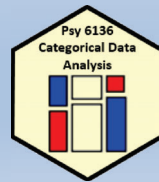


Models & graphs for log odds and log odds ratios



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Today's topics

- Logit models → log odds models
 - Two-way tables
 - Three-way + tables
 - Log odds plots
- Models for generalized odds ratios
 - Log odds ratios
 - Bivariate response models

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Main ideas

- Familiar case— Binary responses:
 - Every loglinear model for a binary response has an equivalent form in terms of **log odds** ["logit" models]
 - Log odds models have simple interpretations
 - Data + model plots give simple descriptions of data and models
- Extend to two-way ($I \times J$) and three-way ($I \times J \times K_1 \dots$) tables:
 - Log odds as **contrasts** in $\log(n)$
 - Variety of simple models for log odds (ANOVA-like)
 - Easily incorporate **ordinal** variables
 - Data + model plots give simple descriptions of data and models
- Generalized log odds ratios capture associations between two **focal variables**
 - Simple linear models for LOR
 - Direct visualization (Data + model plots) \Rightarrow more sensitive comparisons

Based on my CARME (2015) presentation, <https://www.datavis.ca/papers/CARME2015-2x2.pdf>

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Logit models → Log odds models

- In an $I \times 2$ table for variables [A B], where B is a binary response, the logit model expresses the log odds that $B=1$ vs. $B=2$

$$\psi_i^A = \log \left(\frac{m_{i1}}{m_{i2}} \right)$$

- Models pertain to the **one-way** log odds
- This generalizes to $I \times J$ tables, where we consider $(J-1)$ log odds for each level of A, e.g.,
 - Adjacent categories

$$\psi_{ij}^{A\bar{B}} = \log \left(\frac{m_{ij}}{m_{i(j+1)}} \right) \quad j = 1, 2, \dots, J-1$$

- In general, $I \times J \rightarrow (J-1)$ log odds **contrasts** of the B categories for each level of A
- Similar to how **polytomous responses** treated in logistic regression
- Can also use comparisons with a baseline category

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2-way example: Hospital visits

How does the **length of stay** in hospital differ among schizophrenic patients, classified by the frequency of visiting by friends and relatives?

```
data(HospVisits, package="vcdExtra")
HospVisits
```

```
##          stay
## visit    2-9 10-19 20+
## Regular   43   16   3
## Infrequent 6   11  10
## Never     9   18  16
```

- Length of stay is the response, and it is **ordered**
- Can model the **adjacent** odds or log odds that stay is category j vs $(j+1)$
 - E.g., stay= 2-9 vs. 10-19; stay= 10-19 vs. 20+
- In general, $I \times J \rightarrow I \times (J-1)$ adjacent comparisons
- visit is also **ordered**. Can consider simpler (e.g., linear) models for the log odds

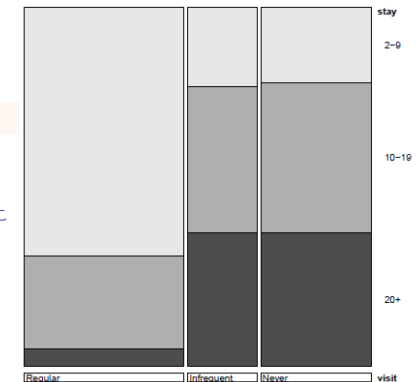
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Exploratory plots: Doubledecker

Doubledecker plot

```
doubledecker(HospVisits)
```

- Shows directly the conditional distributions of **stay** given **visit**
- Length of stay is shorter with frequent visits
- Infrequent and Never don't differ very much

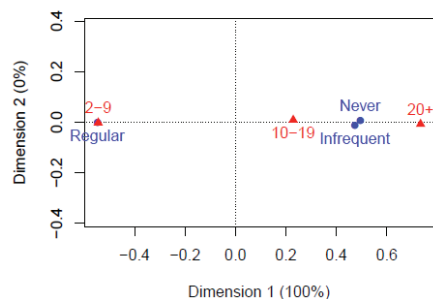


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Exploratory plots: ca

What does CA tell us?

```
plot(ca(HospVisits))
```



- Association is entirely 1D!
- Infrequent and Never category points don't differ much
- Greater visit frequency associated with shorter stay

But, how can we **test** and **visualize** these ideas with models?

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Models for log odds

- Start with the saturated loglinear model for the two-way table

$$\log m_{ij} = \mu + \lambda_i^A + \lambda_j^B + \lambda_{ij}^{AB}$$

- For adjacent categories of the response variable B, the **odds**, ω_{ij}^{AB} and **log odds**, ψ_{ij}^{AB} , that the response is in category j rather than $j+1$ are:

$$\text{odds: } \omega_{ij}^{AB} = \frac{m_{ij}}{m_{i,j+1}} \quad \text{log odds: } \psi_{ij}^{AB} = \log \left(\frac{m_{ij}}{m_{i,j+1}} \right), j = 1, \dots, J-1$$

- For the hospital visits data, this gives:

```
> t(logsds(HospVisits, response = "stay"))
log odds for stay by visit
```

```
visit    stay
visit    2-9:10-19 10-19:20+
Regular    0.989    1.6740
Infrequent -0.606    0.0953
Never      -0.693    0.1178
```

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Models for log odds

A variety of simple models can be specified in terms of log odds:

Table: Models for adjacent log odds in an $I \times J$ table with B as the response

Model	log odds parameters	degrees of freedom
null log odds	$\psi_{ij}^{AB} = 0$	$I(J - 1)$
constant log odds	$\psi_{ij}^{AB} = \psi$	$I(J - 1) - 1$
uniform B log odds	$\psi_{ij}^{AB} = \psi_i^A$	$I(J - 2)$
parallel log odds	$\psi_{ij}^{AB} = \psi_i^A + \psi_j^B$	$(I - 1)(J - 2)$
saturated	ψ_{ij}^{AB} unspecified	

- The log odds, ψ_{ij}^{AB} can be viewed as entries in an $I \times (J - 1)$ table
- These models are analogous to ANOVA tests of the A, B and $A * B$ effects in this table.

