

Package ‘ordinal’

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Type Package

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Imports numDeriv

Depends R (>= 2.13.0), MASS, ucminf, Matrix,

Suggests lme4, nnet, xtable

Description This package implements 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). 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 | <i>Regression Models for Ordinal Data via Cumulative Link (Mixed) Models</i> |
|-----------------|--|

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
Version: 2011.08-11
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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 `c1m` 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 `c1mm` and the main features are:

- Any number of random effect terms can be included.
- The syntax for the model formula resembles that of `lmer`
- 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 are not yet implemented.
- Random slopes (random coefficient models) are not yet implemented.
- 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.

In addition to the reference manual several vignettes describe aspects of the package. Two brief tutorials on `clm` and `clmm` introduces the use of these functions. The Primer vignette is a 30-page introduction to cumulative link models.

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)

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Examples

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

## A simple cumulative link mixed model:
fmm1 <- clmm(rating ~ contact + temp + (1|judge), data=wine)
summary(fmm1)
```

addterm.clm2

Try all one-term additions to and deletions from a model

Description

Try fitting all models that differ from the current model by adding or deleting a single term from those supplied while maintaining marginality.

Usage

```
## S3 method for class 'clm2'
addterm(object, scope, scale = 0, test = c("none", "Chisq"),
        k = 2, sorted = FALSE, trace = FALSE,
        which = c("location", "scale"), ...)
## S3 method for class 'clm2'
dropterm(object, scope, scale = 0, test = c("none", "Chisq"),
```

```
k = 2, sorted = FALSE, trace = FALSE,
which = c("location", "scale"), ...)
```

Arguments

| | |
|--------|--|
| object | A <code>clm2</code> object. |
| scope | for <code>addterm</code> : a formula specifying a maximal model which should include the current one. All additional terms in the maximal model with all marginal terms in the original model are tried. For <code>dropterm</code> : a formula giving terms which might be dropped. By default, the model formula. Only terms that can be dropped and maintain marginality are actually tried. |
| scale | used in the definition of the AIC statistic for selecting the models. Specifying scale asserts that the dispersion is known. |
| test | should the results include a test statistic relative to the original model? The Chisq test is a likelihood-ratio test. |
| k | the multiple of the number of degrees of freedom used for the penalty. Only $k=2$ gives the genuine AIC: $k = \log(n)$ is sometimes referred to as BIC or SBC. |
| sorted | should the results be sorted on the value of AIC? |
| trace | if TRUE additional information may be given on the fits as they are tried. |
| which | should additions or deletions occur in location or scale models? |
| ... | arguments passed to or from other methods. |

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 and the likelihood ratio statistic. If `test = "Chisq"` a column also contains the p-value from the Chisq test.

Author(s)

Rune Haubo B Christensen

See Also

[clm2](#), [anova](#), [addterm.default](#) and [dropterm.default](#)

Examples

```
options(contrasts = c("contr.treatment", "contr.poly"))
data(soup)
mB1 <- clm2(SURENESS ~ PROD + GENDER + SOUPTYPE,
            scale = ~ COLD, data = soup, link = "probit",
```

```

      Hess = FALSE)
dropterm(mB1, test = "Chi")      # or
dropterm(mB1, which = "location", test = "Chi")
dropterm(mB1, which = "scale", test = "Chi")
addterm(mB1, scope = ~.^2, test = "Chi", which = "location")
addterm(mB1, scope = ~ . + GENDER + SOUPTYPE,
        test = "Chi", which = "scale")
addterm(mB1, scope = ~ . + AGEGROUP + SOUPFREQ,
        test = "Chi", which = "location")

## Fit model from polr example:
data(housing, package = "MASS")
fm1 <- clm2(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
addterm(fm1, ~ Infl + Type + Cont, test= "Chisq", which = "scale")
dropterm(fm1, test = "Chisq")

```

anova.clm2

Likelihood ratio test of cumulative link models

Description

Comparison of cumulative link models in likelihood ratio tests. The models may differ by terms in location, scale and nominal formulae, in link, threshold function and random effect structure.

Usage

```

## S3 method for class 'clm2'
anova(object, ..., test = c("Chisq", "none"))
## S3 method for class 'clmm2'
anova(object, ..., test = c("Chisq", "none"))

```

Arguments

| | |
|--------|---|
| object | a <code>clm2</code> object. |
| ... | one or more additional <code>clm2</code> objects. |
| test | if test = "none" the p-value for the likelihood ratio test is suppressed. |

Value

The method returns an object of class `Anova` (for printing) and `data.frame` with the following elements

| | |
|----------|---|
| Model | character description of the cumulative link models being compared. Location, scale and nominal formulae are separated by " "s in this order. |
| Resid.df | the residual degrees of freedom |
| -2logLik | twice the negative log likelihood (proportional to the deviance) |
| Test | indication of which models are being compared. |

| | |
|----------|--|
| DF | the difference in the degrees of freedom in the models being compared, i.e. the degrees of freedom for the chi-squared test. |
| LR stat. | the likelihood ratio statistic. |
| Pr(Chi) | the p-value from the likelihood ratio test. Absent if test = "none". |

Author(s)

Rune Haubo B Christensen

See Also

[clm2](#), [addterm](#), [dropterm](#) and [anova.default](#)

Examples

