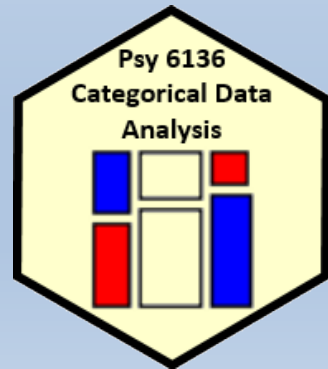


Extending loglinear models



Michael Friendly
Psych 6136

<http://friendly.github.io/psy6136>



Today's topics

- Overview of extended loglinear models
- Logit models for response variables
- Models for ordinal factors
- RC models, estimating row/col scores
- Models for square tables
- More complex models

Visual overview: Models for frequency tables

Generalized nonlinear models

```
gnm(F~A+B+Mult(A,B), family=poisson)
```

Generalized linear models

```
glm(F~A+B, family=poisson)
```

Loglinear models

```
loglm(~A+B)
```

Related models: logistic regression, polytomous regression, log odds models, ...
Goal: connect all with visualization methods

Loglinear models: Perspectives

Loglinear approach

Loglinear models were first developed as an analog of classical ANOVA models, where *multiplicative* relations (under independence) are re-expressed in *additive* form as models for $\log(\text{frequency})$.

$$\log m_{ij} = \mu + \lambda_i^A + \lambda_j^B \equiv [A][B] \equiv \sim A + B$$

- This expresses the model of independence for a two-way table (no A^*B association, or $A \perp B$)
- The notations $[A][B] \equiv \sim A + B$ are shorthands
- Three-way tables: models $[A][B][C]$ (mutual indep.), $[AB][C]$ (joint indep.), $[AB][AC]$ (cond. indep.), ... $[ABC]$ (saturated)

Extending loglinear models

Loglinear models can be extended in a variety of ways

- Models for ordinal factors allow a more parsimonious description of association (linear association)
- Specialized models for square tables provide more nuanced hypotheses (symmetry, quasi-symmetry)
- These ideas apply to higher-way tables
- Some of these extensions are more easily understood when loglinear models are re-cast in an equivalent but simpler or more general form (logit models)

Loglinear models: Perspectives

GLM approach

More generally, loglinear models are also **generalized linear models** (GLMs) for $\log(\text{frequency})$, with a **Poisson** distribution for the cell counts.

$$\log \mathbf{m} = \mathbf{X}\beta$$

- This looks just like the general linear ANOVA, regression model, but for log frequency
- This approach allows **quantitative** predictors and special ways of treating **ordinal factors**

Loglinear models: Perspectives

Logit models

When one table variable is a **binary response**, a **logit model** for that response is equivalent to a loglinear model.

$$\log(m_{1jk}/m_{2jk}) = \alpha + \beta_j^B + \beta_k^C \equiv [AB][AC][BC]$$

- $\log(m_{1jk}/m_{2jk})$ represents the **log odds** of response category 1 vs. 2
- The model formula includes only terms for the effects on A of variables B and C
- The equivalent loglinear model is [AB] [AC] [BC]
- The logit model assumes [BC] association, and [AB] $\rightarrow \beta_j^B$, [AC] $\rightarrow \beta_k^C$

Logit models

Logit models

For a *binary* response, each loglinear model is equivalent to a logit model (logistic regression, with categorical predictors)

- e.g., Admit \perp Gender | Dept (conditional independence \equiv [AD][DG])

$$\log m_{ijk} = \mu + \lambda_i^A + \lambda_j^D + \lambda_k^G + \lambda_{ij}^{AD} + \lambda_{jk}^{DG}$$

So, for admitted ($i = 1$) and rejected ($i = 2$), we have:

$$\log m_{1jk} = \mu + \lambda_1^A + \lambda_j^D + \lambda_k^G + \lambda_{1j}^{AD} + \lambda_{jk}^{DG} \quad (1)$$

$$\log m_{2jk} = \mu + \lambda_2^A + \lambda_j^D + \lambda_k^G + \lambda_{2j}^{AD} + \lambda_{jk}^{DG} \quad (2)$$

Thus, subtracting (1)-(2), terms not involving Admit will cancel:

$$\begin{aligned} L_{jk} &= \log m_{1jk} - \log m_{2jk} = \log(m_{1jk}/m_{2jk}) = \text{log odds of admission} \\ &= (\lambda_1^A - \lambda_2^A) + (\lambda_{1j}^{AD} - \lambda_{2j}^{AD}) \\ &= \alpha + \beta_j^{\text{Dept}} \quad (\text{renaming terms}) \end{aligned}$$

where, α : overall log odds of admission; β_j^{Dept} : effect on admissions of department

Logit models

Other loglinear models have similar, simpler forms as logit models, where only the relations of the response to the predictors appear in the equivalent logit model.