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Fit some models

I'm simply using `lm()` here. Should use WLS: weights = $1/ASE^2$

```
mod.null <- lm(logodds ~ -1, data=hosp.iodds) # null
mod.const <- lm(logodds ~ 1, data=hosp.iodds) # constant
mod.unif <- lm(logodds ~ visit, data=hosp.iodds) # uniform
mod.par <- lm(logodds ~ visit + stay, data=hosp.iodds) # parallel
```

Compare models:

```
anova(mod.null, mod.const, mod.unif, mod.par)

## Analysis of Variance Table
##
## Model 1: logodds ~ -1
## Model 2: logodds ~ 1
## Model 3: logodds ~ visit
## Model 4: logodds ~ visit + stay
##   Res.Df  RSS Df Sum of Sq  F Pr(>F)
## 1      6 4.65
## 2      5 4.24  1      0.41 177 0.0056 **
## 3      4 3.43  1      0.81 345 0.0029 **
## 4      2 0.00  2      3.43 734 0.0014 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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Ordinal variables

When the levels of A are **ordinal**, we can also test for **linear** effects.

```
mod1a <- lm(logodds ~ as.numeric(visit), data=hosp.iodds)
mod2a <- lm(logodds ~ as.numeric(visit) + stay, data=hosp.iodds)
# compare parallel log odds models
anova(mod.const, mod2a, mod.par)
```

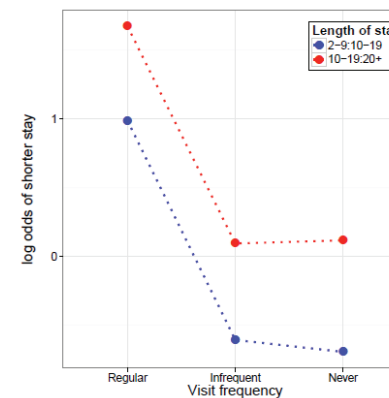
```
## Analysis of Variance Table
##
## Model 1: logodds ~ 1
## Model 2: logodds ~ as.numeric(visit) + stay
## Model 3: logodds ~ visit + stay
##   Res.Df  RSS Df Sum of Sq  F Pr(>F)
## 1      5 4.24
## 2      2 0.00  3      4.23 604 0.0017 **
## 3      2 0.00  0      0.00
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Effects of `visit` are certainly not linear.

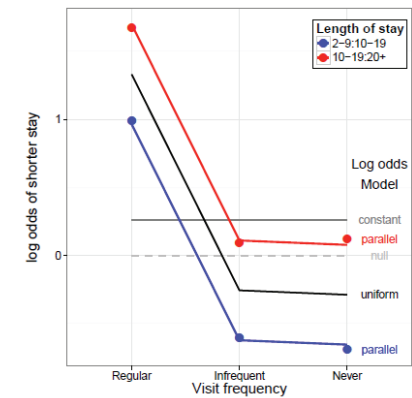
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Visualizing log odds and models

Plots of observed and fitted log odds: easy interpretation of data and models



Data plot: Observed log odds



Data + Model plot (fitted log odds)

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Visualizing log odds and models

Basic plot:

```
gg <- ggplot(hosp.lodds, aes(x=visit, y=logodds,
                           group=stay, color=stay)) +
  geom_point(size=5) +
  geom_line(size=1.2, linetype="dotted")
ylab("log odds of shorter stay\n") +
xlab("Visit frequency") + theme_bw() + ...
```

Add lines for predicted values from the models

```
grid <- hosp.lodds[,1:2]
gg_lines <- function(grid, mod, size=1.2, color=NULL, ...) {
  grid$logodds <- stats::predict(mod, grid)
  if(is.null(color)) geom_line(data=grid, size=size, ...)
  else geom_line(data=grid, size=size, color=color, ...)
}

gg + gg_lines(grid, mod.null, color="gray", size=1, linetype="dashed") +
  gg_lines(grid, mod.const, color=gray(.5), size=1) +
  gg_lines(grid, mod.unif, color="black", size=1) +
  gg_lines(grid, mod.par)
```

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Three-way+ tables: Log odds

These methods naturally extend to three- and higher-way tables:

- Consider a three-way $I \times J \times K$ table of variables A, B and C, where C is the **response** (or **focal variable**)
- The standard loglinear model is:

$$\log m_{ijk} = \mu + \lambda_i^A + \lambda_j^B + \lambda_k^C + \lambda_{ij}^{AB} + \lambda_{ik}^{AC} + \lambda_{jk}^{BC} + \lambda_{ijk}^{ABC}$$

- For categories k and $k+1$ the adjacent log odds for C are

$$\log \text{odds: } \psi_{jk}^{AB\bar{C}} = \log \left(\frac{m_{ijk}}{m_{i,j+1}} \right), \quad k = 1, \dots, K-1$$

- These log odds can be viewed as entries in a two-way, $IJ \times (K-1)$ table.

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Three-way+ tables: Log odds

- The **parallel log odds** model is

$$\begin{aligned} \psi_{ijk}^{AB\bar{C}} &= \Psi_{ij}^{AB} + \psi_k^C \\ &= \psi + \psi_i^A + \psi_j^B + \psi_{ij}^{AB} + \psi_k^C \end{aligned}$$

where the Ψ_{ij}^{AB} are unspecified and the ψ parameters obey standard (sum-to-zero) constraints.