```
options(contrasts = c("contr.treatment", "contr.poly"))
data(soup)
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:
data(housing, package = "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"),
     threshold = c("flexible", "symmetric", "equidistant"), ...)
```

Arguments

| | |
|-----------|--|
| formula | a formula expression as for regression models, of the form <code>response ~ predictors</code> . 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 | an optional formula expression, of the form <code>~ predictors</code> , i.e. with an empty left hand side. An offset may be used. Variables included here will have multiplicative effects and can be interpreted as effects on the scale (or dispersion) of a latent distribution. |
| nominal | an optional formula of the form <code>~ predictors</code> , i.e. with an empty left hand side. The effects of the predictors in this formula are assumed to nominal - 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 formulas. |
| weights | optional case weights in fitting. Defaults to 1. |
| start | initial values for the parameters in the format <code>c(alpha, beta, zeta)</code> , where alpha are the threshold parameters (adjusted for 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 fit 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 <code>"logit"</code> link gives the proportional odds model. |
| threshold | specifies a potential structure for the thresholds (cut-points). <code>"flexible"</code> provides the standard unstructured thresholds, <code>"symmetric"</code> 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 <code>"equidistant"</code> restricts the distance between consecutive thresholds to be of the same size. |
| ... | additional arguments are passed on to clm.control . |

Details

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

There are methods for the standard model-fitting functions, including [summary](#), [anova](#), [model.frame](#), [model.matrix](#), [drop1](#), [dropterm](#), [step](#), [stepAIC](#), [extractAIC](#), [AIC](#), [coef](#), [nobs](#), [profile](#), [confint](#), [vcov](#) and [slice](#).

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 components listed below.

Note that some components are only present if `scale` and `nominal` are used.

| | |
|----------------------------|--|
| <code>alpha</code> | a vector of threshold parameters. |
| <code>beta</code> | a vector of regression parameters. |
| <code>zeta</code> | a vector of scale regression parameters. |
| <code>coefficients</code> | a vector of coefficients of the form <code>c(alpha, beta, zeta)</code> |
| <code>aliased</code> | list of length 3 or less with components <code>alpha</code> , <code>beta</code> and <code>zeta</code> each being logical vectors containing alias information for the parameters of the same names. |
| <code>start</code> | the parameter values at which the optimization has started. An attribute <code>start.iter</code> gives the number of iterations to obtain starting values for models where <code>scale</code> is specified or where the <code>cauchit</code> link is chosen. |
| <code>fitted.values</code> | the fitted probabilities. |
| <code>logLik</code> | the value of the log-likelihood at the estimated optimum. |
| <code>edf</code> | the estimated degrees of freedom, i.e., the number of parameters in the model fit. |
| <code>nobs</code> | the number of observations counted as <code>sum(weights)</code> . |
| <code>n</code> | the number of observations counted as <code>nrow(X)</code> , where <code>X</code> is the design matrix. |
| <code>gradient</code> | a vector of gradients for the coefficients at the estimated optimum. |
| <code>maxGradient</code> | the maximum absolute gradient, i.e., <code>max(abs(gradient))</code> . |
| <code>Hessian</code> | the Hessian matrix for the parameters at the estimated optimum. |
| <code>convergence</code> | convergence code where 0 indicates successful convergence, 1 indicates the iteration limit was reached before convergence and 2 indicates the step factor was reduced below minimum before convergence was reached. |
| <code>link</code> | character, the link function used. |
| <code>threshold</code> | character, the threshold structure used. |
| <code>call</code> | the mathed call. |
| <code>contrasts</code> | (where relevant) the contrasts used for the formula part of the model. |
| <code>S.contrasts</code> | (where relevant) the contrasts used for the scale part of the model. |
| <code>nom.contrasts</code> | (where relevant) the contrasts used for the nominal part of the model. |
| <code>terms</code> | the terms object for the formula part. |
| <code>S.terms</code> | (where relevant) the terms object for the scale part. |
| <code>nom.terms</code> | (where relevant) the terms object for the nominal part. |
| <code>xlevels</code> | (where relevant) a record of the levels of the factors used in fitting for the formula part. |
| <code>S.xlevels</code> | (where relevant) a record of the levels of the factors used in fitting for the scale part. |

| | |
|-------------|--|
| nom.xlevels | (where relevant) a record of the levels of the factors used in fitting for the nominal part. |
| tJac | the transpose of the Jacobian for the threshold structure. |
| y.levels | the levels of the response variable. |
| info | a table of basic model information for printing. |
| model | if requested (the default), the <code>model.frame</code> containing variables from formula, scale and nominal parts. |
| na.action | (where relevant) information returned by <code>model.frame</code> on the special handling of NAs. |

Note

Note that the number of iterations shown in the info table by `print` and `summary` methods can in some cases exceed the maximum number of iterations. This can happen because in a model where scale is specified, the iterations to obtain starting values are added to the main iterations.

Author(s)

Rune Haubo B Christensen

Examples