- Admit \perp Gender \perp Dept (mutual independence \equiv [A][D][G])

$$\begin{aligned}\log m_{ijk} &= \mu + \lambda_i^A + \lambda_j^D + \lambda_k^G \\ &\equiv L_{jk} = (\lambda_1^A - \lambda_2^A) = \alpha \quad (\text{constant log odds})\end{aligned}$$

- Admit \perp Gender | Dept, except for Dept. A

$$\begin{aligned}\log m_{ijk} &= \mu + \lambda_i^A + \lambda_j^D + \lambda_k^G + \lambda_{ij}^{AD} + \lambda_{jk}^{DG} + \delta_{(j=1)} \lambda_{ik}^{AG} \\ &\equiv L_{jk} = \log(m_{1jk} / m_{2jk}) = \alpha + \beta_j^{\text{Dept}} + \delta_{(j=1)} \beta^{\text{Gender}}\end{aligned}$$

where,

- β_j^{Dept} : effect on admissions for department j ,
- $\delta_{(j=1)} \beta^{\text{Gender}}$: 1 df term for effect of gender in Dept. A.

Logit models

- Each logit model for a binary response, C , \equiv a loglinear model
 - The loglin model must include the $[AB]$ association of predictors
 - When the response, C , has $m > 2$ levels, multinomial models have equivalent loglinear form

Table: Equivalent loglinear and logit models for a three-way table, with C as a binary response variable.

Loglinear model	Logit model	Logit formula
$[AB][C]$	α	$C \sim 1$
$[AB][AC]$	$\alpha + \beta_i^A$	$C \sim A$
$[AB][BC]$	$\alpha + \beta_j^B$	$C \sim B$
$[AB][AC][BC]$	$\alpha + \beta_i^A + \beta_j^B$	$C \sim A + B$
$[ABC]$	$\alpha + \beta_i^A + \beta_j^B + \beta_{ij}^{AB}$	$C \sim A * B$

Berkeley data: loglinear approach

Loglinear approach, using `MASS::loglm()`

- Uses `UCBAdmissions` in `table` form
- Fit model of conditional independence of gender and admission given department, $[AD][GD]$

```
library(MASS)
berk.loglm1 <- loglm(~ Dept * (Gender + Admit), data=UCBAdmissions)
berk.loglm1

## Call:
## loglm(formula = ~Dept * (Gender + Admit), data = UCBAdmissions)
##
## Statistics:
##              X^2 df  P(> X^2)
## Likelihood Ratio 21.736  6 0.0013520
## Pearson          19.938  6 0.0028402
```

Berkeley data: glm() approach

GLM approach, using glm()

- Convert `UCBadmissions` to a frequency data frame
- The `Freq` variable is used as the response variable

```
> berkeley <- as.data.frame(UCBadmissions)
> head(berkeley)
  Admit Gender Dept Freq
1 Admitted   Male   A  512
2 Rejected   Male   A  313
3 Admitted Female   A   89
4 Rejected Female   A   19
5 Admitted   Male   B  353
6 Rejected   Male   B  207
```

Berkeley data: glm() approach

GLM approach, using glm()

- Fit the same model of **conditional** independence, [AD][GD]
- This uses family = “**poisson**” to give model for log(Freq)

