 method for class 'clm'
convergence(object, digits = max(3, getOption("digits") - 3),
            tol = sqrt(.Machine$double.eps), ...)
```

**Arguments**

- `object`: for the clm method an object of class "clm", i.e., the result of a call to clm.
- `digits`: the number of digits in the printed table.
- `tol`: numerical tolerance to judge if the Hessian is positive definite from its smallest eigenvalue.
- `...`: arguments to a from methods. Not used by the clm method.

**Details**

The number of correct decimals is defined as...

The number of significant digits is defined as ...

The number of correct decimals and the number of significant digits are determined from the numerical errors in the parameter estimates. The numerical errors are determined from the Method Independent Error Theorem (Elden et al, 2004) and is based on the Newton step evaluated at convergence.

**Value**

Convergence information. In particular a table where the Error column gives the numerical error in the parameter estimates. These numbers express how far the parameter estimates in the fitted model are from the true maximum likelihood estimates for this model. The Cor.Dec gives the number of correct decimals with which the the parameters are determined and the Sig.Dig gives the number of significant digits with which the parameters are determined.

The number denoted logLik.error is the error in the value of log-likelihood in the fitted model at the parameter values of that fit. An accurate determination of the log-likelihood is essential for accurate likelihood ratio tests in model comparison.

**Author(s)**

Rune Haubo B Christensen

**References**

Examples

```r
## Simple model:
fm1 <- clm(rating ~ contact + temp, data=wine)
summary(fm1)
convergence(fm1)
```

---

### drop.coef

Ensure Full Rank Design Matrix

**Description**

Coefficients (columns) are dropped from a design matrix to ensure that it has full rank.

**Usage**

```r
drop.coef(X, silent = FALSE)
```

**Arguments**

- `X` a design matrix, e.g., the result of `model.matrix` possibly of less than full column rank, i.e., with redundant parameters. Works for `ncol(X) >= 0` and `nrow(X) >= 0`.
- `silent` should a message not be issued if `X` is column rank deficient?

**Details**

Redundant columns of the design matrix are identified with the LINPACK implementation of the `qr` decomposition and removed. The returned design matrix will have `qr(X)$rank` columns.

**Value**

The design matrix `X` without redundant columns.

**Author(s)**

Rune Haubo B Christensen

**See Also**

`qr` and `lm`
Examples

```r
X <- model.matrix(~ PRODID * DAY, data = soup)
ncol(X)
newX <- drop.coef(X)
ncol(newX)

## Essentially this is being computed:
qr.X <- qr(X, tol = 1e-7, LAPACK = FALSE)
newX <- X[, qr.X$pivot[1:qr.X$rank], drop = FALSE]
## is newX of full column rank?
ncol(newX) == qr(newX)$rank
## the number of columns being dropped:
ncol(X) - ncol(newX)
```

---

**gfun**  
*Gradients of common densities*

**Description**

Gradients of common density functions in their standard forms, i.e., with zero location (mean) and unit scale. These are implemented in C for speed and care is taken that the correct results are provided for the argument being NA, NaN, Inf, -Inf or just extremely small or large.

**Usage**

```r
gnorm(x)
glogis(x)
gcauchy(x)
```

**Arguments**

- `x` numeric vector of quantiles.

**Details**

The gradients are given by:

- **gnorm:** If \( f(x) \) is the normal density with mean 0 and spread 1, then the gradient is \( f'(x) = -xf(x) \)

- **glogis:** If \( f(x) \) is the logistic density with mean 0 and scale 1, then the gradient is \[ f'(x) = 2 \exp(-x)^2(1 + \exp(-x))^{-3} - \exp(-x)(1 + \exp(-x))^{-2} \]
• pcauhy: If \( f(x) = \pi(1 + x^2)^{-1} \) is the cauchy density with mean 0 and scale 1, then the gradient is
\[
f'(x) = -2x[\pi(1 + x^2)^2]^{-1}
\]
These gradients are used in the Newton-Raphson algorithms in fitting cumulative link models with \texttt{clm} and cumulative link mixed models with \texttt{clmm}.

**Value**

a numeric vector of gradients.

**Author(s)**

Rune Haubo B Christensen

**See Also**

Gradients of densities are also implemented for the extreme value distribution (\texttt{gumbel}) and the log-gamma distribution (\texttt{log-gamma}).

**Examples**

