

## Logistic regression: Extensions



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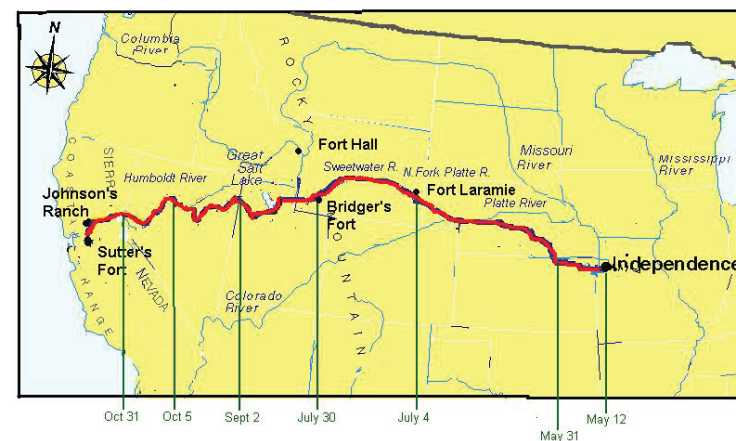


## Donner party: A graphic tale of survival & influence

### History:

- Apr—May, 1846: Donner/Reed families set out from Springfield, IL to CA
- July: Reach Bridger's Fort WY: 87 people, 23 wagons

### TRAIL OF THE DONNER PARTY



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## Donner party: A graphic tale of survival & influence

### History:

- "Hastings cutoff": an untried route through Salt Lake desert (90 people)
- Worst recorded winter: Oct 31 blizzard; stranded at Truckee Lake (nr Reno)
  - Rescue parties sent out ("Dire necessity", "Forelorn hope", ...)
  - Relief parties from CA: 42 survivors (Mar—Apr 1847)

### TRAIL OF THE DONNER PARTY



Who lived? Who died?

Can we explain w/  
logistic regression?

## Donner party: Data

```
> data("Donner", package="vcdExtra")
> Donner$survived <- factor(Donner$survived,
                             labels=c("no", "yes"))

> car::some(Donner, 8)
```

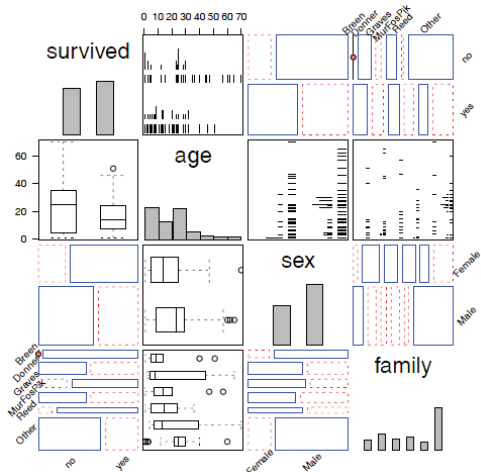
	family	age	sex	survived	death
Breen, Peter	Breen	3	Male	yes	<NA>
Donner, Jacob	Donner	65	Male	no	1846-12-21
Foster, Jeremiah	MurFosPik	1	Male	no	1847-03-13
Graves, Nancy	Graves	9	Female	yes	<NA>
McCutchen, Harriet	McCutchen	1	Female	no	1847-02-02
Reed, James	Reed	46	Male	yes	<NA>
Reinhardt, Joseph	Other	30	Male	no	1846-12-21
Wolfinger, Doris	FosdWolf	20	Female	yes	<NA>

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# Overview: a gpairs() plot

A generalized pairs plot uses different plot types for pairs of continuous, discrete variables

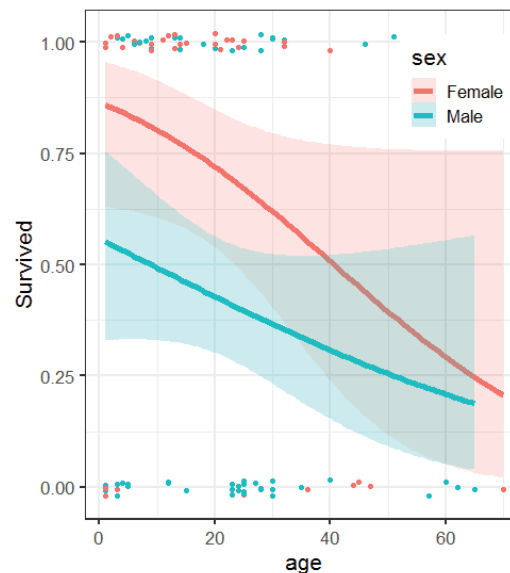


- Binary response: `survived`
- Categorical predictors: `sex`, `family`
- Quantitative predictor: `age`
- Q: Is the effect of age linear?
- Q: Are there interactions among predictors?

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# Exploratory plots

Before fitting models, it is useful to explore the data with conditional ggplots



Survival decreases with age for both men and women

Women more likely to survive, particularly the young

Conf. bands show the data is thin at older ages

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# Using ggplot

Basic plot: survived vs. age, colored by sex, with jittered points

```
gg <- ggplot(Donner,
             aes(age, as.numeric(survived=="yes"), color=sex)) +
  ylab("Survived") +
  geom_jitter(height = 0.02, width = 0)
```

To this we can add conditional logistic fits using `stat_smooth(method="glm")`

```
gg + stat_smooth(method = "glm",
                 method.args = list(family = binomial),
                 formula = y ~ x,
                 alpha = 0.2, size=2, aes(fill = sex)) +
  theme_bw(base_size = 16) +
  theme(legend.position = c(.85, .85))
```

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# Questions

- Is the relation of survival to age well expressed as a **linear** logistic regression model?

- Allow a quadratic or higher power using `poly(age,2)`, `poly(age,3)`

$$\begin{aligned}\text{logit}(\pi_i) &= \alpha + \beta_1 x_i + \beta_2 x_i^2 \\ \text{logit}(\pi_i) &= \alpha + \beta_1 x_i + \beta_2 x_i^2 + \beta_3 x_i^3\end{aligned}$$

- Use **natural spline** functions: `ns(age, df)`
- Use **non-parametric** smooths: `loess(age, span, degree)`

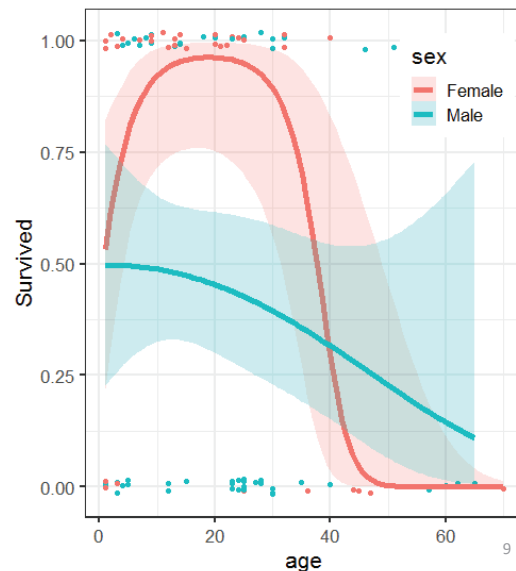
- Is the relation the same for men & women?

