

# A Primer on Cumulative Link Models with the `ordinal2` Package

Rune Haubo B Christensen

April 27, 2011

## **Abstract**

In this primer cumulative link models are introduced using the `ordinal2` package. This is work in progress.

# Contents

<b>1</b>	<b>Introduction</b>	<b>3</b>
<b>2</b>	<b>Cumulative link models</b>	<b>4</b>
2.1	Fitting cumulative link models with <code>clm</code> from package <code>ordinal2</code> . . . . .	5
2.2	Odds ratios and proportional odds . . . . .	7
2.3	Link functions . . . . .	8
2.4	Maximum likelihood estimation of cumulative link models . . . . .	10
2.5	Deviance and model comparison . . . . .	11
2.5.1	Model comparison with likelihood ratio tests . . . . .	11
2.5.2	Deviance and ANODE tables . . . . .	12
2.5.3	Goodness of fit tests with the deviance . . . . .	13
2.6	Latent variable motivation for cumulative link models . . . . .	14
2.6.1	More on parameter interpretation . . . . .	16
<b>3</b>	<b>Assessing the likelihood and model convergence</b>	<b>19</b>
<b>4</b>	<b>Confidence intervals and profile likelihood</b>	<b>21</b>
4.1	Model selection . . . . .	22
4.2	Structured thresholds . . . . .	23
4.3	Predictions . . . . .	23
<b>5</b>	<b>Miscellaneous</b>	<b>23</b>

# 1 Introduction

Ordered categorical data, or simply *ordinal* data, are commonplace in scientific disciplines where humans are used as measurement instruments. Examples include school gradings, ratings of preference in consumer studies, degree of tumor involvement in MR images and animal fitness in field ecology. Cumulative link models are a powerful model class for such data since observations are treated rightfully as categorical, the ordered nature is exploited and the flexible regression framework allows in-depth analyses.

The name *cumulative link models* is adopted from Agresti (2002), but the models are also known as *ordinal regression models* although that term is sometimes also used for other regression models for ordinal responses such as *continuation ratio models* (see e.g., Agresti, 2002). Other aliases are *ordered logit models* and *ordered probit models* (Greene and Hensher, 2010) for the logit and probit link functions. Further, the cumulative link model with a logit link is widely known as the *proportional odds model* due to McCullagh (1980), also with a log-log link<sup>1</sup>, the model is known as *proportional hazards model* for grouped survival times.

Ordinal response variables can be analyzed with omnibus Pearson  $\chi^2$  tests, base-line logit models or log-linear models. This corresponds to assuming that the response variable is nominal and information about the ordering of the categories will be ignored. Alternatively numbers can be attached to the response categories, e.g.,  $1, 2, \dots, J$  and the resulting scores can be analyzed by conventional linear regression and ANOVA models. This approach is in a sense over-confident since the data are assumed to contain more information than they actually do. Observations on an ordinal scale are classified in ordered categories, but the distance between the categories is generally unknown. By using linear models the choice of scoring impose assumptions about the distance between the response categories. Further, standard errors and tests from linear models rest on the assumption that the response, conditional on the explanatory variables, is normally distributed (equivalently the residuals are assumed to be normally distributed). This cannot be the case since the scores are discrete and responses beyond the end categories are not possible. If there are many responses in the end categories, there will most likely be variance heterogeneity to which  $F$  and  $t$  tests can be rather sensitive. If there are many response categories and the response does not pile up in the end categories, we may expect tests from linear models to be accurate enough, but any bias and optimism is hard to quantify.

Cumulative link models provide the regression framework familiar from linear models while treating the response rightfully as categorical. While cumulative link models are not the only type of ordinal regression model, they are by far the most popular class of ordinal regression models.

Common to the application of methods for nominal responses and linear models to ordinal responses is that interpretation of effects on the ordinal response scale is awkward. For example, linear models will eventually give predictions outside the possible range and statements such as “the response increase 1.2 units with each degree increase in temperature” will only be approximately valid in a restricted range of the response variable.

In this document cumulative link models are described for modeling ordinal response variables and the `ordinal2` package is introduced. Our focus will be ...

**Example 1 (The wine data):** As an example of the data set with an ordinal response variable consider the wine data from Randall (1989) available in the object `wine` in package `ordinal2`, cf.

---

<sup>1</sup>or is it the complementary log-log link?

Table 1: Wine data from Randall (1989).

Temperature	Contact	Least—Most bitter				
		1	2	3	4	5
cold	no	4	9	5	0	0
cold	yes	1	7	8	2	0
warm	no	0	5	8	3	2
warm	yes	0	1	5	7	5

Table 1. The data represent a factorial experiment on factors determining the bitterness of wine with 1 = “least bitter” and 5 = “most bitter”. Two treatment factors (temperature and contact) each have two levels. Temperature and contact between juice and skins can be controlled when cruching 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. In table X we have aggregated data over bottles and judges for simplicity, but these variables will be considered later. Initially we only assume that, say, category 4 is larger than 3, but not that the distance between 2 and 3 is half the distance between 2 and 4, for example. The main objective is to examine the effect of contact and temperature on the perceived bitterness of wine.  $\square$

## 2 Cumulative link models

A cumulative link model is a model for an ordinal response variable,  $Y_i$  that can fall in  $j = 1, \dots, J$  categories.<sup>2</sup> Then  $Y_i$  follows a multinomial distribution with parameter  $\boldsymbol{\pi}$  where  $\pi_{ij}$  denote the probability that the  $i$ th observation falls in response category  $j$ . We define the cumulative probabilities as<sup>3</sup>

$$\gamma_{ij} = P(Y_i \leq j) = \pi_{i1} + \dots + \pi_{ij} . \quad (1)$$

Initially we will consider the logit link. The logit function is defined as  $\text{logit}(\pi) = \log[\pi/(1 - \pi)]$  and cumulative logits are defined as:

$$\text{logit}(\gamma_{ij}) = \text{logit}(P(Y_i \leq j)) = \log \frac{P(Y_i \leq j)}{1 - P(Y_i \leq j)} \quad j = 1, \dots, J - 1 \quad (2)$$

so that the cumulative logits are defined for all but the last category.<sup>4</sup>

**Example 2:** For fixed  $j$  the cumulative logit model (3) is just a logistic regression model where the binomial response is divided into those observations falling in category  $j$  or less, and those falling in a higher category than  $j$ . This is a valid analysis approach, but it does not use all the information in the data and the (arbitrary) choice of  $j$  also needs to be made. To improve on this we could make all the ordinary logistic regressions for  $j = 1, \dots, J - 1$ , but it is not easy to draw inference from a collection of models and it would be nice if a plausible data generating mechanism could be summarized in a single model. This is also likely to increase the power of hypothesis tests for the parameters. The cumulative logit model is exactly the model that combines all these ordinary logistic regressions into one. If the cumulative model is correct, the

<sup>2</sup>where  $J \geq 2$ . If  $J = 2$  binomial models also apply, and in fact the cumulative link model is in this situation identical to a generalized linear model for a binomial response.

<sup>3</sup>we have suppressed the conditioning on the covariate vector,  $\mathbf{x}_i$ , so we have that  $\gamma_{ij} = \gamma_j(\mathbf{x}_i)$  and  $P(Y_i \leq j) = P(Y \leq j|\mathbf{x}_i)$ .

<sup>4</sup>since for  $j = J$  the denominator would be  $1 - P(Y_i \leq J) = 1 - 1 = 0$  and thus the fraction is not defined.