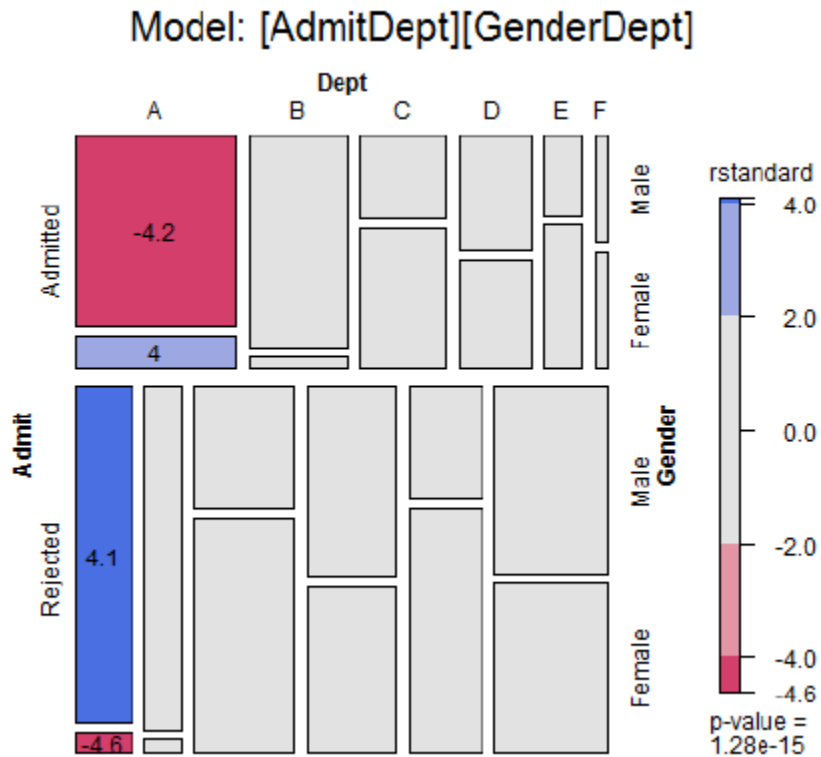
```
> berk.glm1 <- glm(Freq ~ Dept * (Gender+Admit),
                  data=berkeley, family="poisson")

> vcdExtra::LRstats(berk.glm1)
Likelihood summary table:
              AIC  BIC  LR  Chisq  Df  Pr(>Chisq)
berk.glm1  217  238      21.7   6      0.0014  **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Hmm, doesn't look like a very good fit!

What does the mosaic plot tell us?

```
library(vcdExtra)
mosaic(berk.glm1, shade=TRUE, formula=~Admit+Dept+Gender,
       residuals_type="rstandard", labeling=labeling_residuals,
       main="Model: [AdmitDept][GenderDept]")
```



For a glm() model, mosaic() uses residuals from that model

Standardized residuals (“rstandard”) have better statistical properties

Here, we see that the lack of fit is confined to Dept A

Berkeley data: Logit approach

Logit approach, using `glm()`

- The equivalent logit model is $L_{ij} = \alpha + \beta_i^{\text{Dept}} + \beta_j^{\text{Gender}}$
- Fit this with `glm()` using `Admit=="Admitted"` as the response, and `family=binomial`
- Need to specify `weights=Freq` with the data in frequency form

```
> berk.logit2 <- glm(Admit=="Admitted" ~ Dept+Gender,
                    data=berkeley, weights=Freq, family="binomial")
```

```
> Anova(berk.logit2, test="Wald")
```

```
Analysis of Deviance Table (Type II tests)
```

```
Response: Admit == "Admitted"
```

	Df	Chisq	Pr(>Chisq)
Dept	5	534.71	<2e-16 ***
Gender	1	1.53	0.22