```
data(wine)
fm1 <- clm(rating ~ temp * contact, data = wine)
fm1 ## print method
summary(fm1)
fm2 <- update(fm1, ~.-temp:contact)
anova(fm1, fm2)

dropterm(fm1, test = "Chi")
drop1(fm1, test = "Chi")
add1(fm1, ~.+judge, test = "Chi")
addterm(fm1, ~.+judge, test = "Chi")

fm2 <- step(fm1)
summary(fm2)
fm3 <- stepAIC(fm1)
summary(fm3)

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'

## Example from MASS::polr:
data(housing, package = "MASS")
fm1 <- clm(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
summary(fm1)

## Another example:
data(soup, package = "ordinal")

fm.soup <- clm(SURENESS ~ PRODID, data = soup)
summary(fm.soup)

```

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", "ucminf", "nlminb",
  "optim"), ..., trace = 0,
  maxIter = 100, gradTol = 1e-06, maxLineIter = 15)
```

Arguments

| | |
|-------------|---|
| method | "Newton" fits the model by maximum likelihood and "model.frame" cause clm to return the model.frame. |
| 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-6. |
| maxLineIter | the maximum number of step halfings allowed if a Newton(-Raphson) step overshoots. Defaults to 10. |
| ... | 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

```
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,
  link = c("logit", "probit", "cloglog", "loglog", "cauchit"),
  threshold = c("flexible", "symmetric", "equidistant"))
```

Arguments

| | |
|-----------|---|
| y | 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 <code>clm.control</code> . |
| start | an optional list of starting values of the form <code>c(alpha, beta, zeta)</code> for the thresholds and nominal effects (alpha), regression parameters (beta) and scale parameters (zeta). |
| link | the link function. |
| threshold | the threshold structure, see further at <code>clm</code> . |

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.

In contrast to `clm`, `clm.fit` allows non-positive weights.

Value

A list with the following components:

| | |
|-------------|---|
| par | the maximum likelihood estimate of the model parameters on the form <code>c(alpha, beta, zeta)</code> for the thresholds and nominal effects (alpha), regression parameters (beta) and scale parameters (zeta). |
| gradient | gradient of the log-likelihood function for the parameters at the optimum. |
| Hessian | the Hessian of the parameters at the optimum. |
| logLik | the value of the log-likelihood function at the optimum. |
| convergence | a convergence code; 1: successful convergence, 2: iteration limit reached, 3: step factor reduced below minimum. |
| message | convergence message. |
| maxGradient | the maximum absolute gradient: <code>max(abs(gradient))</code> . |
| niter | depends on the optimizer. For the default Newton optimizer it is a vector of length 2: the number of iteration and the number of step halvings respectively. |
| fitted | the fitted values (probabilities). |
| coef.names | a list of vectors of names of the coefficients as inferred from the column names of the design matrices. |
| aliased | a list of logical vectors; TRUE is a parameter is not identified due to column rank deficiency in the design matrices and FALSE otherwise. |

Author(s)

Rune Haubo B Christensen

See Also[clm](#)**Examples**

```
## A simple example:
data(wine)
fm1 <- clm(rating ~ contact + temp, data=wine)
summary(fm1)
## get the model frame containing y and X:
mf1 <- update(fm1, method="model.frame")
clm.fit(mf1$y, mf1$X)
```