- Simpler models:

$$\begin{aligned} \text{uniform log odds: } \psi_k^C &= 0 \\ \text{joint independence: } \Psi_{ij}^{AB} &= \psi \end{aligned}$$

- Even simpler models: null effects of A ($\psi_i^A = 0$) or B ($\psi_j^B = 0$)
- Linear effects models: An ordinal A can use $\psi_i^A = i \times \beta_A$ to test for linearity

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3-way example: Mice depletion data

- Kastenbaum and Lamphiear (1959) gave a $3 \times 5 \times 2$ table of the number of deaths (0, 1, 2+) in 657 litters of mice, classified by litter size (7–11) and treatment ("A", "B")
- How does number of deaths depend on litter size and treatment?

```
data(Mice, package="vcdExtra")
mice.tab <- xtabs(Freq ~ litter + treatment + deaths, data=Mice)
fable(litter + treatment ~ deaths, data=mice.tab)
```

	litter 7		litter 8		litter 9		litter 10		litter 11	
	treatment A	treatment B	treatment A	treatment B	treatment A	treatment B	treatment A	treatment B	treatment A	treatment B
deaths										
0	58	75	49	58	33	45	15	39	4	5
1	11	19	14	17	18	22	13	22	12	15
2+	5	7	10	8	15	10	15	18	17	8

→ Adjacent categories:

- Odds or log odds of 0 vs. 1 deaths
- Odds or log odds of 1 vs. 2+ deaths

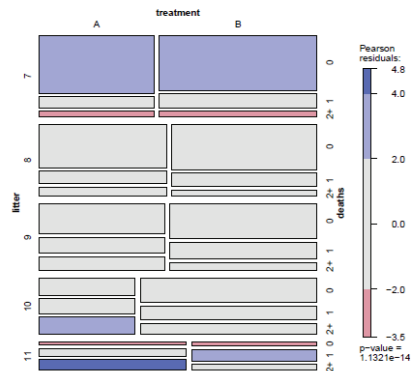
How do these differ with litter size & treatment?

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Mice data: mosaic plot

Fit and display the model of **joint independence**, [litter, treatment] [deaths]

```
mosaic(mice.tab, expected= ~ litter * treatment + deaths)
```

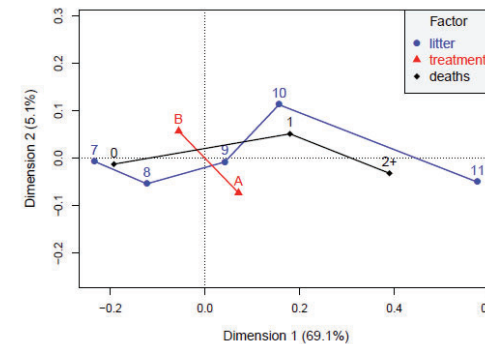


- What can we see?
- Small litters more likely to have 0 deaths
- Large litters more likely to have 2+ deaths
- More deaths with treatment A than B

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Mice data: MCA

```
mice.mca <- mjca(mice.tab)
plot(mice.mca)
```



What can we see?

- Larger litter size associated with more deaths
- More deaths with treatment A than B
- What model? How to simplify?

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Calculating log odds

For a three-way table, a simple way to calculate all (log) odds is to reshape the data as a two-way matrix, T , with $I \times J$ rows and K columns.

```
##      0  1 2+
## 7:A  58 11  5
## 8:A  49 14 10
## 9:A  33 18 15
## 10:A 15 13 15
## 11:A  4 12 17
## ...
```

The $I \times (K - 1)$ table of adjacent log odds can then be calculated as $\log(T)C$, where C is the $K \times K - 1$ matrix of contrasts,

$$C = \begin{bmatrix} 1 & 0 \\ -1 & 1 \\ 0 & -1 \end{bmatrix}$$

Adjacent categories

$$C = \begin{bmatrix} 1 & 1 \\ -1 & 0 \\ 0 & -1 \end{bmatrix}$$

Reference level = 0

In general, any set of $K-1$ $\{1, 0, -1\}$ contrasts can be used

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Calculating log odds

```
mice.tab <- xtabs(Freq ~ litter + treatment + deaths, data=Mice)
```

```
# reshape table to matrix
T <- matrix(mice.tab,
            nrow=prod(dim(mice.tab)[1:2]),
            ncol=dim(mice.tab)[3])
colnames(T) <- dimnames(mice.tab)[[3]]
rn <- expand.grid(dimnames(mice.tab)[1:2])
rownames(T) <- apply(rn, 1, paste, collapse=":")
```

```
C <- matrix(c(1, -1, 0,
              0, 1, -1), nrow=3)
logds <- log(T) %*% C
colnames(logds) <- c("0:1", "1:2+")
```

```
> logds
      0:1  1:2+
7:A  1.663  0.788
8:A  1.253  0.336
9:A  0.606  0.182
10:A  0.143 -0.143
11:A -1.099 -0.348
7:B  1.373  0.999
8:B  1.227  0.754
9:B  0.716  0.788
10:B  0.573  0.201
11:B -1.099  0.629
```

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Calculating log odds

More generally,

- Consider an $R \times K_1 \times K_2 \times \dots$ frequency table $n_{ij\dots}$, with factors $K_1, K_2 \dots$ considered as **strata**.
- Let $\mathbf{n} = \text{vec}(n_{ij\dots})$ be the $N \times 1$ vectorization of the table.
- Then, all log odds and their asymptotic covariance matrix \mathbf{S} can be calculated as:

$$\begin{aligned} \hat{\psi} &= \mathbf{C} \log(\mathbf{n}) \\ \mathbf{S} &= \text{Var}[\psi] = \mathbf{C} \text{diag } \mathbf{n}^{-1} \mathbf{C}^T \end{aligned}$$

where \mathbf{C} is an N -column matrix containing all zeros, except for one +1 elements and one -1 elements in each row.