```r
x <- -5:5
gnorm(x)
glogis(x)
gcauchy(x)
```

---

**gumbel**

*The Gumbel Distribution*

**Description**

Density, distribution function, quantile function, random generation, and gradient of density of the extreme value (maximum and minimum) distributions. The Gumbel distribution is also known as the extreme value maximum distribution, the double-exponential distribution and the log-Weibull distribution.

**Usage**

```r
dgumbel(x, location = 0, scale = 1, log = FALSE, max = TRUE)
pgumbel(q, location = 0, scale = 1, lower.tail = TRUE, max = TRUE)
qgumbel(p, location = 0, scale = 1, lower.tail = TRUE, max = TRUE)
rgumbel(n, location = 0, scale = 1, max = TRUE)
```
ggumbel(x, max = TRUE)

Arguments

- **x, q**: numeric vector of quantiles.
- **p**: vector of probabilities.
- **n**: number of observations.
- **location**: numeric scalar.
- **scale**: numeric scalar.
- **lower.tail**: logical; if TRUE (default), probabilities are $P[X \leq x]$ otherwise, $P[X > x]$.
- **log**: logical; if TRUE, probabilities $p$ are given as log($p$).
- **max**: distribution for extreme maxima (default) or minima? The default corresponds to the standard right-skew Gumbel distribution.

Details
dgumbel, pgumbel and ggumbel are implemented in C for speed and care is taken that 'correct' results are provided for values of NA, NaN, Inf, -Inf or just extremely small or large.

The distribution functions, densities and gradients are used in the Newton-Raphson algorithms in fitting cumulative link models with clm and cumulative link mixed models with clmm.

Value

pgumbel gives the distribution function, dgumbel gives the density, ggumbel gives the gradient of the density, qgumbel is the quantile function, and rgumbel generates random deviates.

Author(s)

Rune Haubo B Christensen

References

https://en.wikipedia.org/wiki/Gumbel_distribution

See Also

Gradients of densities are also implemented for the normal, logistic, cauchy, cf. gfun and the log-gamma distribution, cf. lgamma.

Examples

```r
## Illustrating the symmetry of the distribution functions:
pgumbel(5) == 1 - pgumbel(-5, max=FALSE) ## TRUE
dgumbel(5) == dgumbel(-5, max=FALSE) ## TRUE
ggumbel(5) == -ggumbel(-5, max=FALSE) ## TRUE
```
income

## More examples:
```r
x <- -5:5

(pp <- pgumbel(x))
dgumbel(x)
ggumbel(x)

(ppp <- pgumbel(x, max=FALSE))
## Observe that probabilities close to 0 are more accurately determined than
## probabilities close to 1:
qgumbel(ppp, max=FALSE)
dgumbel(x, max=FALSE)
ggumbel(x, max=FALSE)

## random deviates:
set.seed(1)
(r1 <- rgumbel(10))
set.seed(1)
r2 <- -rgumbel(10, max = FALSE)
all(r1 == r2) ## TRUE
```

---

### income

*Income distribution (percentages) in the Northeast US*

<table>
<thead>
<tr>
<th>year</th>
<th>pct</th>
<th>income</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

#### Description


#### Usage

```r
income
```

#### Format

- year: year.
- pct: percentage of population in income class per year.
- income: income groups. The unit is thousands of constant (1973) US dollars.

#### Source

Data are adopted from McCullagh (1980).

#### References

Examples