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

```
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 \sim 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 \sim 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 <code>c(alpha, beta, log(zeta), lambda)</code> . |
| 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 <code>Hess = TRUE</code> if you intend to call <code>summary</code> or <code>vcov</code> on the fit and <code>Hess = FALSE</code> in all other instances to save computing time. The argument is ignored if <code>method = "Newton"</code> where the Hessian is always computed and returned. Defaults to <code>TRUE</code> . |
| 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, <code>lambda</code> . The Aranda-Ordaz link (Aranda-Ordaz, 1983) equals the logistic link, when <code>lambda = 1</code> and approaches the loglog link when <code>lambda</code> approaches zero. The log-gamma link (Genter and Farewell, 1985) equals the loglog link when <code>lambda = 1</code> , the probit link when <code>lambda = 0</code> and the cloglog link when <code>lambda = -1</code> . |
| lambda | numerical scalar: the link function parameter. Used in combination with link Aranda-Ordaz or log-gamma and otherwise ignored. If <code>lambda</code> is specified, the model is estimated with <code>lambda</code> fixed at this value and otherwise <code>lambda</code> is estimated by ML. For Aranda-Ordaz <code>lambda</code> 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 <code>clm2.control</code> . |
| 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 <code>clm2.control</code> 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:

| | |
|----------------------------|--|
| <code>beta</code> | the parameter estimates of the location part. |
| <code>zeta</code> | the parameter estimates of the scale part on the log scale; the scale parameter estimates on the original scale are given by <code>exp(zeta)</code> . |
| <code>Alpha</code> | vector or matrix of the threshold parameters. |
| <code>Theta</code> | vector or matrix of the thresholds. |
| <code>xi</code> | vector of threshold parameters, which, given a threshold function (e.g. "equidistant"), and possible nominal effects define the class boundaries, <code>Theta</code> . |
| <code>lambda</code> | the value of <code>lambda</code> if <code>lambda</code> is supplied or estimated, otherwise missing. |
| <code>coefficients</code> | the coefficients of the intercepts (<code>theta</code>), the location (<code>beta</code>), the scale (<code>zeta</code>), and the link function parameter (<code>lambda</code>). |
| <code>df.residual</code> | the number of residual degrees of freedoms, calculated using the weights. |
| <code>fitted.values</code> | 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. |
| <code>convergence</code> | TRUE if the gradient based convergence criterion is met and FALSE otherwise. |
| <code>gradient</code> | vector of gradients for all the parameters at termination of the optimizer. |
| <code>optRes</code> | list with results from the optimizer. The contents of the list depends on the choice of optimizer. |
| <code>logLik</code> | the log likelihood of the model at optimizer termination. |
| <code>Hessian</code> | if the model was fitted with <code>Hess = TRUE</code> , this is the Hessian matrix of the parameters at the optimum. |
| <code>scale</code> | <code>model.frame</code> for the scale model. |
| <code>location</code> | <code>model.frame</code> for the location model. |
| <code>nominal</code> | <code>model.frame</code> 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

- Agresti, A. (2002) *Categorical Data Analysis*. Second edition. Wiley.
- Aranda-Ordaz, F. J. (1983) An Extension of the Proportional-Hazards Model for Grouped Data. *Biometrics*, 39, 109-117.
- Genter, F. C. and Farewell, V. T. (1985) Goodness-of-link testing in ordinal regression models. *The Canadian Journal of Statistics*, 13(1), 37-44.
- Christensen, R. H. B., Cleaver, G. and Brockhoff, P. B. (2011) Statistical and Thurstonian models for the A-not A protocol with and without sureness. *Food Quality and Preference*, 22, pp. 542-549.

Examples

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

## More manageable 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 = "nlnmb")
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:
data(housing, package = "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:
library(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. <code>model.frame</code> 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 overshoots. 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

Usage

```
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", "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 <code>c(alpha, beta, tau)</code> , 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 <code>Hess = TRUE</code> if you intend to call <code>summary</code> or <code>vcov</code> on the fit and <code>Hess = FALSE</code> 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 <code>"logit"</code> 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 <code>c1mm.control</code> |
| 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). <code>"flexible"</code> provides the standard unstructured thresholds, <code>"symmetric"</code> 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 <code>"equidistant"</code> restricts the distance between consecutive thresholds to the same value. |
| ... | additional arguments are passed on to <code>c1m.control</code> . |

Details

This is a new (as of August 2011) improved implementation of CLMMs. The old implementation is available in `c1mm2`. Some features are not yet available in `c1mm`; for instance quadrature methods, scale effects, nominal effects and flexible link functions are currently only available in `c1mm2`. `c1mm` is expected to take over `c1mm2` at some point.

There are standard print, summary and anova methods implemented for `"c1mm"` objects.

Value

a list containing

alpha threshold parameters.

| | |
|---------------|---|
| beta | fixed effect regression parameters. |
| stDev | standard deviation of the random effect terms. |
| tau | $\log(\text{stDev})$ - the scale at which the log-likelihood function is optimized. |
| coefficients | the estimated model parameters = $c(\text{alpha}, \text{beta}, \text{tau})$. |
| Hessian | Hessian of the model coefficients. |
| edf | the estimated degrees of freedom used by the model = $\text{length}(\text{coefficients})$. |
| nobs | $\text{sum}(\text{weights})$. |
| n | $\text{length}(y)$. |
| fitted.values | fitted values evaluated with the random effects at their conditional modes. |
| df.residual | residual degrees of freedom; $\text{length}(y) - \text{sum}(\text{weights})$ |
| 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

```
## Get test data:
data(soup)

## 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)
```