- With strata, \mathbf{C} can be calculated as the Kronecker product $\mathbf{C} = \mathbf{C}_R \otimes \mathbf{I}_{K_1} \otimes \mathbf{I}_{K_2} \otimes \dots$
- Linear models for log odds: $\psi = \mathbf{X}\beta$

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Mice data: Log odds

The vcd package contains a general implementation of these ideas:

- `odds()` and `lodds()` : calculate odds or log odds for 1 variable in an n-way table
- Provides methods (`coef()`, `vcov()`, `confint()`, ...) for "lodds" objects

```
> (mice.lodds <- as.data.frame(lodds(mice.tab, response="deaths")))
```

	deaths	litter	treatment	logodds	ASE
1	0:1	7	A	1.663	0.329
2	1:2+	7	A	0.788	0.539
3	0:1	8	A	1.253	0.303
4	1:2+	8	A	0.336	0.414
5	0:1	9	A	0.606	0.293
6	1:2+	9	A	0.182	0.350
7	0:1	10	A	0.143	0.379
8	1:2+	10	A	-0.143	0.379
9	0:1	11	A	-1.099	0.577
10	1:2+	11	A	-0.348	0.377

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Mice data: Fit models

Use WLS, with weights $\sim \text{ASE}^{-2}$

```
mod0 <- lm(logodds ~ 1, weights=1/ASE^2, data=mice.lodds)
mod1 <- lm(logodds ~ litter + treatment, weights=1/ASE^2, data=mice.lodds)
mod2 <- lm(logodds ~ litter * treatment, weights=1/ASE^2, data=mice.lodds)
mod3 <- lm(logodds ~ litter * treatment + deaths, weights=1/ASE^2, data=mice.lodds)
```

Compare models:

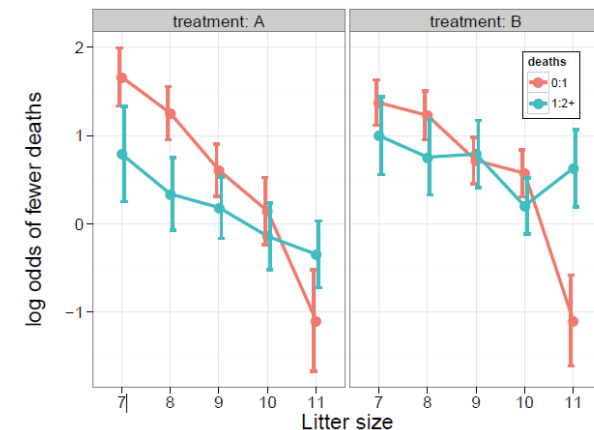
```
anova(mod0, mod1, mod2, mod3)
```

```
## Analysis of Variance Table
##
## Model 1: logodds ~ 1
## Model 2: logodds ~ litter + treatment
## Model 3: logodds ~ litter * treatment
## Model 4: logodds ~ litter * treatment + deaths
## Res.Df RSS Df Sum of Sq    F Pr(>F)
## 1      19 65.0
## 2      14 17.8  5      47.2 18.22 0.00018 ***
## 3      10  6.7  4      11.1  5.36 0.01737 *
## 4       9  4.7  1       2.1  3.98 0.07723 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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Visualize log odds & models: Data plot

- Data plot: log odds with error bars: $\psi_{ijk}^{ABC} \pm 1 \text{ASE}_{\psi}$
- This is equivalent to the saturated model for log odds



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Basic plot:

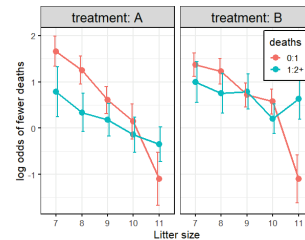
```
gg <- ggplot(mice.iodds, aes(x=litter, y=logodds,
                             color=deaths, group=deaths)) +
  geom_point(size=4) +
  ylab("log odds of fewer deaths") +
  xlab("Litter size") +
  theme_bw(base_size = 16) +
  theme(legend.position = c(.9, .85),
        legend.background = element_rect(colour = "black")) +
  facet_grid(. ~ treatment, labeller=label_both) +
  theme(strip.text = element_text(size = rel(1.2)))
```

Add error bars, dodged

