

Reference: Agresti, Sections 6.2-6.3

Cumulative link models

- Suppose the response categories, $1, 2, \dots, c$ are ordered.
- Let $\pi_{ij} = p(y_i = j)$ then the corresponding cumulative probability is

$$P(y_i \leq j) = \pi_{i1} + \pi_{i2} + \dots + \pi_{ij}, \quad j = 1, \dots, c.$$

- The class of models that we consider are of the form

$$g(P(y_i \leq j)) = \alpha_j + \mathbf{x}_i' \boldsymbol{\beta}.$$

- α_j represents the baseline value of the transformed cumulative probability for category j .
- β_k represents the increase in *all* transformed cumulative probabilities for a one-unit increase in x_{ik} .

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Proportional odds cumulative logit model

- A direct extension of the usual logistic regression model applies the logit transformation to the cumulative probabilities,

$$\text{logit}(P(y_i \leq j)) = \log \frac{P(y_i \leq j)}{1 - P(y_i \leq j)} = \alpha_j + \mathbf{x}_i' \boldsymbol{\beta}.$$

- The cumulative logits are defined

$$\begin{aligned} & \log \left(\frac{\pi_{i1}}{\pi_{i2} + \pi_{i3} + \dots + \pi_{ic}} \right) \\ & \log \left(\frac{\pi_{i1} + \pi_{i2}}{\pi_{i3} + \pi_{i4} + \dots + \pi_{ic}} \right) \\ & \vdots \\ & \log \left(\frac{\pi_{i1} + \pi_{i2} + \dots + \pi_{i,r-1}}{\pi_{ic}} \right) \end{aligned}$$

- Each cumulative logit uses all c response categories.

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- The log-**cumulative odds ratio** is proportional to the distance between $\mathbf{x}_i = \mathbf{u}$ and $\mathbf{x}_i = \mathbf{v}$

$$\log \frac{p(y_i \leq j | \mathbf{x}_i = \mathbf{u}) / p(y_i > j | \mathbf{x}_i = \mathbf{u})}{p(y_i \leq j | \mathbf{x}_i = \mathbf{v}) / p(y_i > j | \mathbf{x}_i = \mathbf{v})} = (\mathbf{u} - \mathbf{v})' \boldsymbol{\beta}.$$

- For each j , adjusting for the other covariates in the model, for a 1-unit increase in x_{ik} , the odds that $y_i \leq j$ is multiplied by $\exp(\beta_k)$.
- The model constrains the $c - 1$ response curves to have the same shape. The same proportionality constant applies to each logit. Hence the name **proportional odds model**.

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- The odds of $y_i \leq j$ are

$$\frac{P(y_i \leq j)}{1 - P(y_i \leq j)} = \exp(\alpha_j + \mathbf{x}_i' \boldsymbol{\beta}).$$

- $\exp(\alpha_j)$ may be interpreted as the **baseline** odds of a response in category j or below when $\mathbf{x} = \mathbf{0}$.
- Note that α_j increases as j increases, since for $j < j'$, $P(y_i \leq j) < P(y_i \leq j')$.
- β_k is the change in log-odds of falling into or below any category for a one unit increase in x_k , holding all other covariates fixed.

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- The likelihood function viewed as a function of $(\{\alpha_j\}, \beta)$ is

$$\begin{aligned} \prod_{i=1}^N \prod_{j=1}^c \pi_{ij}^{y_{ij}} &= \prod_{i=1}^N \prod_{j=1}^c (P(y_i \leq j | \mathbf{x}_i) - P(y_i \leq j-1 | \mathbf{x}_i))^{y_{ij}} \\ &= \prod_{i=1}^N \prod_{j=1}^c \left(\frac{\exp(\alpha_j + \mathbf{x}_i' \beta)}{1 + \exp(\alpha_j + \mathbf{x}_i' \beta)} - \frac{\exp(\alpha_{j-1} + \mathbf{x}_i' \beta)}{1 + \exp(\alpha_{j-1} + \mathbf{x}_i' \beta)} \right)^{y_{ij}}. \end{aligned}$$

- The log-likelihood is

$$\log \mathcal{L} = \sum_{i=1}^N \sum_{j=1}^c y_{ij} \log \left[\frac{\exp(\alpha_j + \mathbf{x}_i' \beta)}{1 + \exp(\alpha_j + \mathbf{x}_i' \beta)} - \frac{\exp(\alpha_{j-1} + \mathbf{x}_i' \beta)}{1 + \exp(\alpha_{j-1} + \mathbf{x}_i' \beta)} \right]$$