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

Description

Set control parameters for cumulative link mixed models

Usage

```
clmm.control(method = c("ucminf", "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 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 halflings allowed if a Newton(-Raphson) step overshoots during the inner optimization. |
| innerCtrl | the use of warnings/errors if the inner optimization fails to converge. |

Value

a list of control parameters

Author(s)

Rune Haubo B Christensen

See Also

[clmm](#)

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 <code>clm2</code> . |
| scale | as in <code>clm2</code> . |
| nominal | as in <code>clm2</code> . |
| random | a factor for the random effects in the location-part of the model. |
| data | as in <code>clm2</code> . |
| weights | as in <code>clm2</code> . |
| start | initial values for the parameters in the format <code>c(alpha, beta, log(zeta), lambda, log(stDev))</code> where <code>stDev</code> is the standard deviation of the random effects. |
| subset | as in <code>clm2</code> . |
| na.action | as in <code>clm2</code> . |
| contrasts | as in <code>clm2</code> . |
| Hess | logical for whether the Hessian (the inverse of the observed information matrix) should be computed. Use <code>Hess = TRUE</code> if you intend to call <code>summary</code> or <code>vcov</code> on the fit and <code>Hess = FALSE</code> in all other instances to save computing time. |
| model | as in <code>clm2</code> . |
| sdFixed | If <code>sdFixed</code> is specified (a positive scalar), a model is fitted where the standard deviation for the random term is fixed at the value of <code>sdFixed</code> . If <code>sdFixed</code> is left unspecified, the standard deviation of the random term is estimated from data. |
| link | as in <code>clm2</code> . |

| | |
|-----------|---|
| lambda | as in clm2 . |
| doFit | as in clm2 although it can also be one of <code>c("no", "R" "C")</code> , 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. |
| ... | 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](#), [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. [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 [clm2](#) to up an environment and to get starting values.

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 "clmm2" with the following components:

| | |
|---------|---|
| stDev | the standard deviation of the random effects. |
| Niter | the total number of iterations in the Newton updates of the conditional modes of the random effects. |
| grFac | the grouping factor defining the random effects. |
| nAGQ | the number of quadrature points used in the adaptive Gauss-Hermite Quadrature approximation to the marginal likelihood. |
| ranef | the conditional modes of the random effects, sometimes referred to as "random effect estimates". |
| condVar | the conditional variances of the random effects at their conditional modes. |
| 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 <code>exp(zeta)</code> . |

| | |
|---------------|--|
| 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 conditional on the values of the random effects. Use 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. |
| convergence | TRUE if the optimizer terminates without error and FALSE otherwise. |
| gradient | vector of gradients for the unit-variance random effects at their conditional modes. |
| 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. |
| 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

Agresti, A. (2002) *Categorical Data Analysis*. Second edition. Wiley.

Examples

```

options(contrasts = c("contr.treatment", "contr.poly"))
data(soup)

## More manageable data set:
dat <- subset(soup, as.numeric(as.character(RESPI)) <= 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 data from the lme4-package:
data(cbpp, package = "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 the adaptive Gauss-Hermite quadrature approximation:
fm2 <- clmm2(incidence ~ period, random = herd, weights = freq,
            data = cbpp2, Hess = 1, nAGQ = 7)
summary(fm2)

```

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. |
| maxLineIter | the maximum number of step halvings allowed if a Newton(-Raphson) step overshoots 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 optimizer's 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](#)

| | |
|---------|--|
| confint | <i>Confidence intervals and profile likelihoods for parameters in cumulative link models</i> |
|---------|--|

Description

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

Usage

```
## 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 = TRUE, approx = root, n = 1e3,
     ask = prod(par("mfcol")) < length(which.par) && dev.interactive(),
     ..., ylim = NULL)
```

Arguments

| | |
|---|--|
| object, fitted, x | a fitted <code>clm</code> object or a <code>profile.clm</code> 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 <code>confint.clm</code> 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? |

| | |
|------------------------|--|
| <code>relative</code> | should the relative or the absolute likelihood be plotted? |
| <code>root</code> | should the (approximately linear) likelihood root statistic be plotted? |
| <code>approx</code> | should the Gaussian or quadratic approximation to the (log) likelihood be included? |
| <code>fig</code> | should the profile likelihood be plotted? |
| <code>ask</code> | logical; if TRUE, the user is asked before each plot, see <code>par(ask=.)</code> . |
| <code>n</code> | the no. points used in the spline interpolation of the profile likelihood. |
| <code>ylim</code> | overrides default y-limits on the plot of the profile likelihood. |
| <code>alpha</code> | The likelihood is profiled in the $100*(1-\alpha)\%$ confidence region as determined by the profile likelihood. |
| <code>control</code> | a list of control parameters for <code>clm</code> . Possibly use <code>clm.control</code> to set these. |
| <code>max.steps</code> | the maximum number of profiling steps in each direction for each parameter. |
| <code>nsteps</code> | 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 <code>nsteps</code> , but will deviate when the log-likelihood functions is irregular. |
| <code>step.warn</code> | a warning is issued if the number of steps in each direction (up or down) for a parameter is less than <code>step.warn</code> . If few steps are taken, the profile will be unreliable and derived confidence intervals will be inaccurate. |
| <code>...</code> | 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 $(1-\text{level})/2$ and $1 - (1-\text{level})/2$ 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