```
bars <- aes(ymin=logodds-ASE,
            ymax=logodds+ASE)
gg + geom_line(size=1.2) +
  geom_errorbar(bars,
               width=0.25, size=1,
               position=position_dodge(width=.2))
```

ggplot thinking:

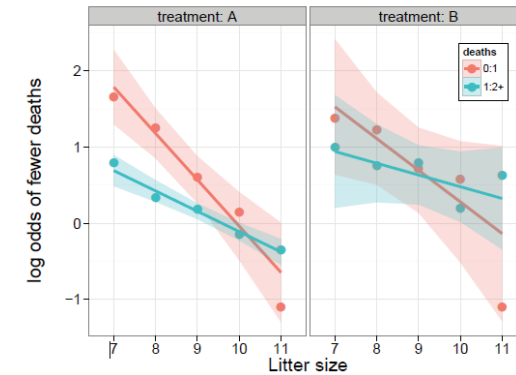
- gg is my basic plot of points
- I can add other layers to it



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Visualize log odds & models: Smoothing

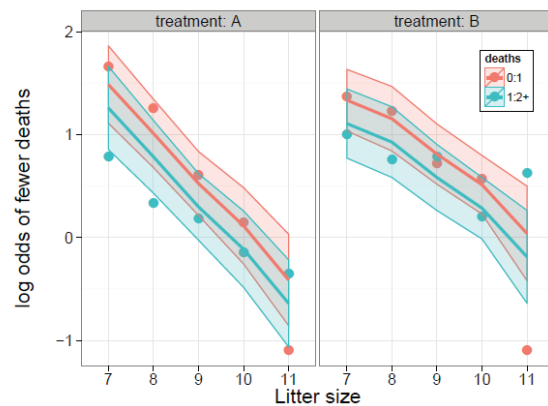
- Apply a **linear smoother** (weighed linear regression) to each
- This is equivalent to a model with a three-way term, `as.numeric(litter)*treatment*deaths`
- Error bands show model uncertainty



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Visualize log odds & models: Data + Model

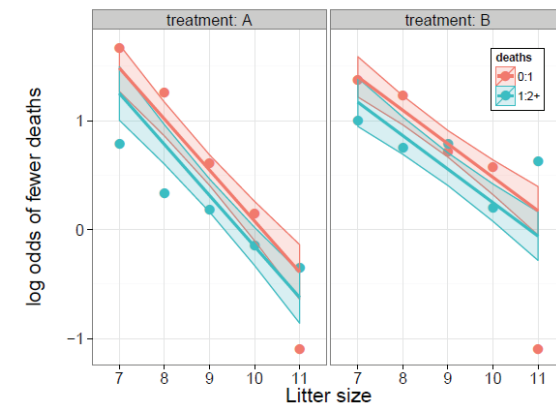
- Display the fit of the parallel log odds model, $\psi_{ijk}^{ABC} = \psi_{ij}^{AB} + \psi_k^C$



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Visualize log odds & models: Data + Model

- Simplify the model: fit only **linear** effects of `litter`
- `lm(logodds ~ as.numeric(litter)*treatment + deaths)`
- Error bands show **smaller** model uncertainty



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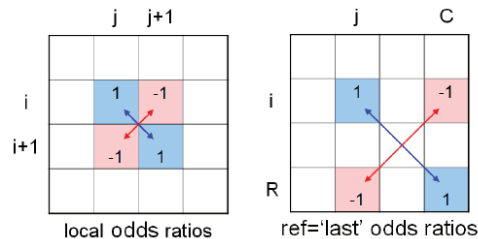
Generalized log odds ratios

- In any two-way, $R \times C$ table, **all** associations can be represented by a set of $(R-1) \times (C-1)$ **odds ratios**,

$$\theta_{ij} = \frac{n_{ij}/n_{i+1,j}}{n_{i,j+1}/n_{i+1,j+1}} = \frac{n_{ij} \times n_{i+1,j+1}}{n_{i+1,j} \times n_{i,j+1}}$$

Simpler in terms of **log odds ratios**:

$$\log(\theta_{ij}) = \begin{pmatrix} 1 & -1 & -1 & 1 \end{pmatrix} \log \begin{pmatrix} n_{ij} & n_{i+1,j} & n_{i,j+1} & n_{i+1,j+1} \end{pmatrix}^T$$



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Generalized log odds ratios

- $\log \theta_{ij} \sim \mathcal{N}(0, \sigma^2)$, with estimated asymptotic standard error:

$$\hat{\sigma}(\log \theta_{ij}) = (n_{ij}^{-1} + n_{i+1,j}^{-1} + n_{i,j+1}^{-1} + n_{i+1,j+1}^{-1})^{1/2}$$

- This extends naturally to $\theta_{ij|k}$ in higher-way tables, stratified by one or more "control" variables.
- Many models have a simpler form expressed in terms of $\log(\theta_{ij})$.
 - e.g., Uniform association model

$$\log(m_{ij}) = \mu + \lambda_i^A + \lambda_j^B + \gamma \mathbf{a}_i \mathbf{b}_j \equiv \log(\theta_{ij}) = \gamma$$

- Direct visualization of log odds ratios permits more sensitive comparisons than area-based displays.

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Models for log odds ratios: Computation

- Consider an $R \times C \times K_1 \times K_2 \times \dots$ frequency table $n_{ij\dots}$, with factors K_1, K_2, \dots considered as **strata**.
- Let $\mathbf{n} = \text{vec}(n_{ij\dots})$ be the $N \times 1$ vectorization of the table.
- Then, all log odds ratios and their asymptotic covariance matrix \mathbf{S} can be calculated as:

- $\log(\hat{\theta}) = \mathbf{C} \log(\mathbf{n})$
- $\mathbf{S} = \text{Var}[\log(\theta)] = \mathbf{C} \text{diag } \mathbf{n}^{-1} \mathbf{C}^T$

where \mathbf{C} is an N -column matrix containing all zeros, except for two +1 elements and two -1 elements in each row.

- With strata, \mathbf{C} can be calculated as $\mathbf{C} = \mathbf{C}_{RC} \otimes \mathbf{I}_{K_1} \otimes \mathbf{I}_{K_2} \otimes \dots$
- `loddsratio()` in `vcd` provides generic methods (`coef()`, `vcov()`, `confint()`, ...)
- `plot()` method gives reasonable data and model plots.

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Models for log odds ratios: Computation

For example, for a 2×3 table, there are two adjacent odds ratios

```
##      Age
## Sex Yng Mid Old
## M   30  20  10
## F    5  15  25
## log odds ratios for Sex and Age
##
## Yng:Mid Mid:Old
##  1.504  1.204
```

These are calculated as:

$$\log(\theta) = \mathbf{C} \log(\mathbf{n}) = \begin{bmatrix} 1 & -1 & -1 & 1 & 0 & 0 \\ 0 & 0 & 1 & -1 & -1 & 1 \end{bmatrix} \log \begin{pmatrix} n_{11} \\ n_{12} \\ n_{13} \\ n_{21} \\ n_{22} \\ n_{23} \end{pmatrix}$$

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Models for log odds ratios: Estimation

- A **log odds ratio linear model** for the $\log(\theta)$ is

$$\log(\theta) = \mathbf{X}\beta$$

where \mathbf{X} is the design matrix of covariates

- The (asymptotic) ML estimates $\hat{\beta}$ are obtained by GLS via

$$\hat{\beta} = (\mathbf{X}^T \mathbf{S}^{-1} \mathbf{X})^{-1} \mathbf{X}^T \mathbf{S}^{-1} \log(\hat{\theta})$$

where $\mathbf{S} = \text{Var}[\log(\theta)]$ is the estimated covariance matrix

- ⇒ Standard graphical and diagnostic methods can be adapted to this case.
 - visualization: full-model plots, effect plots, ...
 - diagnostics: influence plots, added-variable plots, ...

Technical note: for simplicity, I use `lm()` for WLS, with $\mathbf{S}^{-1} = \text{diag}(1/\text{ASE}^2)$
Should probably use `nlme::gls()` instead

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Example: Breathlessness & wheeze in coal miners

- Ashford & Sowden (1970) gave data on the association between two pulmonary conditions: breathlessness and wheeze, in a large sample of coal miners
- Age is the primary covariate
- How does the association between breathlessness and wheeze vary with age?

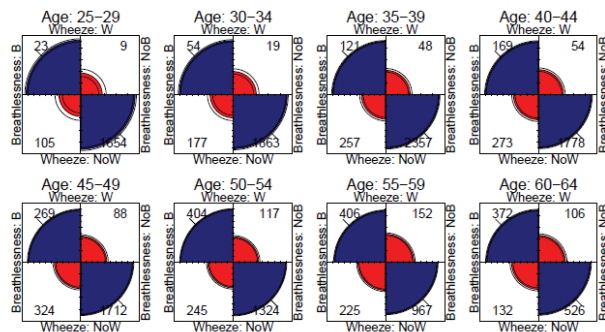
```
fctable(CoalMiners)
```

		Age 25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64
##	Breathlessness Wheeze								
##	B W	23	54	121	169	269	404	406	3
##	NoW	9	19	48	54	88	117	152	1
##	NoB W	105	177	257	273	324	245	225	1
##	NoW	1654	1863	2357	1778	1712	1324	967	5

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Example: Breathlessness & wheeze in coal miners