```
print(income)
## Convenient table:
(tab <- xtabs(pct ~ year + income, income))
## small rounding error in 1970:
rowSums(tab)
## compare link functions via the log-likelihood:
links <- c("logit", "probit", "cloglog", "loglog", "cauchit")
sapply(links, function(link) {
  clm(income ~ year, data=income, weights=pct, link=link)$logLik })
## a heavy tailed (cauchy) or left skew (cloglog) latent distribution
## is fitting best.
## The data are defined as:
income.levels <- c(0, 3, 5, 7, 10, 12, 15)
income <- paste(income.levels, c(rep("-", 6), "+"),
  c(income.levels[-1], ""), sep = "")
income <- data.frame(year=factor(rep(c("1960", "1970"), each = 7)),
  pct = c(6.5, 8.2, 11.3, 23.5, 15.6, 12.7, 22.2,
  4.3, 6, 7.7, 13.2, 10.5, 16.3, 42.1),
  income=factor(rep(income, 2), ordered=TRUE,
  levels=income))
```

---

**lgamma**  
*The log-gamma distribution*

Description

Density, distribution function and gradient of density for the log-gamma distribution. These are implemented in C for speed and care is taken that the correct results are provided for values of NA, NaN, Inf, -Inf or just extremely small or large values.

The log-gamma is a flexible location-scale distribution on the real line with an extra parameter, \( \lambda \). For \( \lambda = 0 \) the distribution equals the normal or Gaussian distribution, and for \( \lambda \) equal to 1 and -1, the Gumbel minimum and maximum distributions are obtained.

Usage

```
plgamma(q, lambda, lower.tail = TRUE)

dlgamma(x, lambda, log = FALSE)

lgamma(x, lambda)
```
Arguments

x, q  numeric vector of quantiles.
lambda numerical scalar
lower.tail logical; if TRUE (default), probabilities are \( P[X \leq x] \) otherwise, \( P[X > x] \).
log logical; if TRUE, probabilities p are given as log(p).

Details

If \( \lambda < 0 \) the distribution is right skew, if \( \lambda = 0 \) the distribution is symmetric (and equals the normal distribution), and if \( \lambda > 0 \) the distribution is left skew.

These distribution functions, densities and gradients are used in the Newton-Raphson algorithms in fitting cumulative link models with \texttt{clm2} and cumulative link mixed models with \texttt{clmm2} using the log-gamma link.

Value

\texttt{plgamma} gives the distribution function, \texttt{dlgamma} gives the density and \texttt{glgamma} gives the gradient of the density.

Author(s)

Rune Haubo B Christensen

References


See Also

Gradients of densities are also implemented for the normal, logistic, cauchy, cf. \texttt{gfun} and the Gumbel distribution, cf. \texttt{gumbel}.

Examples

```r
## Illustrating the link to other distribution functions:
x <- -5:5
plgamma(x, lambda = 0) == pnorm(x)
all.equal(plgamma(x, lambda = -1), pgumbel(x)) ## TRUE, but:
plgamma(x, lambda = -1) == pgumbel(x)
plgamma(x, lambda = 1) == pgumbel(x, max = FALSE)

dlgamma(x, lambda = 0) == dnorm(x)
dlgamma(x, lambda = -1) == dgumbel(x)
dlgamma(x, lambda = 1) == dgumbel(x, max = FALSE)