```
---
```

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


Plots for logit models

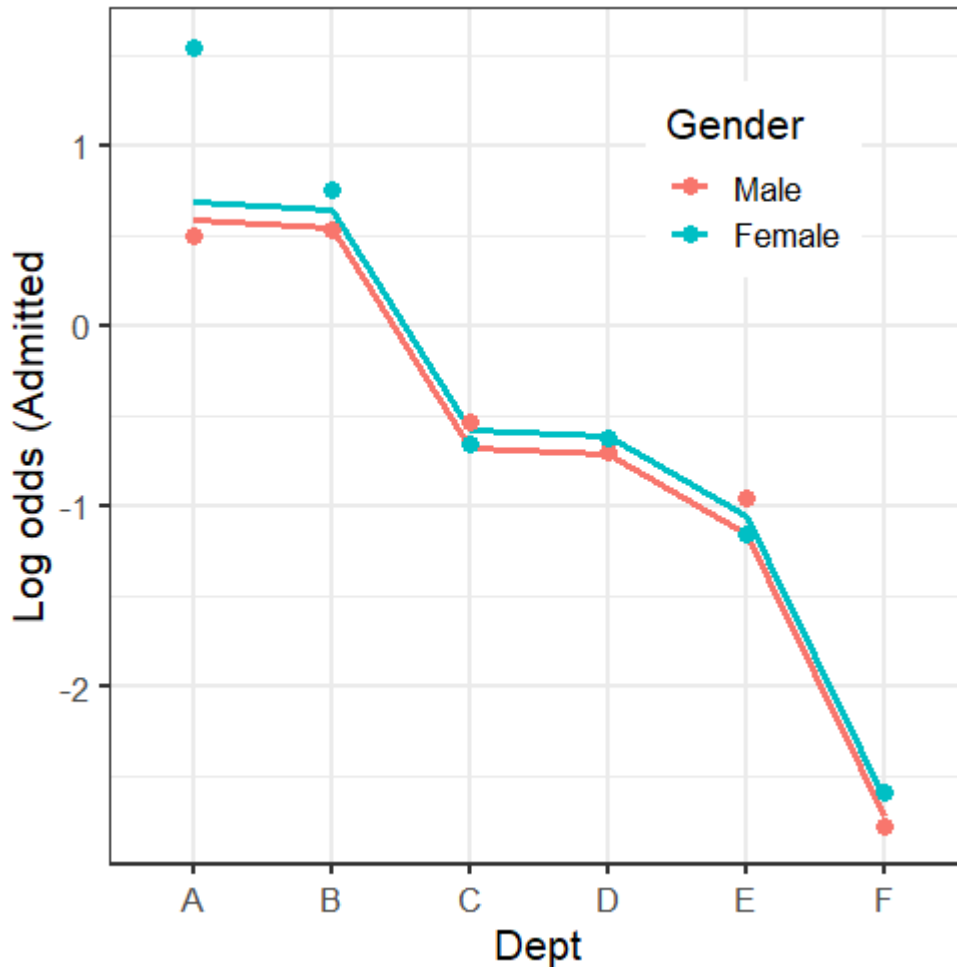
Logit models are easier to interpret because there are fewer parameters

Easiest to interpret from plots of the fitted & observed odds

Get these using the `predict()` method for the model

```
> obs <- log(UCBAdmissions[1,,] / UCBAdmissions[2,,])
> pred2 <- cbind(berkeley[,1:3],
                 fit=predict(berk.logit2))
> pred2 <- cbind(subset(pred2, Admit=="Admitted"),
                 obs=as.vector(obs))
> head(pred2)
      Admit Gender Dept   fit   obs
1  Admitted  Male   A  0.58  0.49
3  Admitted Female  A  0.68  1.54
5  Admitted  Male   B  0.54  0.53
7  Admitted Female  B  0.64  0.75
9  Admitted  Male   C -0.68 -0.54
11 Admitted Female  C -0.58 -0.66
```