```
fourfold(CoalMiners, mfcol=c(2,4), fontsize=18)
```



- There is a strong + association at all ages
- But can you see the trend?

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Coal miners: Log odds & models

```
(lor.CM <- loddsratio(CoalMiners))
```

```
## log odds ratios for Breathlessness and Wheeze by Age
##
## 25-29 30-34 35-39 40-44 45-49 50-54 55-59 60-64
## 3.695 3.398 3.141 3.015 2.782 2.926 2.441 2.638
```

How does LOR vary with Age?

- Uniform association: $\ln(\theta) = \beta_0$
- Linear association: $\ln(\theta) = \beta_0 + \beta_1 \text{ Age}$
- Quadratic association: $\ln(\theta) = \beta_0 + \beta_1 \text{ Age} + \beta_2 \text{ Age}^2$

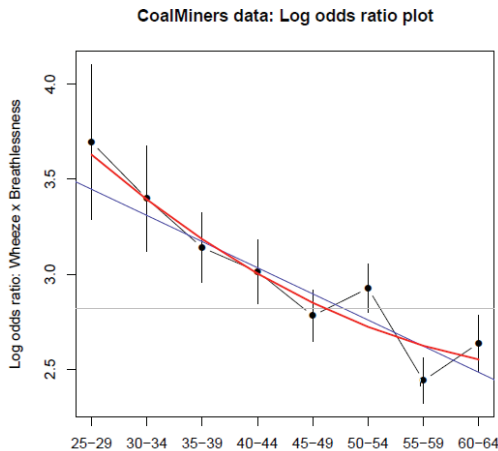
Fit models using WLS:

```
lor.CM.df <- as.data.frame(lor.CM)
age <- seq(25, 60, by = 5)
CM.mod0 <- lm(LOR ~ 1, weights=1/ASE^2, data=lor.CM.df)
CM.mod1 <- lm(LOR ~ age, weights=1/ASE^2, data=lor.CM.df)
CM.mod2 <- lm(LOR ~ poly(age, 2), weights=1/ASE^2, data=lor.CM.df)
```

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Coal miners: LOR plot

Plot log odds ratios and fitted regressions: The trend is now clear!



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Coal miners: Model comparisons

Standard ANOVA procedures allow tests of nested competing models:

```
anova(CM.mod0, CM.mod1, CM.mod2)

## Analysis of Variance Table
##
## Model 1: LOR ~ 1
## Model 2: LOR ~ age
## Model 3: LOR ~ poly(age, 2)
##   Res.Df  RSS Df Sum of Sq    F Pr(>F)
## 1      7 25.61
## 2      6  6.34  1    19.28 17.23 0.0089 **
## 3      5  5.60  1     0.74  0.66 0.4525
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

`(vcdExtra::LRstats())` gives direct tests of each model, and AIC, BIC
The linear model, $\ln(\theta) = \beta_0 + \beta_1 \text{Age}$, gives the best fit.

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Going further: Bivariate response models

- In this example, breathlessness and wheeze are two binary responses
- A **bivariate logistic response** model fits simultaneously
 - the **marginal** log odds of each response, ψ_1, ψ_2 vs. predictors (\mathbf{x})
 - the **joint** log odds ratio, ϕ_{12} , vs. \mathbf{x}
- This model has the form

$$\eta(\mathbf{x}) = \begin{pmatrix} \eta_1 \\ \eta_2 \\ \eta_{12} \end{pmatrix} \equiv \begin{pmatrix} \log \text{odds}_1(\mathbf{x}) \\ \log \text{odds}_2(\mathbf{x}) \\ \log \text{OR}_{12}(\mathbf{x}) \end{pmatrix} \equiv \begin{pmatrix} \psi_1 \\ \psi_2 \\ \log \theta_{12} \end{pmatrix} = \begin{pmatrix} \mathbf{x}_1^T \beta_1 \\ \mathbf{x}_2^T \beta_2 \\ \mathbf{x}_{12}^T \beta_{12} \end{pmatrix}$$

where $\mathbf{x}_1, \mathbf{x}_2, \mathbf{x}_{12} \subset \mathbf{x}$

- For example, with one x , the following model allows linear effects on log odds, with a constant log odds ratio

$$\begin{pmatrix} \eta_1 \\ \eta_2 \\ \eta_{12} \end{pmatrix} = \begin{pmatrix} \alpha_1 + \beta_1 x \\ \alpha_2 + \beta_2 x \\ \log(\theta) \end{pmatrix} \quad (1)$$

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Calculating...