- Allow an **interaction** of `sex * age` or `sex * f(age)`
- Test goodness of fit relative to the main effects model

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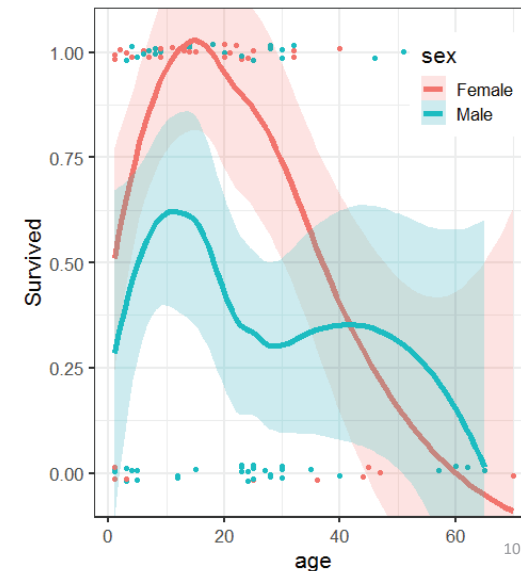
```
gg + stat_smooth(method = "glm",
  method.args = list(family = binomial),
  formula = y ~ poly(x,2), alpha = 0.2, size=2, aes(fill = sex)) + ...
```

Fit separate quadratics for  
M & F



```
gg + stat_smooth(method = "loess", span=0.9,
  alpha = 0.2, size=2,
  aes(fill = sex)) + coord_cartesian(ylim=c(-.05,1.05)) +
```

Fit separate loess smooths for  
M & F



## Fitting models

Models with **linear** effect of age:

```
> donner.mod1 <- glm(survived ~ age + sex,
  data=Donner, family=binomial)
> donner.mod2 <- glm(survived ~ age * sex,
  data=Donner, family=binomial)
> Anova(donner.mod2)
Analysis of Deviance Table (Type II tests)
```

```
Response: survived
      LR Chisq Df Pr(>Chisq)
age      5.52  1  0.0188 *
sex      6.73  1  0.0095 **
age:sex   0.40  1  0.5269
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Fitting models

Models with **quadratic** effect of age:

```
> donner.mod3 <- glm(survived ~ poly(age,2) + sex,
  data=Donner, family=binomial)
> donner.mod4 <- glm(survived ~ poly(age,2) * sex,
  data=Donner, family=binomial)
> Anova(donner.mod4)
Analysis of Deviance Table (Type II tests)
```

```
Response: survived
      LR Chisq Df Pr(>Chisq)
poly(age, 2)    9.91  2  0.0070 **
sex             8.09  1  0.0044 **
poly(age, 2):sex 8.93  2  0.0115 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

# Comparing models

These models are only nested in **pairs**. We can compare them using AIC &  $\Delta\chi^2$

```
> library(vcdExtra)
> LRstats(donner.mod1, donner.mod2, donner.mod3, donner.mod4)
Likelihood summary table:
      AIC BIC LR Chisq Df Pr(>Chisq)
donner.mod1 117 125   111.1 87    0.042 *
donner.mod2 119 129   110.7 86    0.038 *
donner.mod3 115 125   106.7 86    0.064 .
donner.mod4 110 125    97.8 84    0.144
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

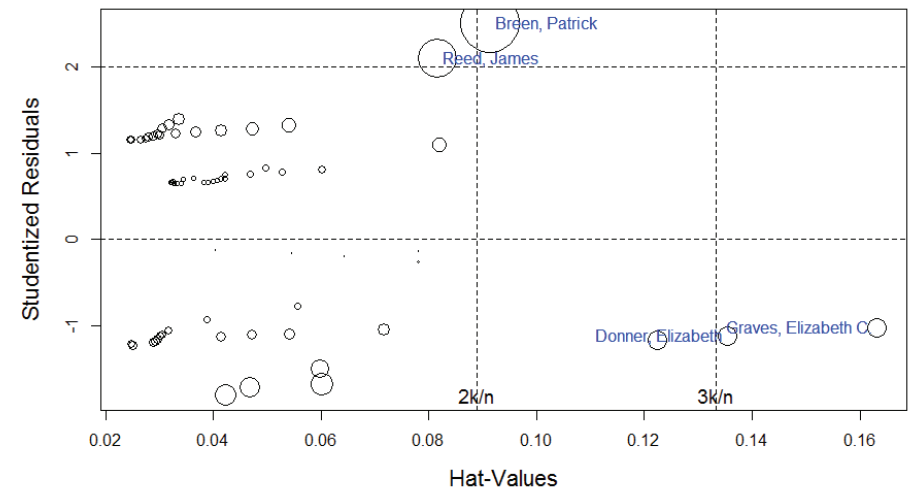
	linear	non-linear	$\Delta\chi^2$	p-value	
additive	111.128	106.731	4.396	0.036	✓
non-additive	110.727	97.799	12.928	0.000	✓
$\Delta\chi^2$	0.400	8.932			
p-value	0.527	0.003			

✓

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# Who was influential?

```
res <- influencePlot(donner.mod3, id = list(col="blue", n=2), scale=8)
```



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# Why were they influential?