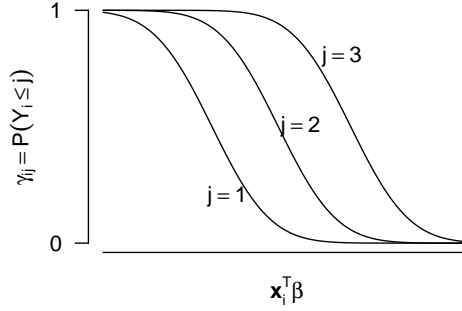


Figure 1: Illustration of a cumulative link model with four response categories.

regression parameter estimates from the individual logistic regression models will be similar and approximately identical to the regression parameter estimates from the cumulative probit model. Thus the cumulative link model saves the estimation of  $J - 2$  sets of  $\boldsymbol{\beta}$ —this is where the power gain comes from. Further, we also expect the intercept parameter estimates from the logistic regression models to be approximately the same as estimates of  $\{\theta_j\}$  from the cumulative link model.  $\square$

A cumulative link model with a logit link, or simply *cumulative logit model* is a regression model for cumulative logits:

$$\text{logit}(\gamma_{ij}) = \theta_j - \mathbf{x}_i^T \boldsymbol{\beta} \quad (3)$$

where  $\mathbf{x}_i$  is a vector of explanatory variables for the  $i$ th observation and  $\boldsymbol{\beta}$  is the corresponding set of regression parameters. The  $\{\theta_j\}$  parameters provide each cumulative logit (for each  $j$ ) with its own intercept. A key point is that the regression part  $\mathbf{x}_i^T \boldsymbol{\beta}$  is independent of  $j$ , so  $\boldsymbol{\beta}$  has the same effect for each of the  $J - 1$  cumulative logits. Note that  $\mathbf{x}_i^T \boldsymbol{\beta}$  does not contain an intercept, since the  $\{\theta_j\}$  act as intercepts. The cumulative logit model is illustrated in Fig. 1 for data with four response categories. For small values of  $\mathbf{x}_i^T \boldsymbol{\beta}$  the response is likely to fall in the first category and for large values of  $\mathbf{x}_i^T \boldsymbol{\beta}$  the response is likely to fall in the last category. The horizontal displacements of the curves are given by the values of  $\{\theta_j\}$ .

Some sources write the cumulative logit model, (3) with a plus on the right-hand-side, but there are two good reasons for the minus. First, it means that the larger the value of  $\mathbf{x}_i^T \boldsymbol{\beta}$ , the higher the probability of the response falling in a category at the upper end of the response scale. Thus  $\boldsymbol{\beta}$  has the same direction of effect as the regression parameter in an ordinary linear regression or ANOVA model. The second reason is related to the latent variable interpretation of cumulative link models that we will consider in section 2.6.

## 2.1 Fitting cumulative link models with `clm` from package `ordinal2`

Cumulative link models can be fitted with `clm` from package `ordinal2`. The function takes the following arguments:

```
clm(formula, data, weights, start, subset, doFit = TRUE, na.action,
    contrasts, model = TRUE, control, link = c("logit", "probit",
```

```
"cloglog", "loglog", "cauchit"), threshold = c("flexible",
"symmetric", "equidistant"), ...)
```

Most arguments are standard and well-known from `lm` and `glm`, so they will not be introduced. The `formula` argument is of the form `response ~ covariates` and specifies the linear predictor. The `response` should be an *ordered factor* (see `help(factor)`) with levels corresponding to the response categories. A number of link functions are available and the logit link is the default. The `doFit` and `threshold` arguments will be introduced in later sections. For further information about the arguments see the help page for `clm`<sup>5</sup>.

**Example 3:** In this example we fit a cumulative logit model to the wine data presented in example 1 with `clm` from package `ordinal2`. A cumulative logit model that includes additive effects of temperature and contact is fitted and summarized with

```
> fm1 <- clm(rating ~ contact + temp, data = wine)
> summary(fm1)
```

Call:

```
clm(formula = rating ~ contact + temp, data = wine)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
contactyes	1.5278	0.4766	3.2055	0.0013484
tempwarm	2.5031	0.5287	4.7346	2.1946e-06

Threshold coefficients:

	Estimate	Std. Error	z value
1 2	-1.3444	0.5171	-2.5998
2 3	1.2508	0.4379	2.8565
3 4	3.4669	0.5978	5.7998
4 5	5.0064	0.7309	6.8496

log-likelihood: -86.49192

AIC: 184.9838

Condition number of Hessian: 26.59441

The summary provides basic information about the model fit. There are two coefficient tables: one for the regression variables and one for the thresholds or cutpoints. Often the thresholds are not of primary interest, but they are an integral part of the model. It is not relevant to test whether the thresholds are equal to zero, so no *p*-values are provided for this test. The condition number of the Hessian is a measure of how identifiable the model is; large values, say larger than `1e4` indicate that the model may be ill defined. From this model it appears that contact and high temperature both lead to higher probabilities of observations in the high categories as we would also expect from examining Table 1.

The Wald tests provided by `summary` indicate that both contact and temperature effects are strong. More accurate likelihood ratio tests can be obtained using the `drop1` and `add1` methods (equivalently `dropterm` or `addterm`). The Wald tests are marginal tests so the test of e.g., `temp` is measuring the effect of temperature while *controlling* for the effect of contact. The equivalent likelihood ratio tests are provided by the `drop`-methods:

```
> drop1(fm1, test = "Chi")
```

Single term deletions

Model:

---

<sup>5</sup>Typing `?clm` or `help(clm)` in the command prompt should display the help page for `clm`.

```

rating ~ contact + temp
      Df    AIC    LRT   Pr(Chi)
<none>      184.98
contact  1 194.03 11.043 0.0008902 ***
temp     1 209.91 26.928 2.112e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

In this case the likelihood ratio tests are slightly more significant than the Wald tests. We could also have tested the effect of the variables while *ignoring* the effect of the other variable. For this test we use the `add-methods`:

```

> fm0 <- clm(rating ~ 1, data = wine)
> add1(fm0, scope = ~contact + temp, test = "Chi")

```

Single term additions

```

Model:
rating ~ 1
      Df    AIC    LRT   Pr(Chi)
<none>      215.44
contact  1 209.91  7.5263  0.00608 **
temp     1 194.03 23.4113 1.308e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

where we used the `scope` argument to indicate which terms to include in the model formula. These tests are a little less significant than the tests controlling for the effect of the other variable.

Conventional symmetric so-called Wald confidence intervals for the parameters are available as

```

> confint(fm1, type = "Wald")

              2.5 %    97.5 %
contactyes 0.5936345 2.461961
tempwarm   1.4669081 3.539296

```

More accurate profile likelihood confidence intervals are also available and these are discussed in section 4. □

## 2.2 Odds ratios and proportional odds

The odds ratio of the event  $Y \leq j$  at  $\mathbf{x}_1$  relative to the same event at  $\mathbf{x}_2$  is

$$\text{OR} = \frac{\gamma_j(\mathbf{x}_1)/[1 - \gamma_j(\mathbf{x}_1)]}{\gamma_j(\mathbf{x}_2)/[1 - \gamma_j(\mathbf{x}_2)]} = \frac{\exp(\theta_j - \mathbf{x}_1\boldsymbol{\beta})}{\exp(\theta_j - \mathbf{x}_2\boldsymbol{\beta})} = \exp[(\mathbf{x}_2 - \mathbf{x}_1)\boldsymbol{\beta}]$$

which is independent of  $j$ . Thus the cumulative odds ratio is proportional to the distance between  $\mathbf{x}_1$  and  $\mathbf{x}_2$  which made McCullagh (1980) call the cumulative logit model a *proportional odds model*. If  $x$  represent a treatment variable with two levels (e.g., placebo and treatment), then  $x_2 - x_1 = 1$  and the odds ratio is  $\exp(-\beta_{\text{treatment}})$ . Similarly the odds ratio of the event  $Y \geq j$  is  $\exp(\beta_{\text{treatment}})$ .

Confidence intervals for the odds ratios are obtained by transforming the limits of confidence intervals for  $\boldsymbol{\beta}$ , which will lead to asymmetric confidence intervals for the odds ratios. Symmetric confidence intervals constructed from the standard error of the odds ratios will not be appropriate and should be avoided.

Table 2: Summary of various link functions

Name	logit	probit	log-log	clog-log <sup>a</sup>	cauchit
Distribution	logistic	Normal	Gumbel (min) <sup>b</sup>	Gumbel (max) <sup>b</sup>	Cauchy ( $t_1$ ) <sup>c</sup>
Shape	symmetric	symmetric	right skew (?)	left (?) skew	kurtotic
Link function ( $F^{-1}$ )	$\log[\gamma/(1 - \gamma)]$	$\Phi^{-1}(\gamma)$			
Inverse link ( $F$ )	$1/[1 + \exp(\eta)]$	$\Phi(\eta)$		$\exp(\exp(-\eta))$	$\arctan(\eta)/\pi + 0.5$
Density ( $f = F'$ )	$\exp(-\eta)/[1 + \exp(-\eta)]^2$	$\phi(\eta)$		$\exp(-\exp(-\eta) - \eta)$	$1/\pi(1 + \eta^2)$

<sup>a</sup>: the *complementary log-log* link

<sup>b</sup>: the Gumbel distribution is also known as the extreme value (type I) distribution for extreme minima or maxima. It is also sometimes referred to as the Weibull (or log-Weibull) distribution ([http://en.wikipedia.org/wiki/Gumbel\\_distribution](http://en.wikipedia.org/wiki/Gumbel_distribution)).

<sup>c</sup>: the Cauchy distribution is a  $t$ -distribution with one df

**Example 4:** The (cumulative) odds ratio of `rating`  $\geq j$  (for all  $j = 1, \dots, J - 1$ ) for contact and temperature are