Logits and log odds for a bivariate response can be calculated with `vcdExtra::blogits()`

```
data(coalminers, package = "VGAM")
coalminers <- transform(coalminers, Age = (age - 42) / 5)

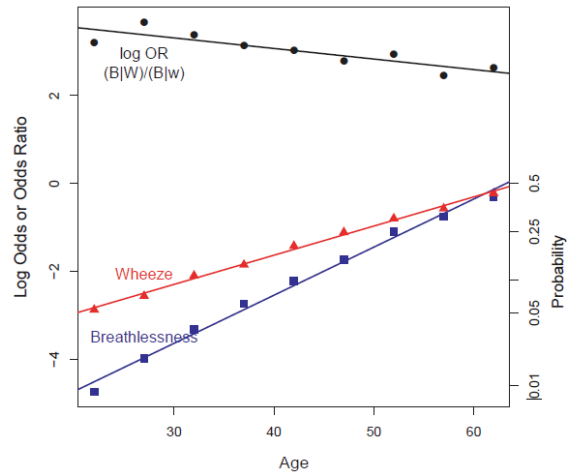
logitsCM <- vcdExtra::blogits(coalminers[, 1:4], add = 0.5)
colnames(logitsCM)[1:2] <- c("logitB", "logitW")
logitsCM <- cbind(logitsCM,
                  coalminers[, c("age", "Age")])

logitsCM
```

```
logitB logitW logOR age Age
1 -4.736 -2.868  3.20  22  -4
2 -3.977 -2.557  3.66  27  -3
3 -3.317 -2.094  3.38  32  -2
4 -2.733 -1.848  3.13  37  -1
5 -2.215 -1.420  3.01  42   0
6 -1.739 -1.109  2.78  47   1
7 -1.101 -0.797  2.92  52   2
8 -0.758 -0.572  2.44  57   3
9 -0.319 -0.226  2.63  62   4
```

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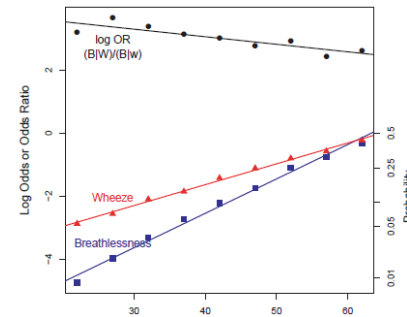
Linear model for log odds and log odds ratios



Log odds & LORs have similar scales, so it is not terrible to plot them together

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Linear model for log odds and log odds ratios

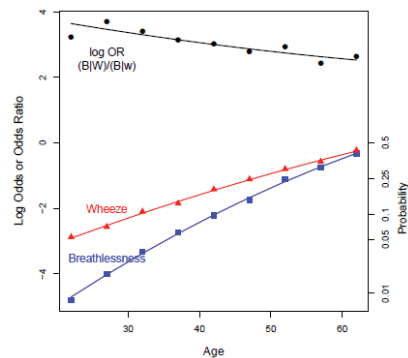


This data + model plot has a simple interpretation:

- Prevalence of breathlessness and wheeze both increase with age
- Breathlessness is less prevalent at young age, but increases faster
- Their association decreases approx. linearly, but is still strong

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Quadratic model for log odds and log odds ratios



- Allowing quadratic fits in age serves as a sensitivity check
- The story is pretty much the same

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Plotting ...

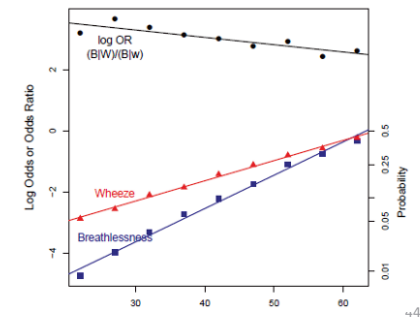
With the data in this form, we can use `matplot()` to plot each column against age

```
matplot(age, logitsCM[, 1:3], type = "p",
        col = col, pch = pch, cex = 1.2, cex.lab = 1.25,
        xlab = "Age", ylab = "Log Odds or Odds Ratio")
abline(lm(logitsCM[,1] ~ age), col = col[1], lwd = 2)
abline(lm(logitsCM[,2] ~ age), col = col[2], lwd = 2)
abline(lm(logitsCM[,3] ~ age), col = col[3], lwd = 2)
```

To plot the quadratic fit, simply use

```
lm(logitsCM[,1] ~ poly(age,2))
```

But: this is NOT a model. It simply fits each set of odds separately



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Fitting: VGAM::vglm()

VGAM::vglm() can fit a wide class of models for a vector of multivariate responses

- The family `binom2()` is used for bivariate logistic models
- An argument `zero=` allows the logit or odds ratio submodels to be constrained to intercept-only

```
cm.vglm <- vglm(cbind(nBnW, nBW, BnW, BW) ~ Age,
  binom2.or(zero = NULL), data = coalminers)
```

```
exp(coef(cm.vglm, matrix = TRUE))
```

	logitlink(mu1)	logitlink(mu2)	loglink(oratio)	
(Intercept)	0.104	0.226		20.530
Age	1.673	1.385		0.877

Each 5 years of age:

- Multiplies odds of breathlessness by 1.67, a 67% increase
- Multiplies odds of wheeze by 1.38, a 38% increase
- Multiplies the OR for association by 0.88, a 12 % decrease

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Plotting the model fit

VGAM::fitted() returns the **fitted** values on the probability scale

VGAM::depar() returns the **observed** values on the probability scale

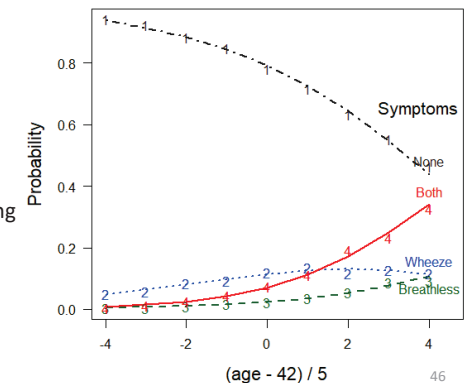
```
> P <- fitted(cm.vglm)
> colnames(P) <- c("bw", "bW",
  "Bw", "BW")
```

```
> P
  bw    bW    Bw    BW
1 0.94 0.049 0.0046 0.0085
2 0.91 0.064 0.0070 0.0148
3 0.88 0.080 0.0105 0.0254
4 0.84 0.097 0.0158 0.0428
5 0.79 0.114 0.0239 0.0704
...
```