glgamma(x, lambda = 0) == gnorm(x)
all.equal(glgamma(x, lambda = -1), ggumbel(x)) ## TRUE, but:
```
nominal_test

\[
\text{lgamma}(x, \lambda = -1) = \text{ggumbel}(x)
\]
\[
\text{all.equal(lgamma}(x, \lambda = 1), \text{ggumbel}(x, \text{max} = \text{FALSE})) \quad \# \text{TRUE, but:}
\]
\[
\text{lgamma}(x, \lambda = 1) = \text{ggumbel}(x, \text{max} = \text{FALSE})
\]
\[
\# \text{There is a loss of accuracy, but the difference is very small:}
\]
\[
\text{lgamma}(x, \lambda = 1) - \text{ggumbel}(x, \text{max} = \text{FALSE})
\]
\[
\# \text{More examples:}
\]
\[
x <- -5:5
\]
\[
\text{plgamma}(x, \lambda = .5)
\]
\[
\text{dlgamma}(x, \lambda = .5)
\]
\[
\text{glgamma}(x, \lambda = .5)
\]

nominal_test

Likelihood ratio tests of model terms in scale and nominal formulae

Description

Add all model terms to scale and nominal formulae and perform likelihood ratio tests. These tests can be viewed as goodness-of-fit tests. With the logit link, nominal_test provides likelihood ratio tests of the proportional odds assumption. The scale_test tests can be given a similar interpretation.

Usage

nominal_test(object, ...)

## S3 method for class 'clm'
nominal_test(object, scope, trace=FALSE, ...)

scale_test(object, ...)

## S3 method for class 'clm'
scale_test(object, scope, trace=FALSE, ...)

Arguments

object for the clm method an object of class "clm", i.e., the result of a call to clm.
scope a formula or character vector specifying the terms to add to scale or nominal. In nominal_test terms in scope already in nominal are ignored. In scale_test terms in scope already in scale are ignored. In nominal_test the default is to add all terms from formula (location part) and scale that are not also in nominal. In scale_test the default is to add all terms from formula (location part) that are not also in scale.
trace if TRUE additional information may be given on the fits as they are tried.
... arguments passed to or from other methods.
predict.clm

Predict Method for CLM fits

Description

Obtains predictions from a cumulative link model.

Details

The definition of AIC is only up to an additive constant because the likelihood function is only defined up to an additive constant.

Value

A table of class "anova" containing columns for the change in degrees of freedom, AIC, the likelihood ratio statistic and a p-value based on the asymptotic chi-square distribution of the likelihood ratio statistic under the null hypothesis.

Author(s)

Rune Haubo B Christensen

Examples

```r
## Fit cumulative link model:
fm <- clm(rating ~ temp + contact, data=wine)
summary(fm)
## test partial proportional odds assumption for temp and contact:
nominal_test(fm)
## no evidence of non-proportional odds.
## test if there are signs of scale effects:
scale_test(fm)
## no evidence of scale effects.

## tests of scale and nominal effects for the housing data from MASS:
if(require(MASS)) {
  fm1 <- clm(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
scale_test(fm1)
nominal_test(fm1)
  ## Evidence of multiplicative/scale effect of 'Cont'. This is a breach
  ## of the proportional odds assumption.
}
```
Usage

```r
## S3 method for class 'clm'
predict(object, newdata, se.fit = FALSE, interval = FALSE,
         level = 0.95,
         type = c("prob", "class", "cum.prob", "linear.predictor"),
         na.action = na.pass, ...)
```

Arguments

- **object**: a fitted object of class inheriting from `clm`.
- **newdata**: optionally, a data frame in which to look for variables with which to predict. Note that all predictor variables should be present having the same names as the variables used to fit the model. If the response variable is present in `newdata` predictions are obtained for the levels of the response as given by `newdata`. If the response variable is omitted from `newdata` predictions are obtained for all levels of the response variable for each of the rows of `newdata`.
- **se.fit**: should standard errors of the predictions be provided? Not applicable and ignored when `type = "class"`.
- **interval**: should confidence intervals for the predictions be provided? Not applicable and ignored when `type = "class"`.
- **level**: the confidence level.
- **type**: the type of predictions. "prob" gives probabilities, "class" gives predicted response class membership defined as highest probability prediction, "cum.prob" gives cumulative probabilities (see details) and "linear.predictor" gives predictions on the scale of the linear predictor including the boundary categories.
- **na.action**: function determining what should be done with missing values in `newdata`. The default is to predict NA.
- **...**: further arguments passed to or from other methods.

Details

If `newdata` is omitted and `type = "prob"` a vector of fitted probabilities are returned identical to the result from `fitted`.

If `newdata` is supplied and the response variable is omitted, then predictions, standard errors and intervals are matrices rather than vectors with the same number of rows as `newdata` and with one column for each response class. If `type = "class"` predictions are always a vector.

If `newdata` is omitted, the way missing values in the original fit are handled is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclude` they will appear (in predictions, standard errors or interval limits), with residual value NA. See also `napredict`.

If `type = "cum.prob"` or `type = "linear.predictor"` there will be two sets of predictions, standard errors and intervals; one for j and one for j-1 (in the usual notation) where j = 1, ..., J index the response classes.
If `newdata` is supplied and the response variable is omitted, then `predict.clm` returns much the same thing as `predict.polr` (matrices of predictions). Similarly, if `type = "class"`. If the fit is rank-deficient, some of the columns of the design matrix will have been dropped. Prediction from such a fit only makes sense if `newdata` is contained in the same subspace as the original data. That cannot be checked accurately, so a warning is issued (cf. `predict.lm`). If a flexible link function is used (Aranda-Ordaz or log-gamma) standard errors and confidence intervals of predictions do not take the uncertainty in the link-parameter into account.

Value

A list containing the following components

- `fit`: predictions or fitted values if `newdata` is not supplied.
- `se.fit`: if `se.fit=TRUE` standard errors of the predictions otherwise NULL.
- `upr, lwr`: if `interval=TRUE` lower and upper confidence limits.

Author(s)

Rune Haubo B Christensen

See Also

clm, clmm.

Examples