```
> idx <- which(rownames(Donner) %in% rownames(res))
> # show data together with diagnostics
> cbind(Donner[idx,2:4], res)
      age sex survived StudRes   Hat   CookD
Breen, Patrick    51  Male      yes    2.50 0.0915 0.3235
Donner, Elizabeth  45 Female     no   -1.11 0.1354 0.0341
Graves, Elizabeth C. 47 Female     no   -1.02 0.1632 0.0342
Reed, James       46  Male      yes    2.10 0.0816 0.1436
```

- Patrick Breen, James Reed: Older men who survived
- Elizabeth Donner, Elizabeth Graves: Older women who died
- Moral lessons of this story:
  - Don't try to cross the Donner Pass in late October; if you do, bring lots of food
  - Plots of fitted models show *only* what is included in the model
  - Discrete data often need smoothing (or non-linear terms) to see the pattern
  - Always examine model diagnostics — preferably graphic

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# Polytomous responses: Overview

When Response categories are:

**Unordered**

for example,

Hall  
Rowlands  
Meinzer

the analysis can use:

**Multinomial  
logistic  
regression**

we model these logits:

None    Some or marked  
None or Some    Marked

**Ordered**

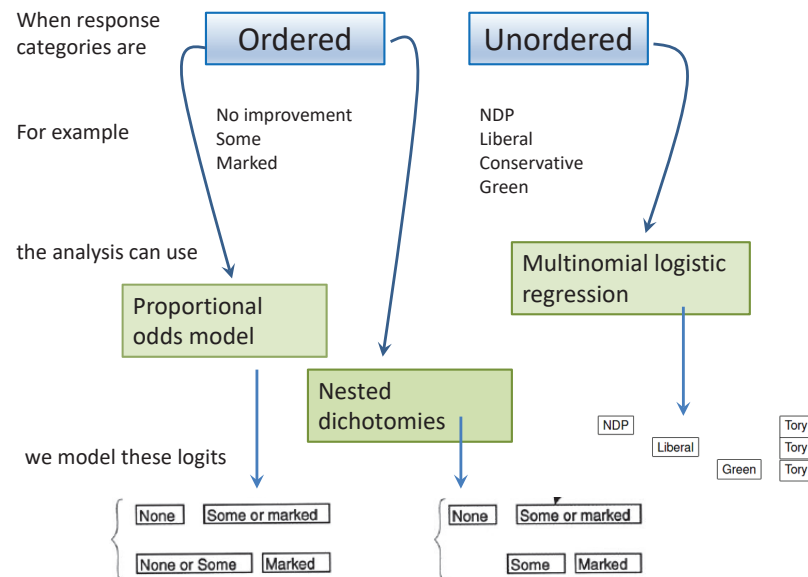
No improvement  
Some improvement  
Marked improvement

**Proportional  
odds model**

**Nested  
dichotomies**

None    Some or marked  
Some    Marked

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## Polytomous responses: Ordered

### Polytomous responses

- $m$  categories  $\rightarrow (m-1)$  comparisons (logits)
- One part of the model for each logit
- Similar to ANOVA where an  $m$ -level factor  $\rightarrow (m-1)$  contrasts (df)

**Ordered** response categories, e.g., None, Some, Marked improvement

#### Proportional odds model

- Uses adjacent-category logits
- Assumes slopes are **equal** for all  $m - 1$  logits; only intercepts vary
- R: `polr()` in **MASS**

#### Nested dichotomies

- Model each logit separately
- $G^2$  s are additive  $\rightarrow$  combined model

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## Polytomous responses: Unordered

**Unordered** response categories, e.g., vote: NDP, Liberal, Green, Tory

- Multinomial logistic regression
  - Fits  $m - 1$  logistic models for logits of category  $i = 1, 2, \dots, m - 1$  vs. category  $m$



- This is the most general approach
- R: `multinom()` function in **nnet**
- Can also use nested dichotomies

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## Proportional odds model

Arthritis treatment data:

Sex	Treatment	Improvement			Total
		None	Some	Marked	
F	Active	6	5	16	27
F	Placebo	19	7	6	32
M	Active	7	2	5	14
M	Placebo	10	0	1	11

The **proportional odds** model uses logits for  $(m-1) = 2$  **adjacent category** cutpoints

$$\text{logit}(\theta_{ij1}) = \log \frac{\pi_{ij1}}{\pi_{ij2} + \pi_{ij3}} = \text{logit}(\text{None vs. [Some or Marked]})$$

$$\text{logit}(\theta_{ij2}) = \log \frac{\pi_{ij1} + \pi_{ij2}}{\pi_{ij3}} = \text{logit}(\text{[None or Some] vs. Marked})$$

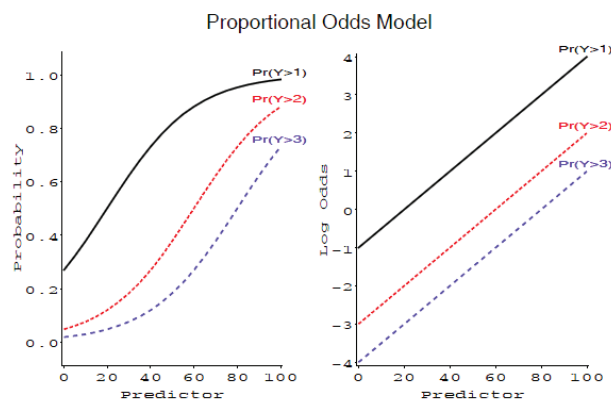
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- Consider a logistic regression model for each logit:

$$\text{logit}(\theta_{ij1}) = \alpha_1 + \mathbf{x}_{ij}'\beta_1 \quad \text{None vs. Some/Marked}$$

$$\text{logit}(\theta_{ij2}) = \alpha_2 + \mathbf{x}_{ij}'\beta_2 \quad \text{None/Some vs. Marked}$$

- Proportional odds assumption: regression functions are parallel on the logit scale i.e.,  $\beta_1 = \beta_2$ .



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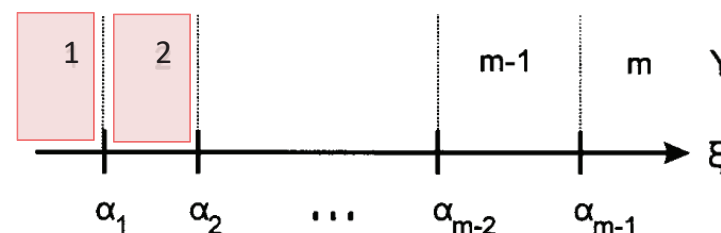
## Proportional odds: Latent variable interpretation

A simple motivation for the proportional odds model:

- Imagine a continuous, but *unobserved* response,  $\xi$ , a linear function of predictors

$$\xi_i = \beta^T \mathbf{x}_i + \epsilon_i$$

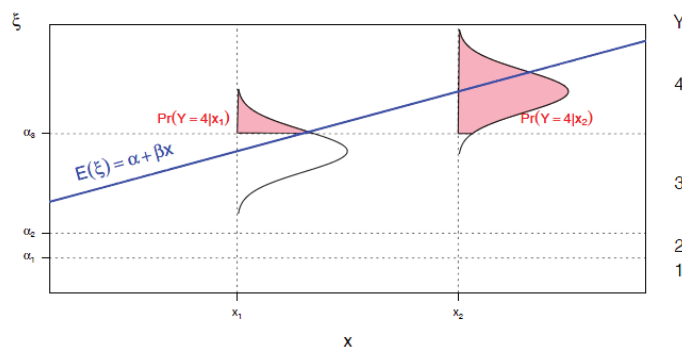
- The *observed* response,  $Y$ , is discrete, according to some *unknown* thresholds,  $\alpha_1 < \alpha_2 < \dots < \alpha_{m-1}$
- That is, the response,  $Y = i$  if  $\alpha_i \leq \xi_i < \alpha_{i+1}$
- Thus, intercepts in the proportional odds model  $\sim$  thresholds on  $\xi$



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## Proportional odds: Latent variable interpretation

We can visualize the relation of the latent variable  $\xi$  to the observed response  $Y$ , for two values,  $x_1$  and  $x_2$ , of a single predictor,  $X$  as shown below:

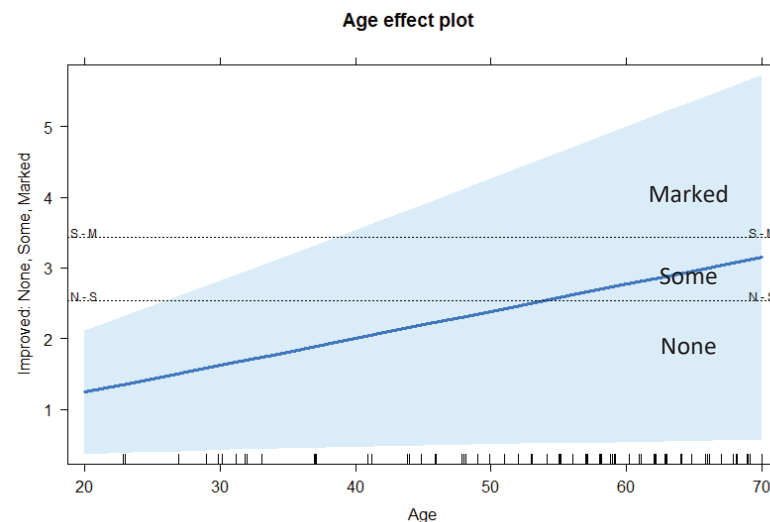


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## Proportional odds: Latent variable interpretation

Plotting the effect of Age on the latent variable scale