```
> round(exp(fm1$beta), 1)
```

```
contactyes    tempwarm
      4.6         12.2
```

attesting to the strong effects of contact and temperature. Asymmetric confidence intervals for the odds ratios based on the Wald statistic are:

```
> round(exp(confint(fm1, type = "Wald")), 1)
```

```
                2.5 % 97.5 %
contactyes      1.8   11.7
tempwarm        4.3   34.4
```

□

## 2.3 Link functions

Cumulative link models are not formally a member of the class of (univariate) generalized linear models<sup>6</sup> (McCullagh and Nelder, 1989), but they share many similarities with generalized linear models. Notably a link function and a linear predictor ( $\eta_{ij} = \theta_j - \mathbf{x}_i^T \boldsymbol{\beta}$ ) needs to be specified as in generalized linear models while the response distribution is just the multinomial. Fahrmeir and Tutz (2001) argues that cumulative link models are members of a class of multivariate generalized linear models. In addition to the logit link other choices are the probit, cauchit, log-log and clog-log links. These are summarized in Table 2. The cumulative link model may be written as

$$F^{-1}(\gamma_{ij}) = \theta_j - \mathbf{x}_i^T \boldsymbol{\beta} \quad (4)$$

where  $F^{-1}$  is the link function—the motivation for this particular notation will be given in section 2.6.

The probit link is often used when the model is interpreted with reference to a latent variable, cf. section 2.6. When the response variable represent grouped duration or survival times

<sup>6</sup>the distribution of the response, the multinomial, is not a member of the (univariate) exponential family of distributions.



Table 3: Income distribution (percentages) in the Northeast US adopted from McCullagh (1980).

Year	Income						
	0-3	3-5	5-7	7-10	10-12	12-15	15+
1960	6.50	8.20	11.30	23.50	15.60	12.70	22.20
1970	4.30	6.00	7.70	13.20	10.50	16.30	42.10

the complementary log-log link is often used. This leads to the proportional hazard model for grouped responses:

$$-\log\{1 - \gamma_j(\mathbf{x}_i)\} = \exp(\theta_j - \mathbf{x}_i^T \boldsymbol{\beta})$$

or equivalently

$$\log[-\log\{1 - \gamma_j(\mathbf{x}_i)\}] = \theta_j - \mathbf{x}_i^T \boldsymbol{\beta}. \quad (5)$$

Here  $1 - \gamma_j(\mathbf{x}_i)$  is the probability of survival beyond category  $j$  given  $\mathbf{x}_i$ . Thus, similar to the proportional odds model, the ratio of hazard functions beyond category  $j$  at  $\mathbf{x}_1$  relative to  $\mathbf{x}_2$  (the hazard ratio,  $HR$ ) is:

$$HR = \frac{-\log\{1 - \gamma_j(\mathbf{x}_2)\}}{-\log\{1 - \gamma_j(\mathbf{x}_1)\}} = \frac{\exp(\theta_j - \mathbf{x}_1^T \boldsymbol{\beta})}{\exp(\theta_j - \mathbf{x}_2^T \boldsymbol{\beta})} = \exp[(\mathbf{x}_2 - \mathbf{x}_1)\boldsymbol{\beta}]$$

In addition to the standard links in Table 2, flexible link functions are available for `clm` in package `ordinal` and these are described in section XX.

**Example 5:** McCullagh (1980) present data on income distribution in the Northeast US reproduced in Table 3. The numbers are percentages summing to 100 in each row<sup>7</sup>, so these are not the original observations. The uncertainty of parameter estimates depends on the sample size, which is unknown here, so we will not consider hypothesis tests. Rather the most important systematic component is an upward shift in the income distribution from 1960 to 1970 which can be estimated from a cumulative link model. This is possible since the parameter estimates themselves only depend on the relative proportions and not the absolute numbers.

McCullagh considers which of the logit or cloglog links best fit the data in a model with an additive effect of `year`. He concludes that a the complementary log-log link corresponding to a right-skew distribution is a good choice. We can compare the relative merit of the links by comparing the value of the log-likelihood of models with different link functions:

```
> links <- c("logit", "probit", "cloglog", "loglog", "cauchit")
> sapply(links, function(link) {
  clm(income ~ year, data = income, weights = freq, link = link)$logLik
})