```r
## simple model:
fm1 <- clm(rating ~ contact + temp, data=wine)
summary(fm1)

## Fitted values with standard errors and confidence intervals:
predict(fm1, se.fit=TRUE, interval=TRUE) # type="prob"
## class predictions for the observations:
predict(fm1, type="class")

newData <- expand.grid(temp = c("cold", "warm"),
                        contact = c("no", "yes"))

## Predicted probabilities in all five response categories for each of
## the four cases in newData:
predict(fm1, newdata=newData, type="prob")
## now include standard errors and intervals:
predict(fm1, newdata=newData, se.fit=TRUE, interval=TRUE, type="prob")
```
Confidence intervals and profile likelihoods for the standard deviation for the random term in cumulative link mixed models

Description

Computes confidence intervals from the profiled likelihood for the standard deviation for the random term in a fitted cumulative link mixed model, or plots the associated profile likelihood function.

Usage

```r
## S3 method for class 'profile.clmm2'
confint(object, parm = seq_along(Pnames), level = 0.95, ...)
```

```r
## S3 method for class 'clmm2'
profile(fitted, alpha = 0.01, range, nSteps = 20, trace = 1, ...)
```

```r
## S3 method for class 'profile.clmm2'
plot(x, parm = seq_along(Pnames), level = c(0.95, 0.99),
     Log = FALSE, relative = TRUE, fig = TRUE, n = 1e3, ..., ylim = NULL)
```

Arguments

- `object` a fitted `profile.clmm2` object.
- `fitted` a fitted `clmm2` object.
- `x` a `profile.clmm2` object.
- `parm` For `confint.profile.clmm2`: a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered. Currently only "stDev" or 1 are supported.

For `plot.profile.clmm2`: a specification of which parameters the profile likelihood are to be plotted for, either a vector of numbers or a vector of names. If missing, all parameters are considered. Currently only "stDev" or 1 are supported.

- `level` the confidence level required. Observe that the model has to be profiled in the appropriate region; otherwise the limits are NA.

- `trace` logical. Should profiling be traced? Defaults to TRUE due to the time consuming nature of the computation.

- `alpha` Determines the range of profiling. By default the likelihood is profiled approximately in the 99% confidence interval region as determined by the Wald approximation. This is usually sufficient for 95% profile likelihood confidence limits.

- `range` if range is specified, this overrules the range computation based on alpha. range should be all positive and stDev is profiled in range(range).
**nSteps**
the number of points at which to profile the likelihood function. This determines
the resolution and accuracy of the profile likelihood function; higher values gives
a higher resolution, but also longer computation times.

**Log**
should the profile likelihood be plotted on the log-scale?

**Relative**
should the relative or the absolute likelihood be plotted?

**fig**
should the profile likelihood be plotted?

**n**
the no. points used in the spline interpolation of the profile likelihood for plot-
ting.

**ylim**
overrides default y-limits on the plot of the profile likelihood.

**...**
additional argument(s), e.g. graphical parameters for the plot method.

**Details**
A `confint.clmm2` method deliberately does not exist due to the time consuming nature of the
computations. The user is required to compute the profile object first and then call `confint` on the
profile object to obtain profile likelihood confidence intervals.

In `plot.profile.clm2`: at least one of `Log` and `relative` arguments have to be TRUE.

**Value**
confint: A matrix with columns giving lower and upper confidence limits. These will be labelled
as (1-level)/2 and 1 - (1-level)/2 in % (by default 2.5% and 97.5%).

`plot.profile.clm2` invisibly returns the profile object.

**Author(s)**
Rune Haubo B Christensen

**See Also**
`profile` and `confint`

**Examples**
```r
options(contrasts = c("contr.treatment", "contr.poly"))