```

data(wine)
fm1 <- clm(rating ~ temp * contact, data = wine)

## Accurate profile likelihood confidence intervals compared to the
## conventional Wald intervals:
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:
data(housing, package = "MASS")
fm1 <- clm(Sat ~ Infl + Type + Cont, weights = Freq,
  data = housing)

pr1 <- profile(fm1)
confint(pr1)
par(mfrow=c(2,2))
plot(pr1)

```

confint.clm2

Confidence intervals and profile likelihoods for parameters in cumulative link models

Description

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

Usage

```
## S3 method for class 'clm2'
confint(object, parm, level = 0.95, whichL = seq_len(p),
        whichS = seq_len(k), lambda = TRUE, trace = 0, ...)

## S3 method for class 'profile.clm2'
confint(object, parm = seq_along(Pnames), level = 0.95, ...)

## S3 method for class 'clm2'
profile(fitted, whichL = seq_len(p), whichS = seq_len(k),
        lambda = TRUE, alpha = 0.01, maxSteps = 50, delta = LrootMax/10,
        trace = 0, stepWarn = 8, ...)

## S3 method for class 'profile.clm2'
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 <code>clm2</code> object or a <code>profile.clm2</code> object. |
| fitted | a fitted <code>clm2</code> object. |
| x | a <code>profile.clm2</code> object. |
| parm | not used in <code>confint.clm2</code> . For <code>confint.profile.clm2</code> : 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. For <code>plot.profile.clm2</code> : 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. |
| level | the confidence level required. |
| whichL | a specification of which <i>location</i> parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all location parameters are considered. |
| whichS | a specification of which <i>scale</i> parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all scale parameters are considered. |
| lambda | logical. Should profile or confidence intervals be computed for the link function parameter? Only used when one of the flexible link functions are used; see the link-argument in <code>clm2</code> . |
| trace | logical. Should profiling be traced? |
| alpha | Determines the range of profiling. By default the likelihood is profiled in the 99% confidence interval region as determined by the profile likelihood. |
| maxSteps | the maximum number of profiling steps in each direction (up and down) for each parameter. |

| | |
|----------|--|
| delta | the length of profiling steps. To some extent this parameter determines the degree of accuracy of the profile likelihood in that smaller values, i.e. smaller steps gives a higher accuracy. Note however that a spline interpolation is used when constructing confidence intervals so fairly long steps can provide high accuracy. |
| stepWarn | a warning is issued if the no. steps in each direction (up or down) for a parameter is less than stepWarn (defaults to 8 steps) because this indicates an unreliable profile. |
| 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. |
| ylim | overrides default y-limits on the plot of the profile likelihood. |
| ... | additional argument(s) for methods including range (for the hidden function profileLambda) that sets the range of values of lambda at which the likelihood should be profiled for this parameter. |

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.

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

Value

confint: A matrix (or vector) 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%). The parameter names are preceded with "loc." or "sca." to indicate whether the confidence interval applies to a location or a scale parameter.

plot.profile.clm2 invisibly returns the profile object.

Author(s)

Rune Haubo B Christensen

See Also

[profile](#) and [confint](#)

Examples

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

## More manageable 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")

## profile
pr1 <- profile(m1)
par(mfrow = c(2, 2))
plot(pr1)

m9 <- update(m1, link = "log-gamma")
pr9 <- profile(m9, whichL = numeric(0), whichS = numeric(0))
par(mfrow = c(1, 1))
plot(pr9)

plot(pr9, Log=TRUE, relative = TRUE)
plot(pr9, Log=TRUE, relative = TRUE, ylim = c(-4, 0))
plot(pr9, Log=TRUE, relative = FALSE)

## confint
confint(pr9)
confint(pr1)

## Extend example from polr in package MASS:
## Fit model from polr example:
data(housing, package = "MASS")
fm1 <- clm2(Sat ~ Inf1 + Type + Cont, scale = ~ Cont, weights = Freq,
            data = housing)

pr1 <- profile(fm1)
confint(pr1)
par(mfrow=c(2,2))
plot(pr1)

```

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 `clm`.

Usage

```
convergence(object, ...)
```

```
## S3 method for class 'clm'
```

```
convergence(object, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

| | |
|---------------------|---|
| <code>object</code> | for the <code>clm</code> method an object of class " <code>clm</code> ", i.e., the result of a call to <code>clm</code> . |
| <code>digits</code> | the number of digits in the printed table. |
| <code>...</code> | arguments to a from methods. Not used by the <code>clm</code> 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

Elden, L., Wittmeyer-Koch, L. and Nielsen, H. B. (2004) *Introduction to Numerical Computation — analysis and Matlab illustrations*. Studentlitteratur.