      logit      probit    cloglog    loglog    cauchit
-353.3589 -353.8036 -355.6028 -352.8980 -352.8434
```

The `cauchit` link attains the highest log-likelihood closely followed by the complementary log-log link. This indicates that a symmetric heavy tailed distribution such as the cauchy provides an even slightly better description of these data than a right skew distribution.

Adopting the complementary log-log link we can summarize the connection between the income in the two years by the following: If  $p_{1960}(x)$  is proportion of the population with an income

---

<sup>7</sup>save rounding error

larger than \$x\$ in 1960 and \$p\_{1970}(x)\$ is the equivalent in 1970, then approximately

$$\begin{aligned}\log p_{1960}(x) &= \exp(\hat{\beta}) \log p_{1970}(x) \\ &= \exp(0.568) \log p_{1970}(x)\end{aligned}$$

□

## 2.4 Maximum likelihood estimation of cumulative link models

Cumulative link models are usually estimated by maximum likelihood (ML) and this is also the criterion used in package `ordinal2`. The log-likelihood function (ignoring additive constants) can be written as

$$\ell(\boldsymbol{\theta}, \boldsymbol{\beta}; \mathbf{y}) = \sum_{i=1}^n w_i \log \pi_i \quad (6)$$

where  $i$  index all scalar observations (not multinomial vector observations),  $w_i$  are potential case weights and  $\pi_i$  is the probability of the  $i$ th observation falling in the response category that it did, i.e.,  $\pi_i$  are the non-zero elements of  $\pi_{ij} \mathbf{I}(Y_i = j)$ . Here  $\mathbf{I}(\cdot)$  is the indicator function being 1 if its argument is true and zero otherwise. The ML estimates of the parameters;  $\hat{\boldsymbol{\theta}}$  and  $\hat{\boldsymbol{\beta}}$  are those values of  $\boldsymbol{\theta}$  and  $\boldsymbol{\beta}$  that maximize the log-likelihood function in (6).

Not all data sets can be summarized in a table like Table 1. If a continuous variable takes a unique value for each observation, each row of the resulting table would contain a single 1 and zeroes for the rest. In this case all  $\{w_i\}$  are one unless the observations are weighted for some other reason. If the data can be summarized as in Table 1, a multinomial observation vector such as  $[3, 1, 2]$  can be fitted using  $\mathbf{y} = [1, 1, 1, 2, 3, 3]$  with  $\mathbf{w} = [1, 1, 1, 1, 1, 1]$  or by using  $\mathbf{y} = [1, 2, 3]$  with  $\mathbf{w} = [3, 1, 2]$ . The latter construction is considerably more computationally efficient (and therefore faster) since the log-likelihood function contains three rather than six terms and the design matrix,  $\mathbf{X}$  will have three rather than six rows.

The details of the actual algorithm by which the likelihood function is optimized is deferred to a later section.

Have I got the signs right in the following?

According to standard likelihood theory, the variance-covariance matrix of the parameters can be obtained as the inverse of the observed Fisher information matrix. This matrix is given by the negative Hessian of the log-likelihood function evaluated at the maximum likelihood estimates. Standard errors can be obtained as the square root of the diagonal of the variance-covariance matrix.

Let  $\boldsymbol{\alpha} = [\boldsymbol{\theta}, \boldsymbol{\beta}]$  denote the full set of parameters. The Hessian matrix is then given as the second order derivative of the log-likelihood function evaluated at the ML estimates:

$$\mathbf{H} = \left. \frac{\partial^2 \ell(\boldsymbol{\alpha}; \mathbf{y})}{\partial \boldsymbol{\alpha} \partial \boldsymbol{\alpha}^T} \right|_{\boldsymbol{\alpha} = \hat{\boldsymbol{\alpha}}} \quad (7)$$

The observed Fisher information matrix is then  $I(\hat{\boldsymbol{\alpha}}) = -\mathbf{H}$  and the standard errors are given by

$$\text{se}(\hat{\boldsymbol{\alpha}}) = \sqrt{\text{diag}[I(\hat{\boldsymbol{\alpha}})^{-1}]} \quad (8)$$

Another general way to obtain the variance-covariance matrix of the parameters is to use the expected Fisher information matrix. The choice of whether to use the observed or the expected Fisher information matrix is often dictated by the fitting algorithm: re-weighted

least squares methods often produce the expected Fisher information matrix as a by-product of the algorithm, and Newton-Raphson algorithms (such as the one used for `clm` in `ordinal2`) similarly produce the observed Fisher information matrix.

Mention which is better and refer to Efron and Hinkley

Pratt (1981) and Burridge (1981) showed (seemingly independent of each other) that the log-likelihood function of cumulative link models with the link functions considered in Table 2, except for the cauchit link, is concave. This means that there is a unique global optimum so there is no risk of convergence to a local optimum. It also means that the step of a Newton-Raphson algorithm is guaranteed to be in the direction of a higher likelihood although the step may be too large to cause an increase in the likelihood. Successively halving the step whenever this happens effectively ensures convergence.

Notably the log likelihood of cumulative cauchit models is not guaranteed to be concave, so convergence problems may occur with the Newton-Raphson algorithm. Using the estimates from a cumulative probit models as starting values seems to be a widely successful approach.

Observe also that the concavity property does not extend to cumulative link models with scale effects, but that structured thresholds (cf. section 4.2) are included.

## 2.5 Deviance and model comparison

### 2.5.1 Model comparison with likelihood ratio tests

A general way to compare models is by means of the likelihood ratio statistic. Consider two models,  $m_0$  and  $m_1$ , where  $m_0$  is a submodel of model  $m_1$ , that is,  $m_0$  is simpler than  $m_1$  and  $m_0$  is *nested* in  $m_1$ . The likelihood ratio statistic for the comparison of  $m_0$  and  $m_1$  is

$$LR = -2(\ell_0 - \ell_1) \quad (9)$$

where  $\ell_0$  is the log-likelihood of  $m_0$  and  $\ell_1$  is the log-likelihood of  $m_1$ . The likelihood ratio statistic measures the evidence in the data for the extra complexity in  $m_1$  relative to  $m_0$ . The likelihood ratio statistic asymptotically follows a  $\chi^2$  distribution with degrees of freedom equal to the difference in the number of parameter of  $m_0$  and  $m_1$ . The likelihood ratio test is generally more accurate than Wald tests. Cumulative link models can be compared by means of likelihood ratio tests with the `anova` method.

**Example 6:** Consider the additive model for the wine data in example 3 with a main effect of temperature and contact. We can use the likelihood ratio test to assess whether the interaction between these factors are supported by the data:

```
> fm2 <- clm(rating ~ contact * temp, data = wine)
> anova(fm1, fm2)
```

Likelihood ratio tests of cumulative link models

	Model	Resid. df	-2logLik	Test	Df	LR stat.	Pr(Chi)
1	contact + temp	66	172.9838				
2	contact * temp	65	172.8324	1 vs 2	1	0.1514459	0.6971574

The likelihood ratio statistic is small in this case and compared to a  $\chi^2$  distribution with 1 df, the  $p$ -value turns out insignificant. We conclude that the interaction is not supported by the data.  $\square$

## 2.5.2 Deviance and ANODE tables

In linear models ANOVA tables and  $F$ -tests are based on the decomposition of sums of squares. The concept of sums of squares does not make much sense for categorical observations, but a more general measure called the *deviance* is defined for generalized linear models and contingency tables<sup>8</sup>. The deviance can be used in much the same way to compare nested models and to make a so-called analysis of deviance (ANODE) table. The deviance is closely related to sums of squares for linear models (McCullagh and Nelder, 1989).

The deviance is defined as minus twice the difference between the log-likelihoods of a *full* (or *saturated*) model and a reduced model:

$$D = -2(\ell_{\text{reduced}} - \ell_{\text{full}}) \quad (10)$$

The full model has a parameter for each observation and describes the data perfectly while the reduced model provides a more concise description of the data with fewer parameters.

A special reduced model is the *null model* which describes no other structure in the data than what is implied by the design. The corresponding deviance is known as the *null deviance* and analogous to the total sums of squares for linear models. The null deviance is therefore also denoted the *total deviance*. The *residual deviance* is a concept similar to a residual sums of squares and simply defined as

$$D_{\text{resid}} = D_{\text{total}} - D_{\text{reduced}} \quad (11)$$

A *difference in deviance* between two nested models is identical to the likelihood ratio statistic for the comparison of these models. Thus the deviance difference, just like the likelihood ratio statistic, asymptotically follows a  $\chi^2$ -distribution with degrees of freedom equal to the difference in the number of parameters in the two models. In fact the deviance in (10) is just the likelihood ratio statistic for the comparison of the full and reduced models.

The likelihood of reduced models are available from fits of cumulative link models, but since it is not always easy to express the full model as a cumulative link model, the log-likelihood of the full model has to be obtained in another way. For a two-way table like Table 1 indexed by  $h$  (rows) and  $j$  (columns), the log-likelihood of the full model (comparable to the likelihood in (6)) is given by

$$\ell_{\text{full}} = \sum_h \sum_j w_{hj} \log \hat{\pi}_{hj} \quad (12)$$

where  $\hat{\pi}_{hj} = w_{hj}/w_{h\cdot}$ ,  $w_{hj}$  is the count in the  $(h, j)$ th cell and  $w_{h\cdot}$  is the sum in row  $h$ .

**Example 7:** We can get the likelihood of the full model for the wine data in Table 1 with

```
> tab <- with(wine, table(temp:contact, rating))
> pi.hat <- tab/rowSums(tab)
> (ll.full <- sum(tab * ifelse(pi.hat > 0, log(pi.hat), 0)))