if(require(lme4)) {  ## access cbpp data
  cbpp2 <- rbind(cbpp[,-(2:3)], cbpp[,-(2:3)])
  cbpp2 <- within(cbpp2, {
    incidence <- as.factor(rep(0:1, each=nrow(cbpp)))
    freq <- with(cbpp, c(incidence, size - incidence))
  })

  ## Fit with Laplace approximation:
  fm1 <- clmm2(incidence ~ period, random = herd, weights = freq,
                data = cbpp2, Hess = 1)
  pr.fm1 <- profile(fm1)
```
slice (pr.fm1)
confint(pr.fm1)
par(mfrow = c(2,2))
plot(pr.fm1)
plot(pr.fm1, Log=TRUE, relative = TRUE)
plot(pr.fm1, Log=TRUE, relative = FALSE)
}

slice  Slice the likelihood of a clm

Description
Slice likelihood and plot the slice. This is useful for illustrating the likelihood surface around the MLE (maximum likelihood estimate) and provides graphics to substantiate (non-)convergence of a model fit. Also, the closeness of a quadratic approximation to the log-likelihood function can be inspected for relevant parameters. A slice is considerably less computationally demanding than a profile.

Usage
slice(object, ...)

## S3 method for class 'clm'
slice(object, parm = seq_along(par), lambda = 3,
       grid = 100, quad.approx = TRUE, ...)

## S3 method for class 'slice.clm'
plot(x, parm = seq_along(x),
     type = c("quadratic", "linear"), plot.mle = TRUE,
     ask = prod(par("mfcol")) < length(parm) && dev.interactive(), ...)

Arguments
object  for the clm method an object of class "clm", i.e., the result of a call to clm.
x  a slice.clm object, i.e., the result of slice(clm.object).
parm  for slice.clm a numeric or character vector indexing parameters, for plot.slice.clm
only a numeric vector is accepted. By default all parameters are selected.
lambda  the number of curvature units on each side of the MLE the slice should cover.
grid  the number of values at which to compute the log-likelihood for each parameter.
quad.approx  compute and include the quadratic approximation to the log-likelihood function?
type  "quadratic" plots the log-likelihood function which is approximately quadratic, and "linear" plots the signed square root of the log-likelihood function which is approximately linear.
plot.mle

Include a vertical line at the MLE (maximum likelihood estimate) when type = "quadratic"? Ignored for type = "linear".

ask

Logical; if TRUE, the user is asked before each plot, see par(ask=.)

... further arguments to plot.default for the plot method. Not used in the slice method.

Value

The slice method returns a list of data.frames with one data.frame for each parameter slice. Each data.frame contains in the first column the values of the parameter and in the second column the values of the (positive) log-likelihood "logLik". A third column is present if quad.approx = TRUE and contains the corresponding quadratic approximation to the log-likelihood. The original model fit is included as the attribute "original.fit".

The plot method produces a plot of the likelihood slice for each parameter.

Author(s)

Rune Haubo B Christensen

Examples

```r
## fit model:
fm1 <- clm(rating ~ contact + temp, data = wine)
## slice the likelihood:
sl1 <- slice(fm1)

## three different ways to plot the slices:
par(mfrow = c(2,3))
plot(sl1)
plot(sl1, type = "quadratic", plot.mle = FALSE)
plot(sl1, type = "linear")