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Latent variable motivation

- The model can be interpreted in terms of a *latent variable*.
- Suppose the observed response y_i results from grouping an underlying continuous variable y_i^* using cut-points $\alpha_1 < \alpha_2 < \dots < \alpha_{c-1}$, so that

$$y_i = j \quad \text{if } \alpha_{j-1} < y_i^* \leq \alpha_j$$

$$\text{then,} \quad P(y_i \leq j) = P(y_i^* \leq \alpha_j).$$

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- Suppose that the underlying continuous variable follows a linear model of the form

$$y_i^* = \mathbf{x}_i' \boldsymbol{\beta} + \varepsilon_i,$$

where the error term ε_i has c.d.f. $F(\varepsilon_i)$, then

$$P(y_i^* \leq \alpha_j) = P(\varepsilon_i \leq \alpha_j - \mathbf{x}_i' \boldsymbol{\beta}) = F(\alpha_j - \mathbf{x}_i' \boldsymbol{\beta})$$

and

$$F^{-1}(P(y_i \leq j)) = \alpha_j - \mathbf{x}_i' \boldsymbol{\beta}^*$$

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- Note that the latent variable formulation results in linear predictor $\alpha_j - \mathbf{x}_i' \boldsymbol{\beta}$ rather than $\alpha_j + \mathbf{x}_i' \boldsymbol{\beta}$.
- When using software check which parametrization is used, $\alpha_j + \mathbf{x}_i' \boldsymbol{\beta}$ or $\alpha_j - \mathbf{x}_i' \boldsymbol{\beta}$, and interpret β_k accordingly.
- Note that we have the same parameters $\boldsymbol{\beta}$ for the effects on Y regardless of how the cutpoints $\{\alpha_j\}$ are chosen.
- Two investigators who use different response categories in studying an association should reach similar conclusions.

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- If $\varepsilon \sim \text{logistic}$, then F^{-1} is the logit link.
- Normality for ε implies a probit link for the cumulative probabilities.

$$\Phi^{-1}(P(y_i \leq j)) = \alpha_j + \mathbf{x}_i' \boldsymbol{\beta}$$

- In general, the fit of a logit and probit model are quite similar.
- Another choice is the complementary log-log link, which leads to the model

$$\log(-\log(1 - P(y_i \leq j))) = \alpha_j + \mathbf{x}_i' \boldsymbol{\beta}.$$

Example: Cheese-tasting experiment

Data from McCullagh and Nelder (1989), Table 5.1. Subjects were randomly assigned to taste one of four different cheeses. Response categories are 1=strong dislike to 9=excellent taste.

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Cheese	Response category								
	1	2	3	4	5	6	7	8	9
A	0	0	1	7	8	8	19	8	1
B	6	9	12	11	7	6	1	0	0
C	1	1	6	8	23	7	5	1	0
D	0	0	0	1	3	7	14	16	11

Note that the function `polr(.)` in the R package `MASS` uses the following parametrization for the cumulative logit model

$$\log \frac{P(y_i \leq j)}{1 - P(y_i \leq j)} = \alpha_j - \mathbf{x}_i' \boldsymbol{\beta}$$

That is,

$$\begin{aligned} \log \frac{P(y_i \leq 1)}{P(y_i > 1)} &= \alpha_1 - \beta_1 x_{1i} - \beta_2 x_{2i} - \beta_3 x_{3i} \\ \log \frac{P(y_i \leq 2)}{P(y_i > 2)} &= \alpha_2 - \beta_1 x_{1i} - \beta_2 x_{2i} - \beta_3 x_{3i} \\ &\vdots \\ \log \frac{P(y_i \leq 8)}{P(y_i > 8)} &= \alpha_8 - \beta_1 x_{1i} - \beta_2 x_{2i} - \beta_3 x_{3i} \end{aligned}$$

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Using cheese A as the reference, the three dummy variables are

$$\begin{aligned} x_{1i} &= \begin{cases} 1 & \text{if subject } i \text{ tasted cheese B} \\ 0 & \text{otherwise} \end{cases} \\ x_{2i} &= \begin{cases} 1 & \text{if subject } i \text{ tasted cheese C} \\ 0 & \text{otherwise} \end{cases} \\ x_{3i} &= \begin{cases} 1 & \text{if subject } i \text{ tasted cheese D} \\ 0 & \text{otherwise} \end{cases} \end{aligned}$$

A positive β_k indicates a greater liking for cheese x_k compared to the reference.