```
ggplot(pred2, aes(x=Dept, y=fit, group=Gender, color=Gender)) +  
  geom_line(size=1.4) +  
  geom_point(aes(y=obs), size=3) + ...
```



Large effect of Dept on admission

Small effect of Gender (NS)

Reason for lack of fit: Dept A

A better model

Allow an association between *Admit* and *Gender* only in Dept. A

- Loglinear form:

$$\log m_{ijk} = \mu + \lambda_i^A + \lambda_j^D + \lambda_k^G + \lambda_{ij}^{AD} + \lambda_{jk}^{DG} + I(j = 1)\lambda_{ik}^{AG} ,$$

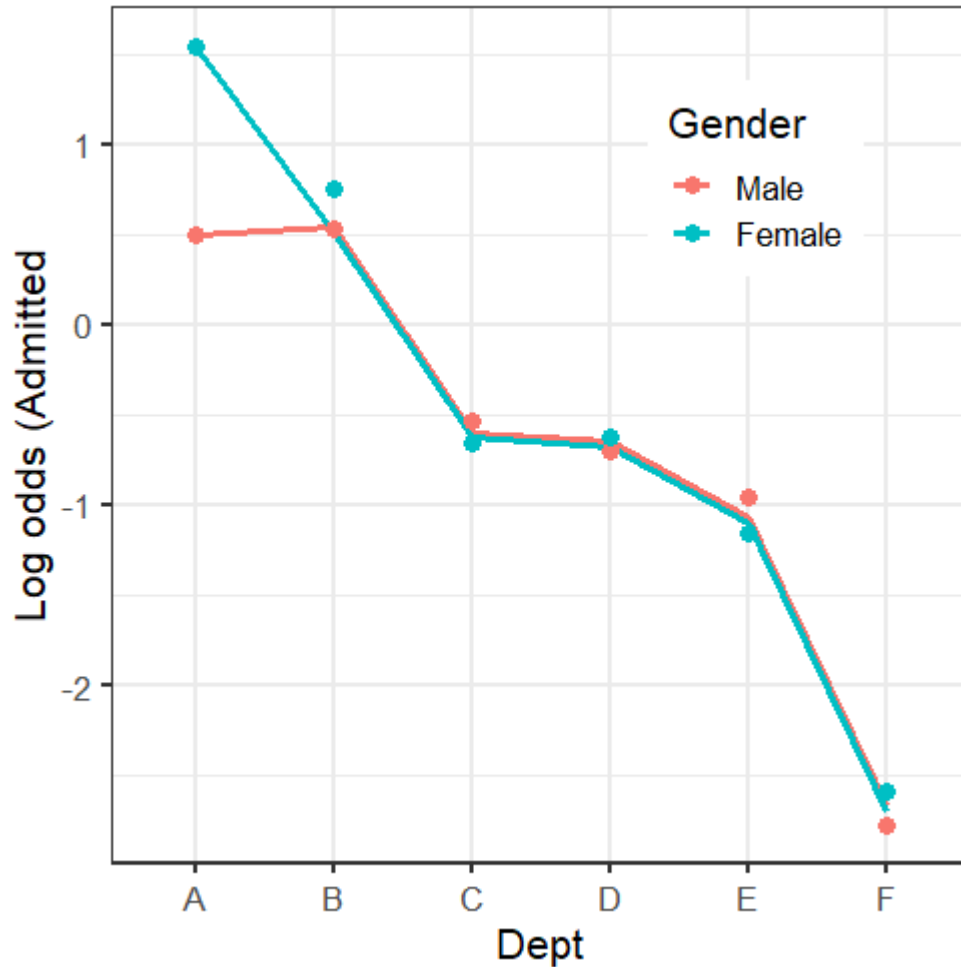
- Equivalent logit form:

$$L_{ij} = \alpha + \beta_i^{\text{Dept}} + I(j = 1)\beta^{\text{Gender}} .$$

```
berkeley <- within(berkeley,
                   dept1AG <- (Dept=='A')*(Gender=='Female'))
berk.logit3 <- glm(Admit=="Admitted" ~ Dept + Gender + dept1AG,
                  data=berkeley, weights=Freq, family="binomial")
Anova(berk.logit3)

## Analysis of Deviance Table (Type II tests)
##
## Response: Admit == "Admitted"
##          LR Chisq Df Pr(>Chisq)
## Dept          647  5  < 2e-16 ***
## Gender           0  1    0.72
## dept1AG         18  1  2.7e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Plot observed and fitted values from this model