```
plot(effect("Age", mod = arth.polr, latent = TRUE))
```



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# Fitting the proportional odds model

The response Improved has been defined as an [ordered](#) factor

```
> data(Arthritis, package = "vcd")
> head(Arthritis$Improved)
[1] Some    None    None    Marked Marked Marked
Levels: None < Some < Marked
```

Fit the model with MASS::polr()

```
> arth.polr <- polr(Improved ~ Sex + Treatment + Age,
  data = Arthritis)

> summary(arth.polr)      # for coefficients
> Anova(arth.polr)        # Type II tests
```

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summary() gives the standard statistical results

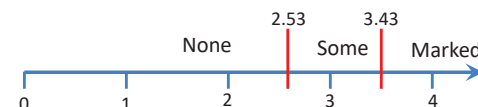
```
> summary(arth.polr)      # for coefficients

Call:
polr(formula = Improved ~ Sex + Treatment + Age, data = Arthritis)

Coefficients:
                Value Std. Error t value
SexMale         -1.2517    0.5464  -2.29
TreatmentTreated  1.7453    0.4759   3.67
Age              0.0382    0.0184   2.07

Intercepts:
                Value Std. Error t value
None|Some       2.532    1.057    2.395
Some|Marked     3.431    1.091    3.144

Residual Deviance: 145.46
AIC: 155.46
```



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car::Anova() gives hypothesis tests for the model terms

```
> Anova(arth.polr)      # Type II tests
Analysis of Deviance Table (Type II tests)

Response: Improved
      LR Chisq Df Pr(>Chisq)
Sex      5.69  1  0.01708 *
Treatment 14.71  1  0.00013 ***
Age       4.57  1  0.03251 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Type II tests are [partial](#) tests, controlling for the effects of all other terms
- e.g.,  $G^2(\text{Sex} \mid \text{Treatment}, \text{Age})$ ,  $G^2(\text{Treatment} \mid \text{Age}, \text{Sex})$
- NB: anova() gives only Type I ([sequential](#)) tests – not usually useful

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# Testing the proportional odds assumption

- The PO model is valid only when the slopes are equal for all predictors
- This can be tested by comparing this model to the [generalized logit](#) NPO model

$$\text{PO: } L_j = \alpha_j + \mathbf{x}^T \beta \quad j = 1, \dots, m-1 \quad (1)$$

$$\text{NPO: } L_j = \alpha_j + \mathbf{x}^T \beta_j \quad j = 1, \dots, m-1 \quad (2)$$

- A likelihood ratio test requires fitting both models calculating  $\Delta G^2 = G_{\text{NPO}}^2 - G_{\text{PO}}^2$  with  $p$  df.
- This can be done using [vglim\(\)](#) in the [VGAM](#) package
- The [rms](#) package provides a visual assessment, plotting the conditional mean  $E(X \mid Y)$  of a given predictor,  $X$ , at each level of the ordered response  $Y$ .
- If the response behaves ordinally in relation to  $X$ , these means should be strictly increasing or decreasing with  $Y$ .

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# Testing the proportional odds assumption

In VGAM, the PO model is fit using `family = cumulative(parallel=TRUE)`

```
library(VGAM)
arth.po <- vglm(Improved ~ Sex + Treatment + Age, data=Arthritis,
               family = cumulative(parallel=TRUE))
```

The more general NPO model is fit using `parallel=FALSE`

```
arth.npo <- vglm(Improved ~ Sex + Treatment + Age, data=Arthritis,
                 family = cumulative(parallel=FALSE))
```

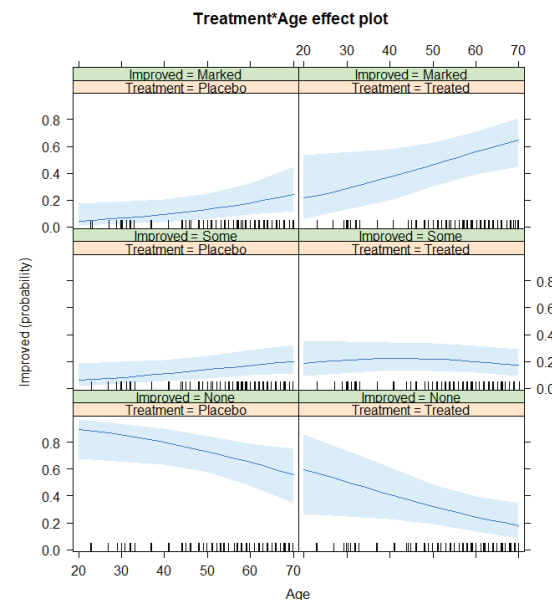
The LR test indicates that the proportional odds model is OK

```
> VGAM::lrtest(arth.npo, arth.po)
Likelihood ratio test
```

```
Model 1: Improved ~ Sex + Treatment + Age
Model 2: Improved ~ Sex + Treatment + Age
#Df LogLik Df Chisq Pr(>Chisq)
1 160 -71.8
2 163 -72.7 3 1.88 0.6
```

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# Plotting effects in the PO model



```
library(effects)
plot(effect("Treatment:Age",
           arth.polr))
```

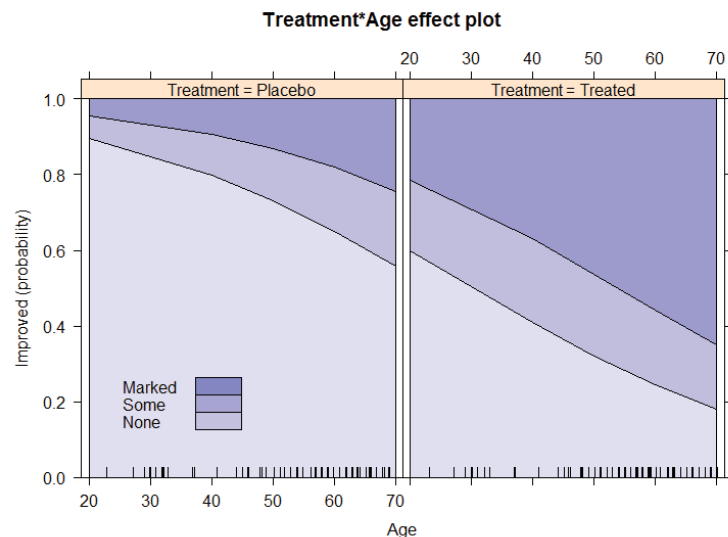
The default style shows separate curves for the response categories