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```
library(MASS)
polr.fit = polr(as.factor(response) ~ type, weights=count, data=cheese)

> summary(polr.fit)
```

Coefficients:

	Value	Std. Error	t value
typeB	-3.352	0.4287	-7.819
typeC	-1.710	0.3715	-4.603
typeD	1.613	0.3805	4.238

Intercepts:

	Value	Std. Error	t value
1 2	-5.4674	0.5236	-10.4413
2 3	-4.4122	0.4278	-10.3148
3 4	-3.3126	0.3700	-8.9522

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4 5	-2.2440	0.3267	-6.8680
5 6	-0.9078	0.2833	-3.2037
6 7	0.0443	0.2646	0.1673
7 8	1.5459	0.3017	5.1244
8 9	3.1058	0.4057	7.6547

Residual Deviance: 711.3479
AIC: 733.3479

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- $\hat{\alpha}_1 = -5.47$ is the estimated log-odds of falling into category 1 (strong dislike) versus all other categories for cheese A.
- $\hat{\alpha}_8 = 3.11$ is the estimated log-odds of responses in $1, \dots, 8$ versus 9 for cheese A.
- $\hat{\beta}_1 = -3.352$ and has p -value $= 9.41 \times 10^{-15}$ (`2*pt(-7.819, 1653)` where $df = 208 \times 8 - 11 = 1653$). This indicates that cheese B does not taste as good as cheese A.
- The results imply that D is the preferred cheese, followed by A, then C, and B comes last.

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We can also use the R package **VGAM** to fit the proportional odds model, but we need to first put the data in an ungrouped format.

```
cheese.ungrp = as.data.frame(lapply(cheese, function(x,p) rep(x,p), cheese$count))
vglm.fit = vglm(response ~ type, family=cumulative(parallel=TRUE), data=cheese.ungrp)
```

```
> summary(vglm.fit)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept):1	-5.46737	0.52022	-10.510	< 2e-16 ***
(Intercept):2	-4.41218	0.42472	-10.389	< 2e-16 ***
(Intercept):3	-3.31262	0.36967	-8.961	< 2e-16 ***
(Intercept):4	-2.24401	0.32617	-6.880	5.99e-12 ***
(Intercept):5	-0.90776	0.27477	-3.304	0.000954 ***
(Intercept):6	0.04426	0.25984	0.170	0.864758
(Intercept):7	1.54592	0.30419	5.082	3.73e-07 ***
(Intercept):8	3.10577	0.40443	7.679	1.60e-14 ***

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```

typeB      3.35184    0.42351    7.914 2.48e-15 ***
typeC      1.70989    0.37305    4.583 4.57e-06 ***
typeD     -1.61279    0.37778   -4.269 1.96e-05 ***
---

```

```

Residual deviance: 711.3479 on 1653 degrees of freedom
Log-likelihood: -355.674 on 1653 degrees of freedom

```

- Note that the function `vglm(.)` with `family = cumulative` uses the parametrization

$$\log \frac{P(y_i \leq j)}{1 - P(y_i \leq j)} = \alpha_j + \mathbf{x}_i' \boldsymbol{\beta}$$

so, a positive β_k indicates a greater dislike for cheese x_k compared to the reference.

- The estimates of α_j are the same as those using `polr(.)`, but the signs for the estimates of β_k are different.

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We can test the proportional odds assumption

H_0 : same slope for all cumulative logits vs. H_1 : different slopes

with a likelihood ratio test comparing the model with varying slopes for the cumulative logits and the model above

```

noprop.fit = vglm(response ~ type, family=cumulative, data=cheese.ungrp)
---

```

```

Residual deviance: 691.0397 on 1632 degrees of freedom
Log-likelihood: -345.5199 on 1632 degrees of freedom
---

```

```

> 1-pchisq(-2*(logLik(vglm.fit)-logLik(noprop.fit)),
           df=df.residual(vglm.fit)-df.residual((noprop.fit)))
[1] 0.5018223

```

We fail to reject the null and can assume a proportional odds structure.