Large effect of Dept on admission

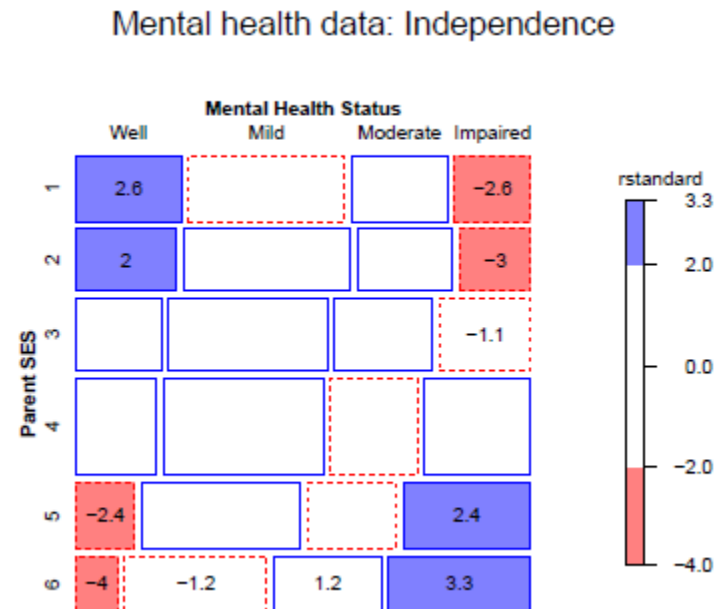
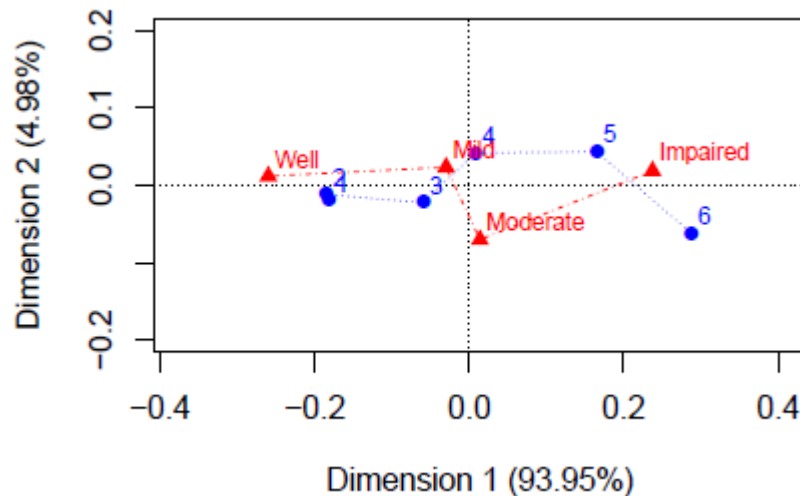
No effect of Gender

Perfect fit now for Dept A (at the expense of 1 df)

Loglinear models for ordinal variables

Ordinal variables reveal themselves in different ways in exploratory plots

- In **correspondence analysis**, one large dimension accounting for most of χ^2
- In **mosaic plots**, an opposite corner pattern of residuals



Advantages of ordinal models

- More focused tests → greater power to detect
- Use fewer df → can fit different models between independence $[A][B]$ and saturated $[AB]$
- Fewer parameters → easier interpretation
- Fewer parameters → smaller std. errors

These are similar to reasons for using:

- Cochran-Mantel-Haenzel (CMH) tests
- Testing linear (or polynomial) contrasts in ANOVA

Models for ordered categories

Consider an $R \times C$ table having **ordered** categories

- In many cases, the RC association may be described more simply by assigning numeric scores to the row & column categories.
- For simplicity, we consider only integer scores, 1, 2, ... here
- These models are easily extended to stratified tables

R:C model	μ_{ij}^{RC}	df	Formula
Uniform association	$i \times j \times \gamma$	1	$i:j$
Row effects	$a_i \times j$	$(I - 1)$	$R:j$
Col effects	$i \times b_j$	$(J - 1)$	$i:C$
Row+Col eff	$ja_i + ib_j$	$I + J - 3$	$R:j + i:C$
RC(1)	$\phi_i \psi_j \times \gamma$	$I + J - 3$	Mult (R, C)
Unstructured (R:C)	μ_{ij}^{RC}	$(I - 1)(J - 1)$	$R:C$

Linear x Linear Model (Uniform association)

- Assume linear ordering of both the row and column variables
- Assign scores (usually integers, 1, 2, ...)

$$\begin{aligned} \mathbf{a} &= \{a_i\}, & a_1 \leq a_2 \leq \cdots a_I \\ \mathbf{b} &= \{b_j\}, & b_1 \leq b_2 \leq \cdots b_J \end{aligned}$$

- Then, the **linear-by-linear model** ($L \times L$) model is:

$$\log(m_{ij}) = \mu + \lambda_i^A + \lambda_j^B + \gamma a_i b_j .$$

- The local odds ratios for adjacent 2×2 tables are:

$$\log(\theta_{ij}) = \gamma(a_{i+1} - a_i)(b_{j+1} - b_j) \quad \implies \quad \log(\theta_{ij}) = \gamma \text{ for integer scores}$$

- Only one more parameter (γ) than the independence model
- Independence model: special case, $\gamma = 0$