Examples

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

`drop.coef`*Insure Full Rank Design Matrix*

Description

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

Usage

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

Arguments

| | |
|---------------------|---|
| <code>X</code> | a design matrix, e.g., the result of <code>model.matrix</code> possibly of less than full column rank, i.e., with redundant parameters. Works for <code>ncol(X) >= 0</code> and <code>nrow(X) >= 0</code> . |
| <code>silent</code> | 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

```
data(soup, package = "ordinal")
X <- model.matrix(~ PRODIG * 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

```
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

$$f'(x) = 2 \exp(-x)^2 (1 + \exp(-x))^{-3} - \exp(-x) (1 + \exp(-x))^{-2}$$

- pcauchy: If $f(x) = [\pi(1 + x^2)]^{-1}$ is the cauchy density with mean 0 and scale 1, then the gradient is

$$f'(x) = -2x[\pi(1 + x^2)]^{-1}$$

These gradients are used in the Newton-Raphson algorithms in fitting cumulative link models with [clm](#) and cumulative link mixed models with [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 ([gumbel](#)) and the the log-gamma distribution ([log-gamma](#)).

Examples

```
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

```
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.

See the 'Primer' vignette for the definition of the Gumbel distribution and its relation to the log-log and complementary-log-log link used in cumulative link models. See the examples for numerical relations between the max and min variants.

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

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

```
## 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

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

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

```
(ppp <- pgumbel(x, max=FALSE))
## Observe lack of precision:
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

Description

Income distribution (percentages) in the Northeast US in 1960 and 1970 adopted from McCullagh (1980).

Usage

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

McCullagh, P. (1980) Regression Models for Ordinal Data. *Journal of the Royal Statistical Society. Series B (Methodological)*, Vol. 42, No. 2., pp. 109-142.

Examples

```

data(income)

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, λ . For $\lambda = 0$ the distribution equals the normal or Gaussian distribution, and for λ 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)

```

```
glgamma(x, lambda)
```

Arguments

| | |
|-------------------------|---|
| <code>x, q</code> | numeric vector of quantiles. |
| <code>lambda</code> | numerical scalar |
| <code>lower.tail</code> | logical; if TRUE (default), probabilities are $P[X \leq x]$ otherwise, $P[X > x]$. |
| <code>log</code> | 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.

The log-gamma distribution function is defined as . . . pending.

The density and gradient of the density are defined as . . . pending.

These distribution functions, densities and gradients are used in the Newton-Raphson algorithms in fitting cumulative link models with `c1m2` and cumulative link mixed models with `c1mm2` using the log-gamma link.

Value

`plgamma` gives the distribution function, `dlgamma` gives the density and `glgamma` gives the gradient of the density.

Author(s)

Rune Haubo B Christensen

References

Genter, F. C. and Farewell, V. T. (1985) Goodness-of-link testing in ordinal regression models. *The Canadian Journal of Statistics*, 13(1), 37-44.

See Also

Gradients of densities are also implemented for the normal, logistic, cauchy, cf. `gfun` and the Gumbel distribution, cf. `gumbel`.

Examples

```
## 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:
glgamma(x, lambda = -1) == ggumbel(x)
all.equal(glgamma(x, lambda = 1), ggumbel(x, max = FALSE)) ## TRUE, but:
glgamma(x, lambda = 1) == ggumbel(x, max = FALSE)
## There is a loss of accuracy, but the difference is very small:
glgamma(x, lambda = 1) - ggumbel(x, max = FALSE)

## More examples:
x <- -5:5
plgamma(x, lambda = .5)
dlgamma(x, lambda = .5)
glgamma(x, lambda = .5)

```

predict.clm

Predict Method for CLM fits

Description

Obtains predictions from a cumulative link model.

Usage

```

## 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. |
| 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 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 predictions are based on the data used for the fit. In that case, 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.

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](#)).

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

```
## simple model:
data(wine)
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")
```

predict.clm2

Predict Method for CLM fits

Description

Obtains predictions from a cumulative link (mixed) model.

Usage