Difficult to compare these in different panels

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Visual comparisons are easier when the response levels are "stacked"

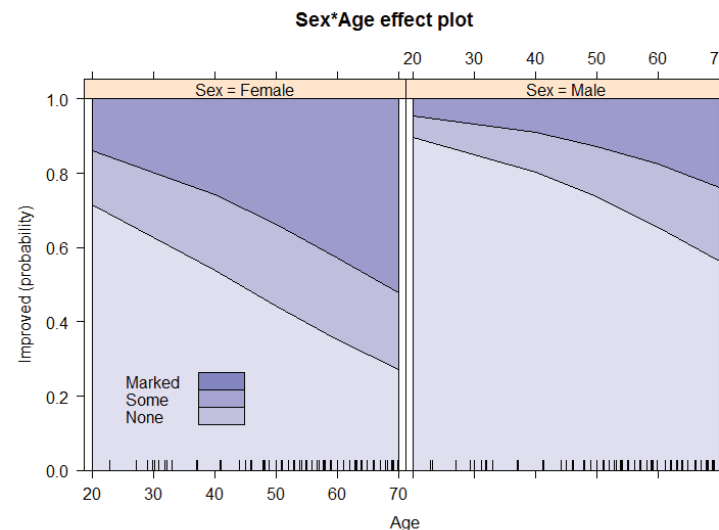
```
plot(effect("Treatment:Age", arth.polr), style='stacked',
     colors=scales::alpha("blue", alpha = (1:3)/8) )
```



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Visual comparisons are easier when the response levels are "stacked"

```
plot(effect("Sex:Age", arth.polr), style='stacked',
     colors=scales::alpha("blue", alpha = (1:3)/8) )
```

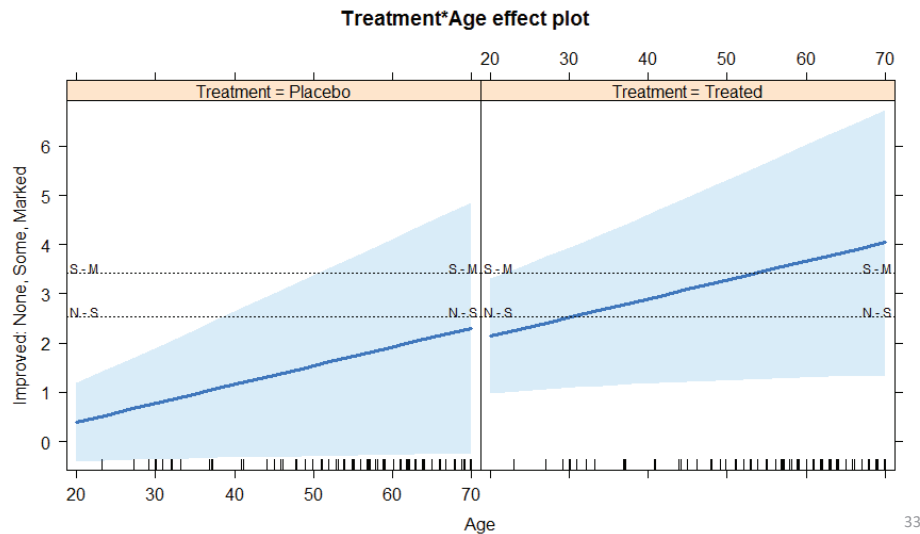


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These plots are even simpler on the logit scale, using `latent = TRUE` to show the cutpoints between adjacent categories

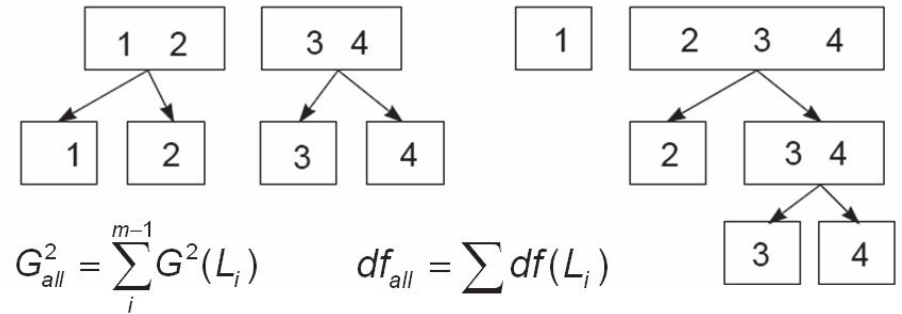
```
plot(effect("Treatment:Age", arth.polr, latent = TRUE))
```



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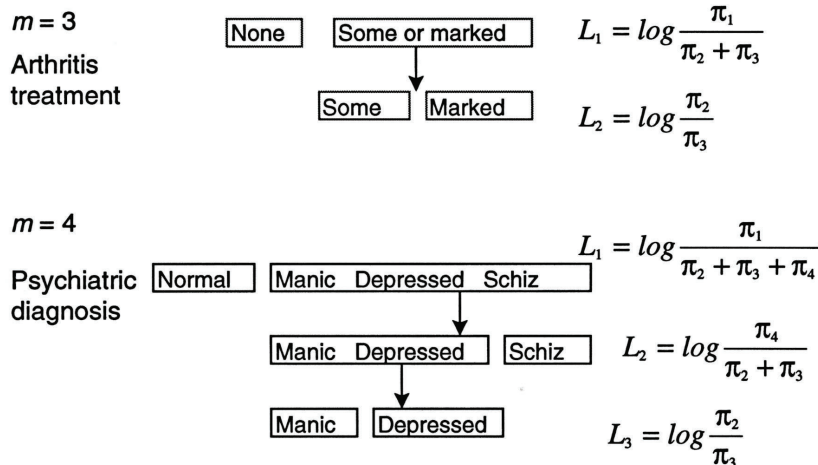
## Nested dichotomies

- $m$  categories  $\rightarrow (m - 1)$  comparisons (logits)
- If these are formulated as  $(m - 1)$  **nested dichotomies**:
  - Each dichotomy can be fit using the familiar binary-response logistic model,
  - the  $m - 1$  models will be statistically independent ( $G^2$  statistics will be additive)
  - (Need some extra work to summarize these as a single, combined model)
- This allows the slopes to differ for each logit



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## Nested dichotomies: Examples

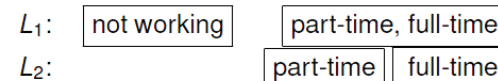


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## Example: Women's Labour-force participation

Data: *Social Change in Canada Project*, York ISR, `car::Women1f` data

- **Response:** not working outside the home ( $n=155$ ), working part-time ( $n=42$ ) or working full-time ( $n=66$ )
- Model as two nested dichotomies:
  - Working ( $n=106$ ) vs. NotWorking ( $n=155$ )
  - Working full-time ( $n=66$ ) vs. working part-time ( $n=42$ ).