Row effects & column effects: R, C, R+C

- In the **row effects model** (R), the row variable, A , is treated as nominal, but B is assigned scores

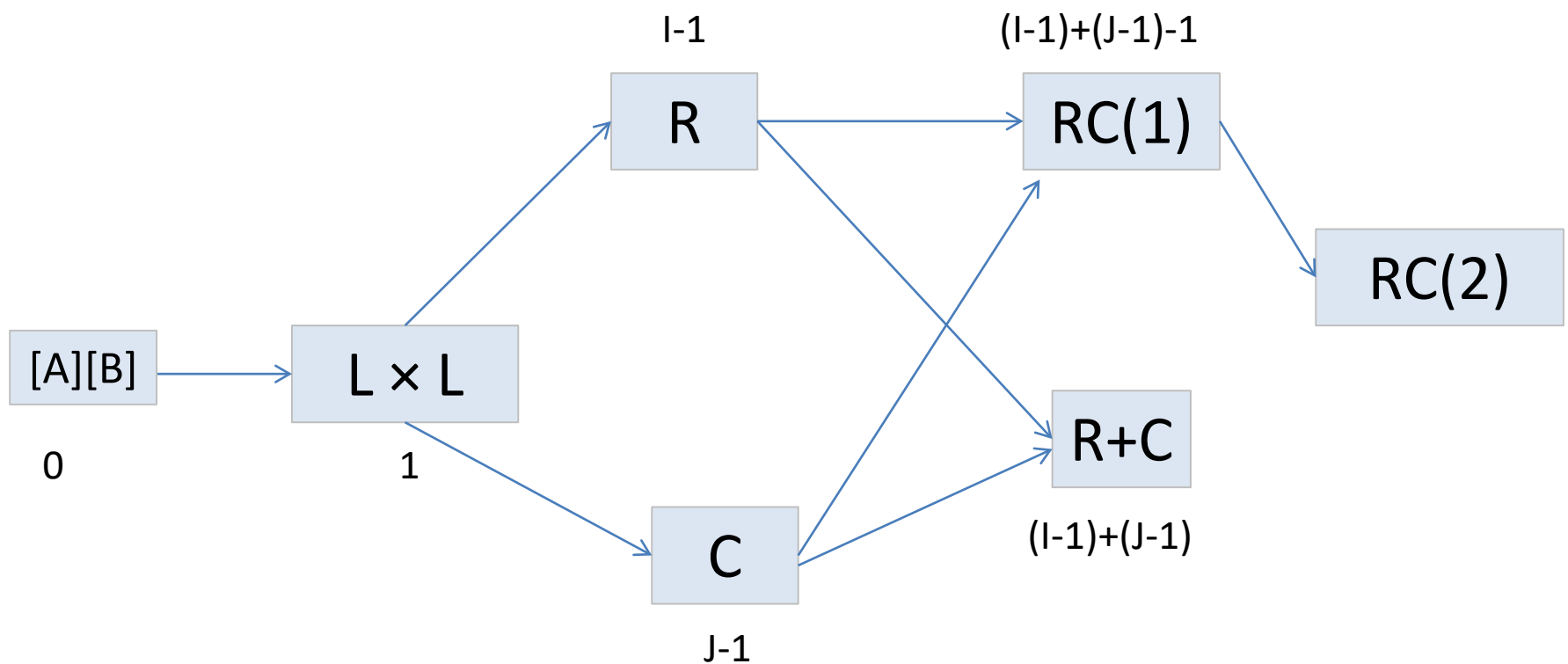
$$\log(m_{ij}) = \mu + \lambda_i^A + \lambda_j^B + \alpha_i b_j \quad \ni \quad \sum_i \alpha_i = 0 \text{ or } \alpha_1 = 0$$

- In the analogous **column effects model** (C), the row variable, A , is assigned scores, but B is nominal
- The **row plus column effects model** (R+C), assigns scores to both the rows and column variables.

$$\log(m_{ij}) = \mu + \lambda_i^A + \lambda_j^B + (\alpha_i b_j + a_i \beta_j)$$