```
## S3 method for class 'clm2'
predict(object, newdata, ...)
```

Arguments

| | |
|---------|---|
| object | a fitted object of class inheriting from clm2 including clmm2 objects. |
| newdata | optionally, a data frame in which to look for variables with which to predict. Observe that the response variable should also be present. |
| ... | further arguments passed to or from other methods. |

Details

This method does not duplicate the behavior of `predict.polr` in package MASS which produces a matrix instead of a vector of predictions. The behavior of `predict.polr` can be mimiced as shown in the examples.

If `newdata` is not supplied, the fitted values are obtained. For `clmm2` fits this means predictions that are controlled for the observed value of the random effects. If the predictions for a random effect of zero, i.e. an average 'subject', are wanted, the same data used to fit the model should be supplied in the `newdata` argument. For `clm2` fits those two sets of predictions are identical.

Value

A vector of predicted probabilities.

Author(s)

Rune Haubo B Christensen

See Also

[clm2](#), [clmm2](#).

Examples

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

## More manageable data set for less voluminous printing:
(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))
dat26

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

mN1 <- clm2(sureness ~ 1, nominal = ~prod, data = dat26,
           weights = wghts)
predict(mN1)

predict(update(m1, scale = ~.-prod))

## Fit model from polr example:
data(housing, package = "MASS")
fm1 <- clm2(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
predict(fm1)

#####
## Mimicing the behavior of predict.polr:
set.seed(123)
```

```

nlev <- 3
y <- gl(nlev, 5)
x <- as.numeric(y) + rnorm(15)
fm.clm <- clm2(y ~ x)
fm.polr <- polr(y ~ x)

## The equivalent of predict.polr(object, type = "probs"):
(pmat.polr <- predict(fm.polr, type = "probs"))
ndat <- expand.grid(y = gl(nlev,1), x = x)
(pmat.clm <- matrix(predict(fm.clm, newdata = ndat), ncol=nlev,
                    byrow = TRUE))
all.equal(c(pmat.clm), c(pmat.polr), tol = 1e-5) # TRUE

## The equivalent of predict.polr(object, type = "class"):
(class.polr <- predict(fm.polr))
(class.clm <- factor(apply(pmat.clm, 1, which.max)))
all.equal(class.clm, class.polr) ## TRUE

```

profile.clmm2

*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

```

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

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

## 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 <code>confint.profile.clmm2</code> : 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 <code>plot.profile.clmm2</code> : 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 plotting. |
| ylim | overrules 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

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

data(cbpp, package = "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)

pr.fm1 <- profile(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 <code>clm</code> method an object of class "clm", i.e., the result of a call to <code>clm</code> . |
| x | a <code>slice.clm</code> object, i.e., the result of <code>slice(clm.object)</code> . |
| parm | for <code>slice.clm</code> a numeric or character vector indexing parameters, for <code>plot.slice.clm</code> 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 <code>type = "quadratic"</code> ? Ignored for <code>type = "linear"</code> . |
| ask | logical; if TRUE, the user is asked before each plot, see <code>par(ask=.)</code> . |
| ... | further arguments to <code>plot.default</code> 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

```
## get data:
data(wine)
## fit model:
fm1 <- clm(rating ~ contact + temp, data = wine)
## slice the likelihood:
s11 <- slice(fm1)

## three different ways to plot the slices:
par(mfrow = c(2,3))
```

```
plot(s11)
plot(s11, type = "quadratic", plot.mle = FALSE)
plot(s11, type = "linear")

## Verify convergence to the optimum:
s12 <- slice(fm1, lambda = 1e-5, quad.approx = FALSE)
plot(s12)
```

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 'reference, sure' = 1 to 'not reference, sure' = 6.

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

Christensen, R. H. B., Cleaver, G. and Brockhoff, P. B.(2011) Statistical and Thurstonian models for the A-not A protocol with and without sureness. *Food Quality and Preference*, 22, pp. 542-549.

update.clm2

Update method for cumulative link models

Description

Update method for cumulative link models fitted with `clm2`. This makes it possible to use e.g. `update(obj, location = ~ . - var1, scale = ~ . + var2)`

Usage

```
## S3 method for class 'clm2'
update(object, formula., location, scale, nominal,...,
       evaluate = TRUE)
## S3 method for class 'clmm2'
update(object, formula., location, scale, nominal,...,
       evaluate = TRUE)
```

Arguments

| | |
|-----------------------|--|
| <code>object</code> | a <code>clm2</code> object. |
| <code>formula.</code> | not used—unfortunately this argument is part of the default method. |
| <code>location</code> | an optional new formula for the location; see update.formula for details. |
| <code>scale</code> | an optional new formula for the scale; see update.formula for details. |
| <code>nominal</code> | an optional new formula for nominal effects; see update.formula for details. |
| <code>...</code> | additional arguments to the call, or arguments with changed values. |
| <code>evaluate</code> | if true evaluate the new call else return the call. |

Value

If `evaluate = TRUE` the fitted object is returned, otherwise the updated call.

Author(s)

Rune Haubo B Christensen

Examples

```

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

m2 <- update(m1, link = "probit")
m3 <- update(m1, link = "cloglog")
m4 <- update(m1, link = "loglog")
anova(m1, update(m1, scale = ~.-PROD))
mT1 <- update(m1, threshold = "symmetric")

## Fit model from polr example:
data(housing, package = "MASS")
fm1 <- clm2(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
update(fm1, location = ~ . - Type, scale = ~ Cont)

```

 wine

Bitterness of wine

Description

The 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

```
wine
```

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

- Randall, J (1989). The analysis of sensory data by generalised linear model. *Biometrical journal* 7, pp. 781–793.
- Tutz, G. and W. Hennevogl (1996). Random effects in ordinal regression models. *Computational Statistics & Data Analysis* 22, pp. 537–557.

Examples

```
data(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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