[1] -84.01558
```

The total deviance (10) for the wine data is given by

```
> fm0 <- clm(rating ~ 1, data = wine)
> ll.null <- fm0$logLik
> (Deviance <- -2 * (ll.null - ll.full))
```

---

<sup>8</sup>i.e., for likelihood based models for contingency tables

Table 4: ANODE table for the data in Table 1.			
Source	df	deviance	$p$ -value
Total	12	39.407	$< 0.001$
Treatment	3	34.606	$< 0.001$
Temperature, $T$	1	26.928	$< 0.001$
Contact, $C$	1	11.043	$< 0.001$
Interaction, $T \times C$	1	0.1514	0.6972
Residual	9	4.8012	0.8513

[1] 39.407

□

**Example 8:** An ANODE table for the wine data in Table 1 is presented in Table 4 where the total deviance is broken up into model deviance (due to treatments) and residual deviance. Further, the treatment deviance is described by contributions from main effects and interaction. Observe that the deviances for the main effects and interaction do not add up to the deviance for Treatment as the corresponding sums of squares would have in an analogous linear model (ANOVA)<sup>9</sup>. The deviances for these terms can instead be interpreted as likelihood ratio tests of nested models: the deviance for the interaction term is the likelihood ratio statistics of the interaction controlling for the main effects, and the deviances for the main effects are the likelihood ratio statistics for these terms while controlling for the other main effect and ignoring the interaction term. As is clear from Table 4, there are significant treatment differences and these seem to describe the data well since the residual deviance is insignificant—the latter is a goodness of fit test for the cumulative logit model describing treatment differences. Further, the treatment differences are well captured by the main effects and there is no indication of an important interaction. □

The terminology can be a bit confusing in this area. Sometimes any difference in deviance between two nested models, i.e., a likelihood ratio statistic is denoted a deviance and sometimes any quantity that is proportional to minus twice the log-likelihood of a model is denoted the deviance of that model.

### 2.5.3 Goodness of fit tests with the deviance

The deviance can be used to test the goodness of fit of a particular reduced model. The deviance asymptotically follows as  $\chi^2$  distribution with degrees of freedom equal to the difference in the number of parameters between the two models. The asymptotics are generally good if the expected frequencies under the reduced model are not too small and as a general rule they should all be at least five. This provides a goodness of fit test of the reduced model. The expectation of a random variable that follows a  $\chi^2$ -distribution is equal to the degrees of freedom of the distribution, so as a rule of thumb, if the deviance in (10) is about the same size as the difference in the number of parameters, there is not evidence of lack of fit.

One problem with the deviance for a particular (reduced) model is that it depends on which model is considered the full model, i.e., how the total deviance is calculated, which often derives from the tabulation of the data. Observe that differences in deviance for

<sup>9</sup>This holds for orthogonal designs including balanced and complete tables like Table 1.

Table 5: Table of the wine data similar to Table 1, but including bottle in the tabulation.

Temperature	Contact	Bottle	Least—Most bitter				
			1	2	3	4	5
cold	no	1	3	4	2	0	0
cold	no	2	1	5	3	0	0
cold	yes	3	1	2	5	1	0
cold	yes	4	0	5	3	1	0
warm	no	5	0	3	4	1	1
warm	no	6	0	2	4	2	1
warm	yes	7	0	1	2	2	4
warm	yes	8	0	0	3	5	1

nested models are independent of the likelihood of a full model, so deviance differences are insensitive to this choice. Collett (2002) recommends that the data are aggregated as much as possible when evaluating deviances and goodness of fit tests are performed.

**Example 9:** In the presentation of the wine data in example 1 and Table 1, the data were aggregated over judges and bottles. Had we included `bottle` in the tabulation of the data we would have arrived at Table 5. A full model for the data in Table 1 has  $(5 - 1)(4 - 1) = 12$  degrees of freedom while a full model for Table 5 has  $(5 - 1)(8 - 1) = 28$  degrees of freedom and a different deviance.

If it is decided that bottle is not an important variable, Collett's recommendation is that we base the residual deviance on a full model defined from Table 1 rather than Table 5.  $\square$

## 2.6 Latent variable motivation for cumulative link models

A cumulative link model can be motivated by assuming an underlying continuous latent variable,  $S$  with cumulative distribution function,  $F$ . The ordinal response variable,  $Y_i$  is then observed in category  $j$  if  $S_i$  is between the thresholds  $\theta_{j-1}^* < S_i \leq \theta_j^*$  where

$$-\infty \equiv \theta_0^* < \theta_1^* < \dots < \theta_{J-1}^* < \theta_J^* \equiv \infty$$

divide the real line on which  $S$  lives into  $J + 1$  intervals. The situation is illustrated in Fig. 2 where a probit link and  $J = 4$  is adopted. The three thresholds,  $\theta_1, \theta_2, \theta_3$  divide the area under the curve into four parts each of which represent the probability of a response falling in the four response categories. The thresholds are fixed on the scale, but the location of the latent distribution, and therefore also the four areas under the curve, changes with  $\mathbf{x}_i$ . A normal linear model for the latent variable is

$$S_i = \alpha + \mathbf{x}_i^T \boldsymbol{\beta}^* + \varepsilon_i, \quad \varepsilon_i \sim N(0, \sigma^2) \quad (13)$$

where  $\{\varepsilon_i\}$  are random disturbances and  $\alpha$  is the intercept, i.e., the mean value of  $S_i$  when  $\mathbf{x}_i$  correspond to a reference level for factors and to zero for continuous covariates. Equivalently we could write:  $S_i \sim N(\alpha + \mathbf{x}_i^T \boldsymbol{\beta}^*, \sigma^2)$ .

The cumulative probability of an observation falling in category  $j$  or below is then:

$$\gamma_{ij} = P(Y_i \leq j) = P(S_i \leq \theta_j^*) = P\left(Z_i \leq \frac{\theta_j^* - \alpha - \mathbf{x}_i^T \boldsymbol{\beta}^*}{\sigma}\right) = \Phi\left(\frac{\theta_j^* - \alpha - \mathbf{x}_i^T \boldsymbol{\beta}^*}{\sigma}\right) \quad (14)$$

Better figure here - see Agresti 2002, p. 278

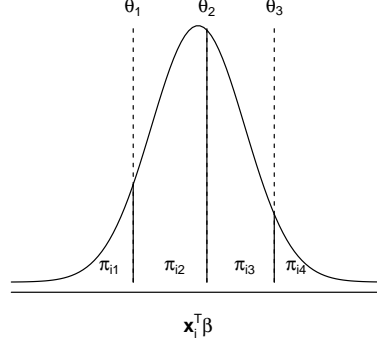


Figure 2: Illustration of a cumulative link model in terms of the latent distribution.

where  $Z_i = (S_i - \alpha - \mathbf{x}_i^T \boldsymbol{\beta}^*) / \sigma \sim N(0, 1)$  and  $\Phi$  is the standard normal CDF.

Since the absolute location and scale of the latent variable,  $\alpha$  and  $\sigma$  respectively, are not identifiable from ordinal observations, an identifiable model is

$$\gamma_{ij} = \Phi(\theta_j - \mathbf{x}_i^T \boldsymbol{\beta}), \quad (15)$$

with identifiable parameter functions:

$$\theta_j = (\theta_j^* - \alpha) / \sigma \quad \text{and} \quad \boldsymbol{\beta} = \boldsymbol{\beta}^* / \sigma. \quad (16)$$

Observe how the minus in (15) entered naturally such that a positive  $\beta$  means a shift of the latent distribution in a positive direction.

Model (15) is exactly a cumulative link model with a probit link. Other distributional assumptions for  $S$  correspond to other link functions. In general assuming that the cumulative distribution function of  $S$  is  $F$  corresponds to assuming the link function is  $F^{-1}$ , cf. Table 2.

Some expositions of the latent variable motivation for cumulative link models get around the identifiability problem by introducing restrictions on  $\alpha$  and  $\sigma$ , usually  $\alpha = 0$  and  $\sigma = 1$  are chosen, which leads to the same definition of the threshold and regression parameters that we use here. However, it seems misleading to introduce restrictions on unidentifiable parameters. If observations really arise from a continuous latent variable,  $\alpha$  and  $\sigma$  are real unknown parameters and it makes little sense to restrict them to take certain values. This draws focus from the appropriate *relative* signal-to-ratio interpretation of the parameters evident from (16).

The standard form of the logistic distribution has mean zero and variance  $\pi^2/3$ . The logistic distribution is symmetric and shows some resemblance with a normal distribution with the same mean and variance in the central part of the distribution; the tails of the logistic distribution are a little heavier than the tails of the normal distribution. In Fig. 3 the normal and logistic distributions are compared with variance  $\pi^2/3$ . Therefore, to a reasonable approximation, the parameters of logit and probit models are related in the following way:

$$\theta_j^{\text{probit}} \approx \theta_j^{\text{logit}} / (\pi / \sqrt{3}) \quad \text{and} \quad \boldsymbol{\beta}^{\text{probit}} \approx \boldsymbol{\beta}^{\text{logit}} / (\pi / \sqrt{3}), \quad (17)$$

where  $\pi / \sqrt{3} \approx 1.81$

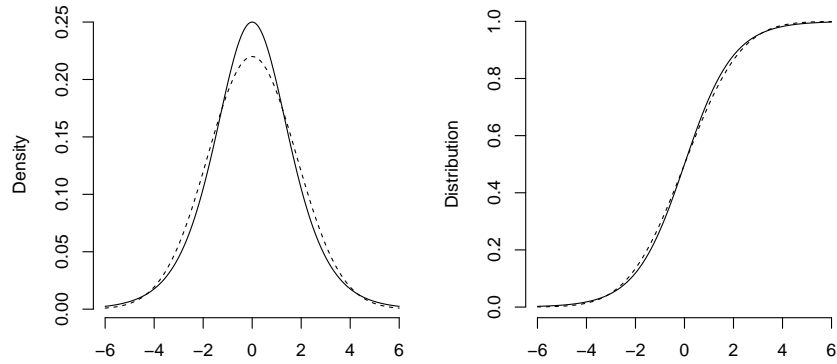


Figure 3: Left: densities. Right: distributions of logistic (solid) and normal (dashed) distributions with mean zero and variance  $\pi^2/3$  which corresponds to the standard form for the logistic distribution.

**Example 10:** Considering once again the wine data the coefficients from logit and probit models with additive effects of temperature and contact are