## Verify convergence to the optimum:
sl2 <- slice(fm1, lambda = 1e-5, quad.approx = FALSE)
plot(sl2)
```

soup

Discrimination study of packet soup

Description

The soup data frame has 1847 rows and 13 variables. 185 respondents participated in an A-not A discrimination test with sureness. Before experimentation the respondents were familiarized with the reference product and during experimentation, the respondents were asked to rate samples on an ordered scale with six categories given by combinations of (reference, not reference) and (sure, not sure, guess) from 'referene, sure' = 1 to 'not reference, sure' = 6.
VarCorr

Usage

soup

Format

RESP factor with 185 levels: the respondents in the study.
PROD factor with 2 levels: index reference and test products.
PRODID factor with 6 levels: index reference and the five test product variants.
SURENESS ordered factor with 6 levels: the respondents ratings of soup samples.
DAY factor with two levels: experimentation was split over two days.
SOUPTYPE factor with three levels: the type of soup regularly consumed by the respondent.
SOUPFREQ factor with 3 levels: the frequency with which the respondent consumes soup.
COLD factor with two levels: does the respondent have a cold?
EASY factor with ten levels: How easy did the respondent find the discrimination test? 1 = difficult, 10 = easy.
GENDER factor with two levels: gender of the respondent.
AGEGROUP factor with four levels: the age of the respondent.
LOCATION factor with three levels: three different locations where experimentation took place.

Source

Data are produced by Unilever Research. Permission to publish the data is granted.

References


| VarCorr | Extract variance and correlation parameters |

Description

The VarCorr function extracts the variance and (if present) correlation parameters for random effect terms in a cumulative link mixed model (CLMM) fitted with clmm.

Usage

```r
## S3 method for class 'clmm'
VarCorr(x, ...)
```
Arguments

x an \texttt{clmm} object.

Details

The \texttt{VarCorr} method returns a list of \texttt{data.frame}s; one for each distinct grouping factor. Each \texttt{data.frame} has as many rows as there are levels for that grouping factor and as many columns as there are random effects for each level. For example a model can contain a random intercept (one column) or a random intercept and a random slope (two columns) for the same grouping factor.

If conditional variances are requested, they are returned in the same structure as the conditional modes (random effect estimates/predictions).

Value

A list of matrices with variances in the diagonal and correlation parameters in the off-diagonal — one matrix for each random effects term in the model. Standard deviations are provided as attributes to the matrices.

Author(s)

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Examples

\begin{verbatim}
fm1 <- clmm(rating ~ contact + temp + (1|judge), data=wine)
VarCorr(fm1)
\end{verbatim}

Bitterness of wine

Description

The \textit{wine} data set is adopted from Randall(1989) and from a factorial experiment on factors determining the bitterness of wine. Two treatment factors (temperature and contact) each have two levels. Temperature and contact between juice and skins can be controlled when crushing grapes during wine production. Nine judges each assessed wine from two bottles from each of the four treatment conditions, hence there are 72 observations in all.

Usage

\begin{verbatim}
wine
\end{verbatim}
### Format

- **response**: scorings of wine bitterness on a 0—100 continuous scale.
- **rating**: ordered factor with 5 levels; a grouped version of **response**.
- **temp**: temperature: factor with two levels.
- **contact**: factor with two levels ("no" and "yes").
- **bottle**: factor with eight levels.
- **judge**: factor with nine levels.

### Source

Data are adopted from Randall (1989).

### References


### Examples

```r
head(wine)
str(wine)

## Variables 'rating' and 'response' are related in the following way:
(intervals <- seq(0,100, by = 20))
all(wine$rating == findInterval(wine$response, intervals)) ## ok

## A few illustrative tabulations:
## Table matching Table 5 in Randall (1989):
temp.contact.bottle <- with(wine, temp:contact:bottle)[drop=TRUE]
xtabs(response ~ temp.contact.bottle + judge, data = wine)

## Table matching Table 6 in Randall (1989):
with(wine, {
  tcb <- temp:contact:bottle
  tcb <- tcb[drop=TRUE]
table(tcb, rating)
})
## or simply: with(wine, table(bottle, rating))

## Table matching Table 1 in Tutz & Hennevogl (1996):
tab <- xtabs(as.numeric(rating) ~ judge + temp.contact.bottle, data = wine)
colnames(tab) <-
  paste(rep(c("c","w"), each = 4), rep(c("n","n","y","y"), 2),
    1:8, sep=".")
tab
```
## A simple model:
m1 <- clm(rating ~ temp * contact, data = wine)
summary(m1)
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