You can get these on the logit scale using the inverse logit function, `qlogis()`

```
LP <- qlogis(P)
LY <- qlogis(Y)
```

The plot is made using `matplot()`



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Other possibilities

We can also model the relations with age as a quadratic, cubic, ...

```
cm.vglm2 <- vglm(cbind(nBnW, nBW, BnW, BW) ~ poly(Age,2),
  binom2.or(zero = NULL), data = coalminers)
```

VGAM also implements vector generalized additive models, fit using `vgam()`

```
cm.vgam <- vgam(cbind(nBnW, nBW, BnW, BW) ~ s(Age, df = 2),
  binom2.or(zero = NULL), data = coalminers)
```

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Example: Attitudes toward corporal punishment

A four-way table, classifying 1,456 persons in Denmark (`Punishment` data in `vcd`).

- Attitude**: approves moderate punishment of children ("moderate"), or refuses any punishment ("no")
- Memory**: Person recalls having been punished as a child?
- Education**: highest level (elementary, secondary, high)
- Age group**: (15–24, 25–39, 40+)

Education	Attitude	Age Memory	15–24		25–39		40+	
			Yes	No	Yes	No	Yes	No
Elementary	No		1	26	3	46	20	109
	Moderate		21	93	41	119	143	324
Secondary	No		2	23	8	52	4	44
	Moderate		5	45	20	84	20	56
High	No		2	26	6	24	1	13
	Moderate		1	19	4	26	8	17

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Attitudes: Questions

Interest focuses on several questions:

- How does Attitude toward punishment depend on Memory, Education and Age?
 - Model log odds approve of moderate corporal punishment
 - Standard logit model:


```
glm(attitude ~ memory + education + age, data=Punishment, weight=Freq, family=binomial)
```
- How does association between Attitude and Memory vary with Education and Age?
 - Model log odds ratio (Attitude, Memory)
 - Visualize: LOR plots

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Log odds model for attitude

Fit the main-effects model for Attitude on other predictors:

```
pun.logit <- glm(attitude ~ memory + education + age,
                  data=Punishment, weight=Freq, family=binomial)
Anova(pun.logit)

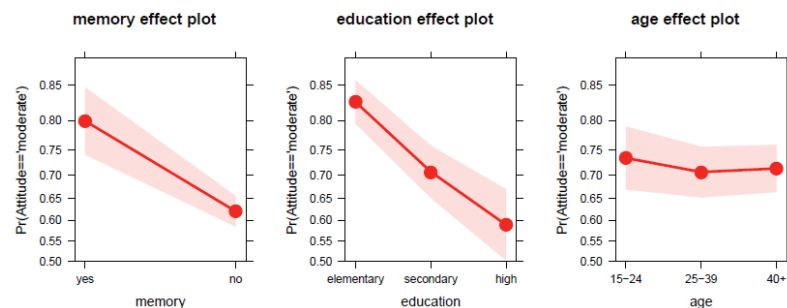
## Analysis of Deviance Table (Type II tests)
##
## Response: attitude
##          LR Chisq Df Pr(>Chisq)
## memory    29.5   1  5.6e-08 ***
## education  50.3   2  1.2e-11 ***
## age         0.6   2    0.73
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Only Memory and Education have significant effects
- A more complex model with all two-way interactions showed no improvement

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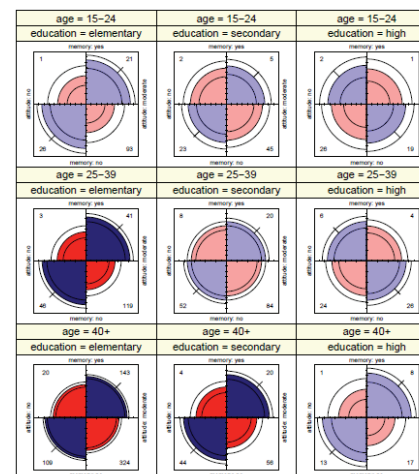
Attitude: Effect plots

- **Model plots**, showing fitted values for **high-order terms** in any model
- Other predictors averaged over in each plot
- Simple interpretation:
 - Those who remembered punishment as children more likely to approve
 - Approval decreases with education
 - No effect of age



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Association of attitude with memory: Fourfold plots



How does the association of attitude and memory vary with education and age?

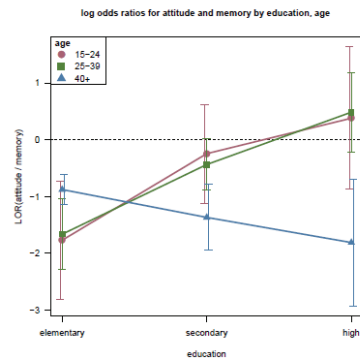
Each fourfold plot visualizes the log odds ratio between them

What's going on here?

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Log odds ratio plot

```
(lor.pun <- loddsratio(punish))  
## log odds ratios for memory and attitude by age, education  
##  
##      education  
## age elementary secondary high  
## 15-24   -1.7700   -0.2451  0.3795  
## 25-39   -1.6645   -0.4367  0.4855  
## 40+     -0.8777   -1.3683 -1.8112
```



- Structure now completely clear
- Little difference between younger groups
- Opposite pattern for the 40+
- Fit an LOR model to confirm appearances (SEs large)!

Summary

- Logit models for a binary response generalize readily to a polytomous response
 - → Models for log odds
 - Handles 3+ way table, ordinal variables
 - Simple plots for interpretation
- Generalized odds ratios handle bivariate responses
 - Simple linear models for LOR
 - Easy to model log odds for each response and the LOR simultaneously
 - Easy to visualize results