- **Predictors:**
  - Children? — 1 or more minor-aged children
  - Husband's Income — in \$1000s
  - Region of Canada (not considered here)

	partic	hincome	children	region
31	not.work	13	present	Ontario
51	parttime	10	present	Prairie
74	not.work	17	present	Ontario
108	not.work	19	present	Ontario
131	parttime	19	present	Ontario
161	not.work	15	present	Ontario
178	fulltime	13	absent	Ontario

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## Nested dichotomies: Recoding

In R, need to create new variables, working and fulltime.

```
> library(dplyr)
> Womenlf <- Womenlf |>
  mutate(working = ifelse(partic=="not.work", 0, 1)) |>
  mutate(fulltime = case_when(
    working & partic == "fulltime" ~ 1,
    working & partic == "parttime" ~ 0
  ))
> some(Womenlf, 8)
```

	partic	hincome	children	region	working	fulltime
76	parttime	38	present	Ontario	1	0
93	parttime	9	present	Ontario	1	0
101	fulltime	11	absent	Atlantic	1	1
107	not.work	13	present	Prairie	0	NA
109	not.work	19	present	Atlantic	0	NA
157	parttime	15	present	BC	1	0
220	fulltime	16	absent	Quebec	1	1
249	not.work	23	absent	Quebec	0	NA

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## Nested dichotomies: Fitting

Then, fit separate models for each dichotomy:

```
Womenlf <- within(Womenlf, contrasts(children)<- 'contr.treatment')
mod.working <- glm(working ~ hincome + children, family=binomial, data=Womenlf)
mod.fulltime <- glm(fulltime ~ hincome + children, family=binomial, data=Womenlf)
```

Some output from summary(mod.working)

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	1.3358	0.3838	3.48	0.0005 ***
hincome	-0.0423	0.0198	-2.14	0.0324 *
childrenpresent	-1.5756	0.2923	-5.39	7e-08 ***

Some output from summary(mod.fulltime)

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	3.4778	0.7671	4.53	5.8e-06 ***
hincome	-0.1073	0.0392	-2.74	0.0061 **
childrenpresent	-2.6515	0.5411	-4.90	9.6e-07 ***

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## Nested dichotomies: Combined tests

- Nested dichotomies →  $\chi^2$  tests and df for the separate logits are **independent**
- → add, to give tests for the full  $m$ -level response (**manually**)

Global tests of BETA=0				
Test	Response	ChiSq	DF	Prob ChiSq
Likelihood Ratio	working	36.4184	2	<.0001
	fulltime	39.8468	2	<.0001
	<b>ALL</b>	<b>76.2652</b>	<b>4</b>	<b>&lt;.0001</b>

Wald tests for each coefficient:

Wald tests of maximum likelihood estimates				
Variable	Response	WaldChiSq	DF	Prob ChiSq
Intercept	working	12.1164	1	0.0005
	fulltime	20.5536	1	<.0001
	<b>ALL</b>	<b>32.6700</b>	<b>2</b>	<b>&lt;.0001</b>
children	working	29.0650	1	<.0001
	fulltime	24.0134	1	<.0001
	<b>ALL</b>	<b>53.0784</b>	<b>2</b>	<b>&lt;.0001</b>
husinc	working	4.5750	1	0.0324
	fulltime	7.5062	1	0.0061
	<b>ALL</b>	<b>12.0813</b>	<b>2</b>	<b>0.0024</b>

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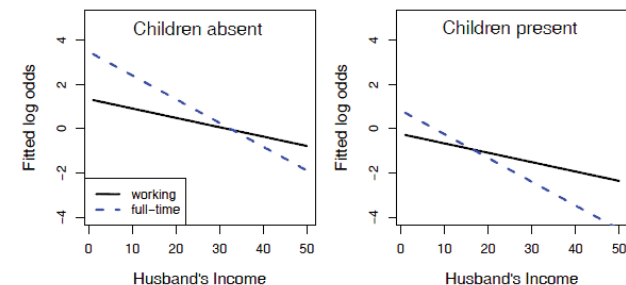
## Nested dichotomies: Interpretation

Write out the predictions for the two logits, and compare coefficients:

$$\log \left( \frac{\Pr(\text{working})}{\Pr(\text{not working})} \right) = 1.336 - 0.042 H\$ - 1.576 \text{ kids}$$

$$\log \left( \frac{\Pr(\text{fulltime})}{\Pr(\text{parttime})} \right) = 3.478 - 0.107 H\$ - 2.652 \text{ kids}$$

Better yet, plot the predicted log odds for these equations:



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## Nested dichotomies: Plotting

For plotting, calculate the predicted probabilities (or logits) over a grid of combinations of the predictors in each sub-model, using `predict()`.

- `type = "response"` gives these on the **probability** scale
- `type = "link"` (default) gives these on the **logit** scale

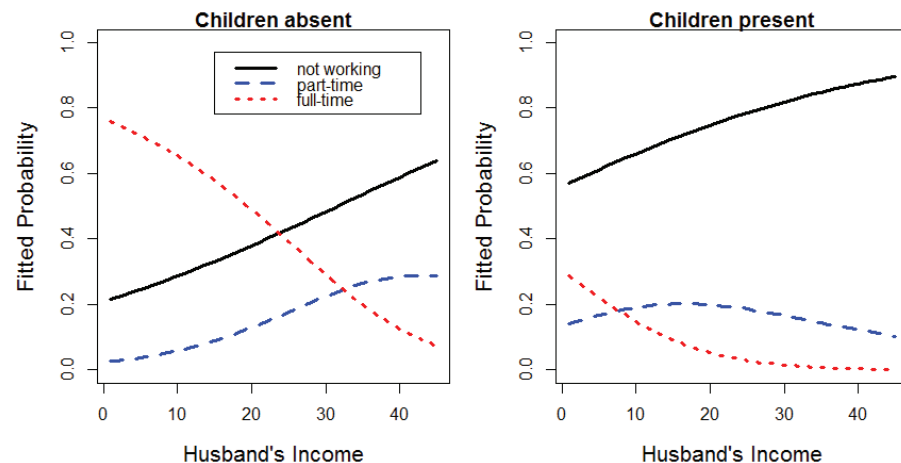
```
predictors <- expand.grid(hincome=1:45, children=c('absent', 'present'))
# get fitted values for both sub-models
p.work <- predict(mod.working, predictors, type='response')
p.fulltime <- predict(mod.fulltime, predictors, type='response')
```