```
> fm1 <- clm(rating ~ contact + temp, data = wine, link = "logit")
> fm2 <- clm(rating ~ contact + temp, data = wine, link = "probit")
> structure(rbind(coef(fm1), coef(fm2)), dimnames = list(c("logit",
  "probit"), names(coef(fm1))))
```

	1 2	2 3	3 4	4 5	contactyes	tempwarm
logit	-1.3443834	1.2508088	3.466887	5.006404	1.5277977	2.503102
probit	-0.7732627	0.7360215	2.044680	2.941345	0.8677435	1.499375

In comparison the approximate probit estimates using (17) are

```
> coef(fm1)/(pi/sqrt(3))
```

	1 2	2 3	3 4	4 5	contactyes	tempwarm
	-0.7411974	0.6896070	1.9113949	2.7601753	0.8423190	1.3800325

These estimates are a great deal closer to the real probit estimates than the unscaled logit estimates. The average difference between the probit and approximate probit estimates being -0.079.  $\square$

### 2.6.1 More on parameter interpretation

Observe that the regression parameter in cumulative link models, cf. (16) are signal-to-noise ratios. This means that adding a covariate to a cumulative link model that reduces the residual noise in the corresponding latent model will increase the signal-to-noise ratios. Thus adding a covariate will (often) increase the coefficients of the other covariates in the cumulative link model. This is different from linear models, where (in orthogonal designs) adding a covariate does not alter the value of the other coefficients<sup>10</sup>. Bauer (Bauer), extending work by Winship and Mare (1984) suggests a way to rescale the coefficients such

<sup>10</sup>but the same thing happens in other generalized linear models, e.g., binomial and Poisson models, where the variance is determined by the mean.



they are comparable in size during model development. See also Fielding (Fielding).

**Example 11:** Consider the estimate of `temp` in models for the wine data ignoring and controlling for `contact`, respectively:

```
> coef(clm(rating ~ temp, data = wine, link = "probit"))["tempwarm"]

tempwarm
1.372290
```

```
> coef(clm(rating ~ temp + contact, data = wine, link = "probit"))["tempwarm"]

tempwarm
1.499375
```

and observe that the estimate of `temp` is larger when controlling for `contact`. In comparison the equivalent estimates in linear models are not affected—here we use the observed scores for illustration:

```
> coef(lm(as.numeric(rating) ~ temp, data = wine))["tempwarm"]

tempwarm
1.166667

> coef(lm(as.numeric(rating) ~ contact + temp, data = wine))["tempwarm"]

tempwarm
1.166667
```

In this case the coefficients are exactly identical, but in designs that are not orthogonal and observed studies with correlated covariates they will only be approximately the same.  $\square$

Regardless of how the threshold parameters discretize the scale of the latent variable, the regression parameters  $\beta$  have the same interpretation. Thus  $\beta$  have the same meaning whether the ordinal variable is measured in, say, five or six categories. Further, the nature of the model interpretation will not change if two or more categories are amalgamated, while parameter estimates will, of course, not be completely identical. This means that regression parameter estimates can be compared (to the extent that the noise level is the same) across studies where response scales with a different number of response categories are adopted. In comparison, for linear models used on scores, it is not so simple to just combine two scores, and parameter estimates from different linear models are not directly comparable.

If the latent variable,  $S_i$  is approximated by scores assigned to the response variable, denote this variable  $Y_i^*$ , then a linear model for  $Y_i^*$  can provide approximate estimates of  $\beta$  by applying (16) for cumulative probit models<sup>11</sup>. The quality of the estimates rest on a number of aspects:

- The scores assigned to the ordinal response variable should be structurally equivalent to the thresholds,  $\theta^*$  that generate  $Y_i$  from  $S_i$ . In particular, if the (equidistant) numbers  $1, \dots, J$  are the scores assigned to the response categories, the thresholds,  $\theta^*$  are also assumed to be equidistant.
- The distribution of  $Y_i^*$  should not deviate too much from a bell-shaped curve; especially there should not be too many observations in the end categories

---

<sup>11</sup>these approximate regression parameters could be used as starting values for an iterative algorithm to find the ML estimates of  $\beta$ , but we have not found it worth the trouble in our Newton algorithm

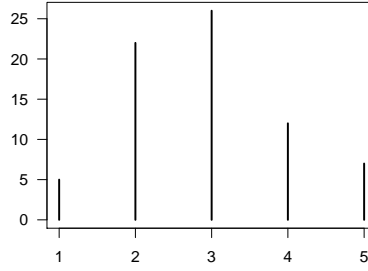


Figure 4: Histogram of the ratings in the wine data, cf. Table 1.

- By appeal to the central limit theorem the coarsening of  $S_i$  into  $Y_i^*$  will “average out” such that bias due to coarsening is probably small.

This approximate estimation scheme extends to other latent variable distributions than the normal where linear models are exchanged with the appropriate location-scale models, cf. Table 2.

**Example 12:** Consider the following linear model for the rating scores of the wine data, cf. Table 1:

$$Y_i^* = \alpha + \beta_1 \text{temp}_i + \beta_2 \text{contact}_i + \varepsilon_i \quad \varepsilon_i \sim N(0, \sigma_\varepsilon^2)$$

The relative parameter estimates,  $\tilde{\beta}$  are

```
> lm1 <- lm(as.numeric(rating) ~ contact + temp, data = wine)
> sd.lm1 <- summary(lm1)$sigma
> coef(lm1)[-1]/sd.lm1
```

```
contactyes    tempwarm
  0.791107    1.384437
```

which should be compared with the estimates from the corresponding cumulative probit model:

```
> fm1 <- clm(rating ~ contact + temp, data = wine, link = "probit")
> coef(fm1)[-1:4]
```

```
contactyes    tempwarm
  0.8677435    1.4993746
```

The relative estimates from the linear model are a lower than the cumulative probit estimates, which is a consequence of the fact that the assumptions for the linear model are not fulfilled. In particular the distance between the thresholds is not equidistant:

```
> diff(coef(fm1)[1:4])

      2|3      3|4      4|5
1.5092842 1.3086590 0.8966645
```

while the distribution is probably sufficiently bell-shaped, cf. Fig 4.

□

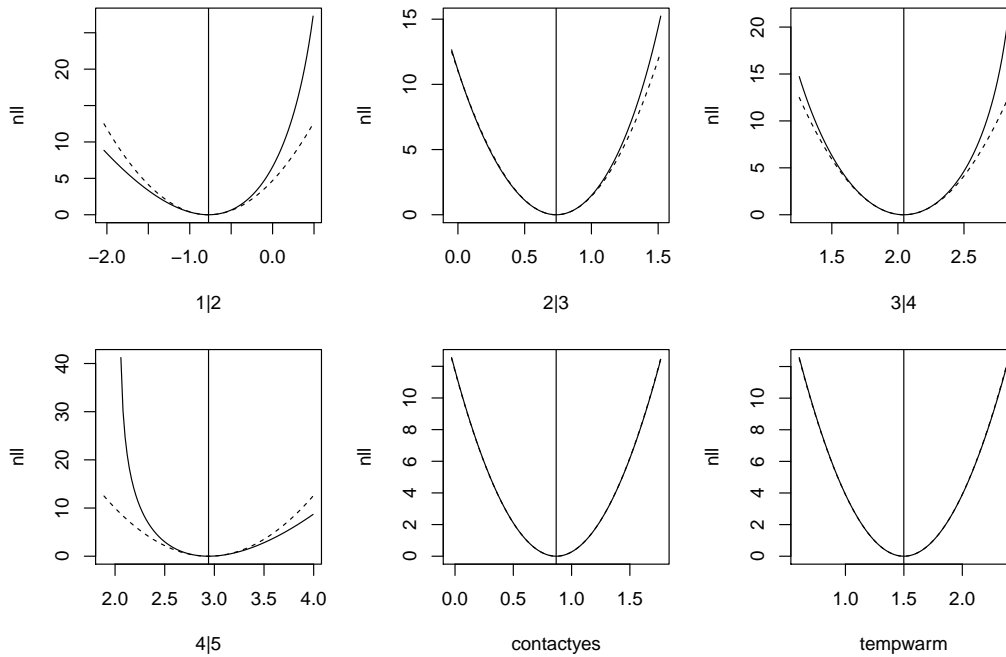


Figure 5: Slices of the (negative) log-likelihood function for parameters in a model for the bitterness-of-wine data. Dashed lines indicate quadratic approximations to the log-likelihood function and vertical bars the indicate maximum likelihood estimates.

### 3 Assessing the likelihood and model convergence

Cumulative link models are non-linear models and in general the likelihood function non-linear models is not guaranteed to be uni-modal or nice and bell-shaped. In cumulative link models, the threshold parameters are even restricted to be ordered and therefore naturally bounded. It can therefore be interesting to visualize the likelihood function in the neighborhood of the optimum. To do this we use the `slice` function. As the name implies, it extracts a (one-dimensional) slice of the likelihood function:

```
> slice.fm1 <- slice(fm1, lambda = 5)
> par(mfrow = c(2, 3))
> plot(slice.fm1)
```

The result is shown in Fig. 5. `lambda` controls the range of parameter values for which the slice is computed. The square root of the diagonal elements of the Hessian at the optimum are measures of curvature in the likelihood functions for each of the parameters, and `lambda` indicates how many of these curvature units away from the optimum the slice is to be computed. Working in curvature units is a way to standardize the parameter range even if some parameters are much better determined (much less curvature in the log-likelihood) than others. Here we wanted to assess the shape of the log-likelihood function, so we chose a relatively large value for `lambda`. By default the quadratic approximation is included for reference in the plot.

Write section example based

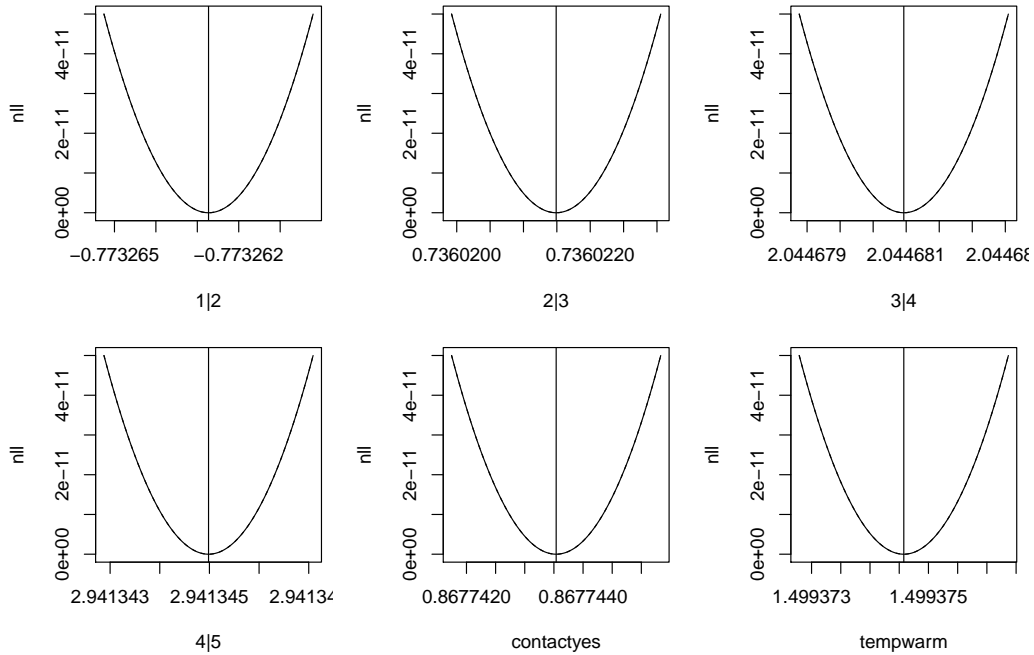


Figure 6: Slices of the (negative) log-likelihood function for parameters in a model for the bitterness-of-wine data very close to the MLEs. Dashed lines indicate quadratic approximations to the log-likelihood function and vertical bars the indicate maximum likelihood estimates.

For this model we see that the log-likelihood function is nicely quadratic for the regression parameters while it is less so for the threshold parameters and particularly bad for the end thresholds. There also appears to be only one optimum.

From Fig. 5 it seems that the parameter estimates as indicated by the vertical bars are close to the optimum indicating successful model convergence. To investigate more closely we slice the likelihood at a much smaller scale:

```
> slice2.fm1 <- slice(fm1, lambda = 1e-05)
> par(mfrow = c(2, 3))
> plot(slice2.fm1)
```

The resulting figure is shown in Fig. 6. Observe that 1) the model has converged and all parameters estimates are correct to at least six decimals and 2) the quadratic approximation is indistinguishable from the log-likelihood at this scale.

Unfortunately there is no general way to infer confidence intervals from the likelihood slices—for that we have to use the computationally more intensive profile likelihoods. Compared to the profile likelihoods discussed in section 4, the slice is much less computationally demanding since the likelihood function is only evaluated—not optimized, at a range of parameter values.

## 4 Confidence intervals and profile likelihood

write section with examples

Confidence intervals are convenient for summarizing the uncertainty about estimated parameters. The classical symmetric estimates given by  $\hat{\beta} \pm z_{1-\alpha/2} \text{se}(\hat{\beta})$  are based on the Wald statistic<sup>12</sup>,  $w(\beta) = (\hat{\beta} - \beta) / \text{se}(\hat{\beta})$  and available by:

```
> confint(fm1, type = "Wald")