The fitted value for the fulltime dichotomy is **conditional** on working outside the home; multiplying by the probability of working gives the **unconditional** probability.

```
p.full <- p.work * p.fulltime
p.part <- p.work * (1 - p.fulltime)
p.not <- 1 - p.work
```

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This plot is produced using base R functions `plot()`, `lines()` and `legend()`  
See the file: wlf-nested.R on the course web page for details



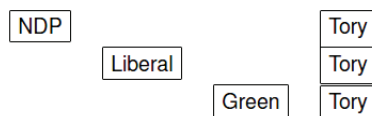
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## Multinomial logistic regression

- Multinomial logistic regression models the probabilities of  $m$  response categories as  $(m-1)$  logits

- Typically, these compare each of the first  $m-1$  categories to the last (reference) category: 1 vs.  $m$ , 2 vs.  $m$ , ...  $m-1$  vs.  $m$

e.g., vote for  
( $m = 4$ )



- Logits for any pair of categories can be calculated from the  $m-1$  fitted ones

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## Multinomial logistic regression

- with  $k$  predictors,  $x_1, x_2, \dots, x_k$  and for  $j=1, 2, \dots, m-1$ , the model fits separate slopes for each logit

$$L_{jm} \equiv \log \left( \frac{\pi_{ij}}{\pi_{im}} \right) = \beta_{0j} + \beta_{1j} x_{i1} + \beta_{2j} x_{i2} + \dots + \beta_{kj} x_{ik} \\ = \beta_j^T \mathbf{x}_i$$

- One set of coefficients,  $\beta_j$  for each response category except the last
- Each coefficient,  $\beta_{hj}$ , gives effect on log odds that response is  $j$  vs.  $m$ , for a one unit change in the predictor  $x_h$
- Probabilities in response categories are calculated as

$$\pi_{ij} = \frac{\exp(\beta_j^T \mathbf{x}_i)}{\sum_{j=1}^{m-1} \exp(\beta_j^T \mathbf{x}_i)}, j = 1, \dots, m-1; \quad \pi_{im} = 1 - \sum_{j=1}^{m-1} \pi_{ij}$$

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# Fitting multinomial regression models

Fit the multinomial model using `nnet::multinom()`  
For ease of interpretation, make `not.work` the reference category

```
> Womenlf$partic <- relevel(Womenlf$partic, ref="not.work")
> library(nnet)
> wlf.multinom <- multinom(partic ~ hincome + children,
                           data=Womenlf, Hess=TRUE)
```

The **Anova()** tests are similar to what we got from summing these tests from the two nested dichotomies

```
> Anova(wlf.multinom)
Analysis of Deviance Table (Type II tests)
```

```
Response: partic
          LR Chisq Df Pr(>Chisq)
hincome    15.2   2  0.00051 ***
children   63.6   2  1.6e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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# Interpreting coefficients

As before, interpret coefficients as increments in log odds or `exp(coef)` as multiples

```
> coef(wlf.multinom)
      (Intercept) hincome childrenpresent
parttime    -1.43  0.00689         0.0215
fulltime     1.98 -0.09723        -2.5586

> exp(coef(wlf.multinom))
      (Intercept) hincome childrenpresent
parttime    0.239  1.007         1.0217
fulltime    7.263  0.907         0.0774
```

$$\log\left(\frac{\Pr(\text{parttime})}{\Pr(\text{notworking})}\right) = -1.43 + 0.0069 \text{ H\$} - 0.215 \text{ kids}$$

$$\log\left(\frac{\Pr(\text{fulltime})}{\Pr(\text{notworking})}\right) = 1.98 - 0.097 \text{ H\$} - 2.55 \text{ kids}$$

Each 1000\$ of husband's income:

- Increases log odds of parttime by 0.0069; multiplies odds by 1.007 (+0.7%)
- Decreases log odds of fulltime by 0.097; multiplies odds by 0.907 (-9%)

Having young children:

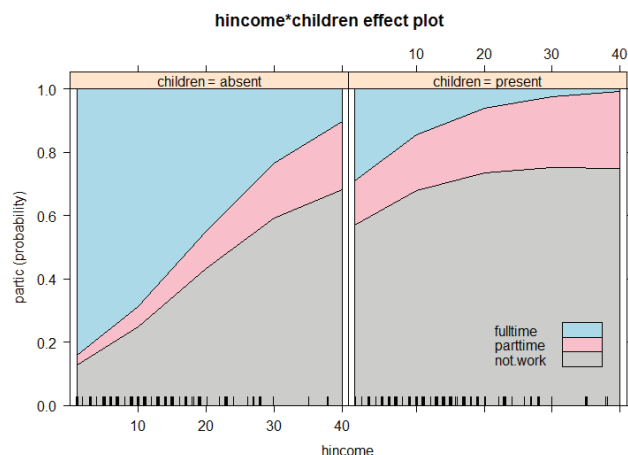
- Increases odds of parttime by 0.0215; multiplies odds by 1.0217 (+2%)
- Decreases odds of fulltime by 2.559; multiplies odds by 0.0774 (-92%)

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# Multinomial models: Plotting

Much easier to interpret a model from a plot, but even more so for polytomous response models

```
library(effects)
plot(Effect(c("hincome", "children"), wlf.multinom), style = "stacked")
```



For multinomial model,  
style="stacked" plots  
cumulative probs.

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# Multinomial models: Plotting

An alternative is to plot the predicted probabilities of each level of participation over a grid of predictor values for husband's income and children.

```
> predictors <- expand.grid(hincome=1:50, children=c('absent', 'present'))
> fit <- data.frame(predictors,
+                   predict(wlf.multinom, predictors, type='probs'))
> fit |> filter(hincome %in% c(10, 25, 40)) # show a few observations
```

hincome	children	not.work	parttime	fulltime
10	absent	0.250	0.0639	0.68627
25	absent	0.520	0.1475	0.33233
40	absent	0.683	0.2150	0.10157
60	10 present	0.678	0.1773	0.14427
75	25 present	0.747	0.2164	0.03693
90	40 present	0.750	0.2411	0.00863

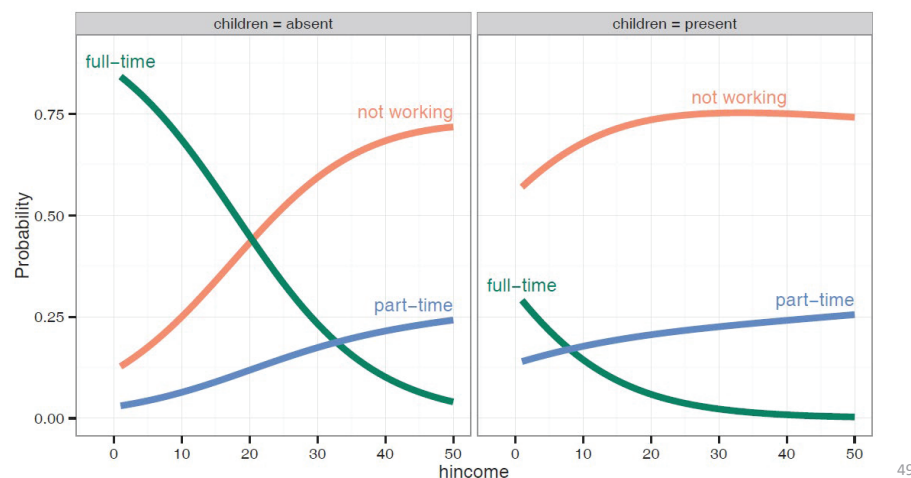
We want to plot predicted probability vs. `hincome`, with separate curves for levels of participation. To do this we need to reshape the fit data from wide to long

```
plotdat <- fit |>
gather(key="Level", value="Probability", not.work:fulltime)
```

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Now, plot Probability ~ hincome, with separate curves for Level of partic

```
library(directlabels)
gg <- ggplot(plotdat, aes(x = hincome, y = Probability, colour = Level)) +
  geom_line(size=1.5) + facet_grid(~ children, labeller = label_both) +
  direct.label(gg, list("top.bumptime", dl.trans(y = y + 0.2)))
```



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## A larger example: BEPS data

### Political knowledge & party choice in Britain

Example from Fox & Anderson (2006); data from 1997 British Election Panel (BEPS), N=1325

- **Response:** Party choice— **Liberal democrat**, **Labour**, **Conservative**
- **Predictors**
  - Europe: 11-point scale of attitude toward European integration (high="Eurosceptic")
  - Political knowledge: knowledge of party platforms on European integration ("low"=0–3="high")
  - Others: Age, Gender, perception of economic conditions, evaluation of party leaders (Blair, Hague, Kennedy)— 1:5 scale
- **Model:**
  - Main effects of Age, Gender, economic conditions (national, household)
  - Main effects of evaluation of party leaders
  - Interaction of attitude toward European integration with political knowledge

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## BEPS data: Fitting

Fit a model with main effects and an interaction of Europe \* political knowledge

```
library(car)      # for Anova()
library(nnet)     # for multinom()
data(BEPS, package = "carData")
BEPS.mod <- multinom(vote ~ age + gender + economic.cond.national +
  economic.cond.household + Blair + Hague + Kennedy +
  Europe*political.knowledge, data=BEPS)
Anova(BEPS.mod)
```

Analysis of Deviance Table (Type II tests)

Response: vote

	LR	Chisq	Df	Pr(>Chisq)
age	13.9	2	0.00097	***
gender	0.5	2	0.79726	
economic.cond.national	30.6	2	2.3e-07	***
economic.cond.household	5.7	2	0.05926	.
Blair	135.4	2	< 2e-16	***
Hague	166.8	2	< 2e-16	***
Kennedy	68.9	2	1.1e-15	***
Europe	78.0	2	< 2e-16	***
political.knowledge	55.6	2	8.6e-13	***
Europe:political.knowledge	50.8	2	9.3e-12	***

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

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## BEPS data: Interpretation?

Coefficients give log odds relative of party choice relative to Conservatives

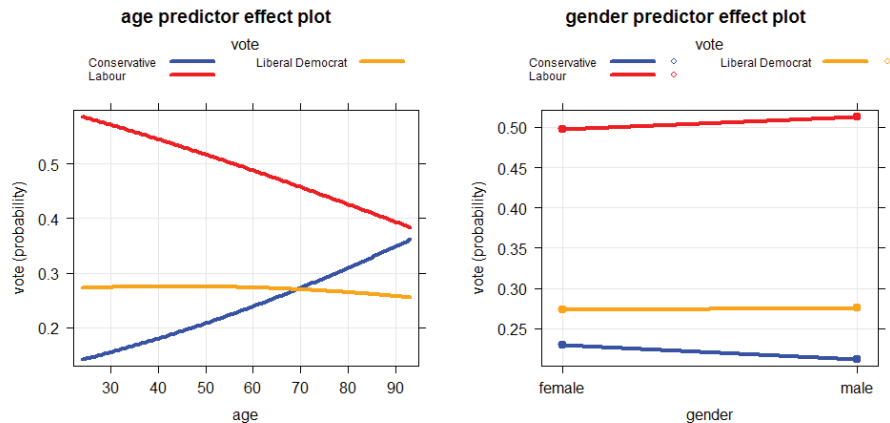
How to understand the **blue** of these effects?

```
> coef(BEPS.mod)
      (Intercept)      age gendermale economic.cond.national
Labour           -0.873 -0.0198      0.1126              0.522
Liberal Democrat -0.718 -0.0146      0.0914              0.145
      economic.cond.household Blair Hague Kennedy Europe
Labour           0.17863 0.824 -0.868      0.240 -0.00171
Liberal Democrat 0.00773 0.278 -0.781      0.656 0.06841
      political.knowledge Europe:political.knowledge
Labour           0.658              -0.159
Liberal Democrat 1.160              -0.183
```

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## BEPS data: Effect plots

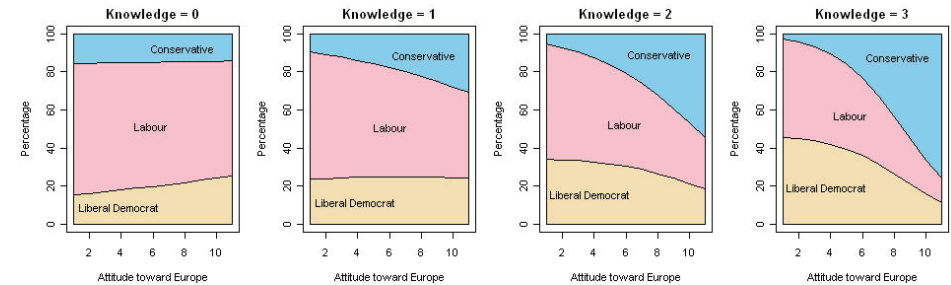
```
plot(predictorEffects(BEPS.mod, ~ age + gender),
     lattice=list(key.args=list(rows=1)),
     lines=list(multiline=TRUE, col=c("blue", "red", "orange")))
```



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## BEPS data: Effect plots

Examine the interaction between political knowledge and attitude toward European integration



- ❖ Low knowledge: little relation between attitude and party choice
- ❖ As knowledge increases: more Eurosceptic view → more likely to support Conservatives
- ❖ Detailed understanding of complex models depends strongly on visualization!

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## Summary

- Polytomous responses
  - m response categories → (m-1) comparisons (logits)
  - Different models for ordered vs. unordered categories
- Proportional odds model
  - Simplest approach for ordered categories
  - Assumes same slopes for all logits
    - Fit with MASS::polr()
    - Test PO assumption with VGAM::vglm()
- Nested dichotomies
  - Applies to ordered or unordered categories
  - Fit m – 1 separate independent models → Additive  $\chi^2$  values
- Multinomial logistic regression
  - Fit m – 1 logits as a single model
  - Results usually comparable to nested dichotomies, but diff interpretation
  - R: nnet::multinom()

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