                2.5 %    97.5 %
contactyes 0.3446154 1.390872
tempwarm   0.9274759 2.071273
```

A similar result could be obtained by `confint.default(fm1)`. However, outside linear models asymmetric confidence intervals often better reflect the uncertainty in the parameter estimates. More accurate, and generally asymmetric, confidence intervals can be obtained by using the likelihood root statistic instead; this relies on the so-called profile likelihood written here for an arbitrary scalar parameter  $\beta_a$ :

$$\ell_p(\beta_a; \mathbf{y}) = \arg \max_{\boldsymbol{\theta}, \boldsymbol{\beta}_{-a}} \ell(\boldsymbol{\theta}, \boldsymbol{\beta}; \mathbf{y}) ,$$

where  $\boldsymbol{\beta}_{-a}$  is the vector of regression parameters without the  $a$ th one. In words, the profile log-likelihood for  $\beta_a$  is given as the full log-likelihood optimized over all parameters but  $\beta_a$ . To obtain a smooth function, the likelihood is optimized over a range of values of  $\beta_a$  around the ML estimate,  $\hat{\beta}_a$ , further, these points are interpolated by a spline to provide an even smoother function.

The likelihood root statistic [refs] is defined as:

should the minus be there?

$$r(\beta_a) = \text{sign}(\hat{\beta}_a - \beta_a) \sqrt{-2[\ell(\hat{\boldsymbol{\theta}}, \hat{\boldsymbol{\beta}}; \mathbf{y}) - \ell_p(\beta_a; \mathbf{y})]}$$

and just like the Wald statistic its reference distribution is the standard normal. Confidence intervals based on the likelihood root statistic are defined as those values of  $\beta_a$  for which  $r(\beta_a)$  is in between, say,  $-1.96$  and  $1.96$  for 95% confidence intervals. Formally the confidence intervals are defined as

$$CI : \{ \beta_a; |r(\beta_a)| < z_{1-\alpha/2} \} .$$

To fix ideas the likelihood root statistic<sup>13</sup> is shown for the `tempwarm` parameter in the model for the wine data given above in Fig. 7. The figure is made with the following code:

```
> pr1 <- profile(fm1, which.beta = "tempwarm")
> plot(pr1, root = TRUE)
```

The horizontal lines indicate 95% and 99% confidence intervals and the dashed line is the Wald statistic. Incidentally, and as is clear from the figure, the Wald statistic is also the tangent line to the likelihood root statistic in the ML estimate. As indicated by the figure, the profile likelihood confidence limits for `tempwarm` are larger than the Wald counterparts and the discrepancy increases with the confidence level.

The profile likelihood confidence intervals are provided by default application of `confint`:

```
> confint(fm1)
```

<sup>12</sup>where  $z_{1-\alpha/2}$  is the  $(1 - \alpha/2)$ -quantile of the standard normal CDF.

<sup>13</sup>actually we reversed the sign of the statistic in the display since a line from lower-left to upper-right looks better than a line from upper-left to lower-right.

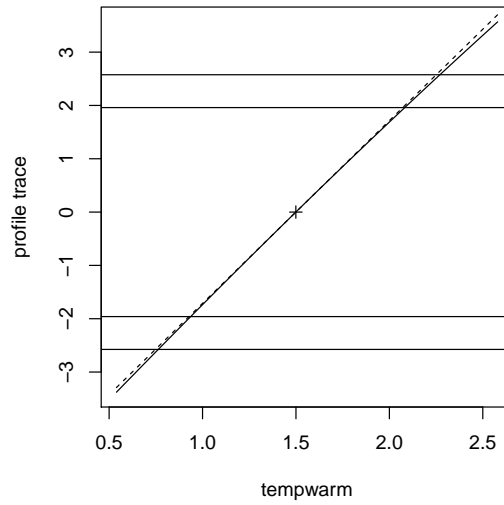


Figure 7: Likelihood root statistic (solid) and Wald statistic (dashed) for the `tempwarm` parameter in the model for the wine data.

```

                2.5 %   97.5 %
contactyes 0.3483889 1.395268
tempwarm   0.9366304 2.082230

```

The visualization of the likelihood root statistic can be helpful in diagnosing non-linearity in the parameterization of the model. The linear scale is particularly suited for this rather than other scales, such as the quadratic scale at which the log-likelihood lives. In summarizing the results of a model's fit, I find the relative likelihood scale,  $\exp(-r(\beta_a)^2/2)$  informative. These relative profile likelihoods are obtained with

```

> pr1 <- profile(fm1, alpha = 1e-04)
> plot(pr1)

```

and provided in Fig. 8. The evidence about the parameters is directly visible; the ML estimate has maximum support, 1 and values away from here are less supported by the data, 95% and 99% confidence intervals are readily read of the plots as intersections with the horizontal lines. Most importantly the plots emphasize that a range of parameter values are actually quite well supported by the data—something which is easy to forget when focus is on the precise numbers of the ML estimates.

## 4.1 Model selection

Several tools are available for variable assessment and model selection.

```

> drop1(fm1, test = "Chi")
> add1(update(fm1, ~1), ~+contact + temp, test = "Chi")
> lm1 <- lm(response ~ contact + temp, data = wine)
> drop1(lm1, test = "F")
> add1(lm(response ~ 1, data = wine), ~. + contact + temp,
      test = "F")

```

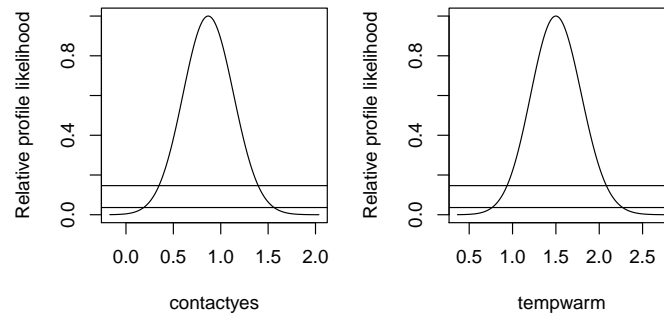


Figure 8: Relative profile likelihoods for the regression parameters in the Wine study.

## 4.2 Structured thresholds

## 4.3 Predictions

# 5 Miscellaneaus

Thompson and Baker (1981) showed that cumulative logit models can be fitted by application of composite link functions.

## References

- Agresti, A. (2002). *Categorical Data Analysis* (Second ed.). Wiley.
- Bauer, D. A note on comparing the estimates of models for cluster-correlated or longitudinal data with binary or ordinal outcomes. *Psychometrika* 74, pp. 97–105.
- Burridge, J. (1981). A note on maximum likelihood estimation for regression models using grouped data. *Journal of the Royal Statistical Society. Series B (Methodological)* 43(1), pp. 41–45.
- Collett, D. (2002). *Modelling binary data* (2nd ed.). London: Chapman & Hall/CRC.
- Fahrmeir, L. and G. Tutz (2001). *Multivariate Statistical Modelling Based on Generalized Linear Models* (2nd ed.). Springer series in statistics. Springer-Verlag New York, Inc.
- Fielding, A. Scaling for residual variance components of ordered category responses in generalised linear mixed multilevel models. *Quality & Quantity* 38, pp. 425–433.
- Greene, W. H. and D. A. Hensher (2010). *Modeling Ordered Choices: A Primer*. Cambridge University Press.
- McCullagh, P. (1980). Regression models for ordinal data. *Journal of the Royal Statistical Society, Series B* 42, pp. 109–142.
- McCullagh, P. and J. Nelder (1989). *Generalized Linear Models* (Second ed.). Chapman & Hall/CRC.

- Pratt, J. W. (1981). Concavity of the log likelihood. *Journal of the American Statistical Association* 76(373), pp. 103–106.
- Randall, J. (1989). The analysis of sensory data by generalised linear model. *Biometrical journal* 7, pp. 781–793.
- Thompson, R. and R. J. Baker (1981). Composite link functions in generalized linear models. *Journal of the Royal Statistical Society. Series C (Applied Statistics)* 30(2), pp. 125–131.
- Winship, C. and R. D. Mare (1984). Regression models with ordinal variables. *American Sociological Review* 49(4), pp. 512–525.