Models for ordered categories

Nesting relations among models for ordinal variables



Example: Mental impairment & SES

Data on mental health status of NYC youth in relation to parents' SES

Note that ses & mental have been declared as **ordered** factors

```
> str(Mental)
'data.frame':      24 obs. of  3 variables:
 $ ses      : Ord.factor w/ 6 levels "1"<"2"<"3"<"4"<...: 1 1 1 1 2 2 2 2 3 3 ...
 $ mental   : Ord.factor w/ 4 levels "Well"<"Mild"<...: 1 2 3 4 1 2 3 4 1 2 ...
 $ Freq     : int   64 94 58 46 57 94 54 40 57 105 ...
```

Display it as a 2-way table

```
> (Mental.tab <- xtabs(Freq ~ mental+ses, data=Mental))
      ses
mental  1   2   3   4   5   6
  Well   64  57  57  72  36  21
  Mild   94  94 105 141  97  71
  Moderate 58  54  65  77  54  54
  Impaired 46  40  60  94  78  71
```

Example: Mental impairment & SES

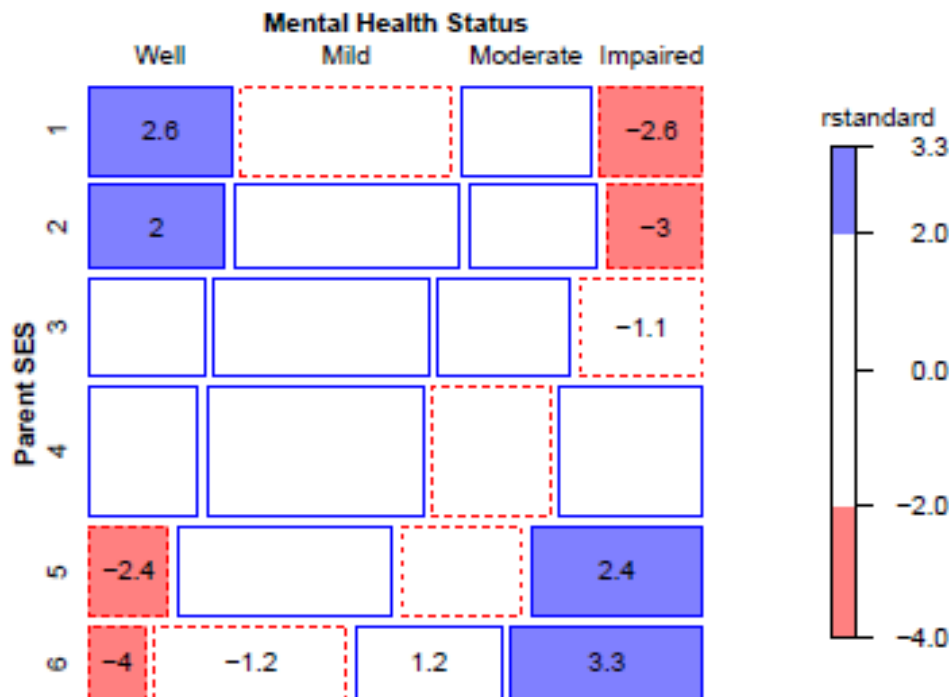
Fit and test the independence model using glm()

```
> indep <- glm(Freq ~ mental+ses,  
               family = poisson, data = Mental)  
  
> vcdExtra::LRstats(indep)  
Likelihood summary table:  
      AIC      BIC LR Chisq Df Pr(>Chisq)  
indep 209.59 220.19  47.418 15 3.155e-05 ***  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Yoda: Look at the mosaic, Luke!

```
> mosaic(indep, residuals_type="rstandard",  
         labeling=labeling_residuals,  
         main="Mental health data: Independence")
```

Mental health data: Independence



Departures from independence show the classic opposite corner pattern

The mosaic uses discrete shading levels, so it is useful to show residuals in the cells

Local odds ratios

For ordered tables, useful to examine the local log odds ratios for successive 2 x 2 sub-tables

These would all be ≈ 0 under independence

```
> (LMT <- loddsratio(t(mental.tab)))
log odds ratios for mental and ses
```

	ses				
mental	1:2	2:3	3:4	4:5	5:6
Well:Mild	0.1158	0.1107	0.0612	0.3191	0.227
Mild:Moderate	-0.0715	0.0747	-0.1254	0.0192	0.312
Moderate:Impaired	-0.0683	0.2201	0.2795	0.1682	-0.094

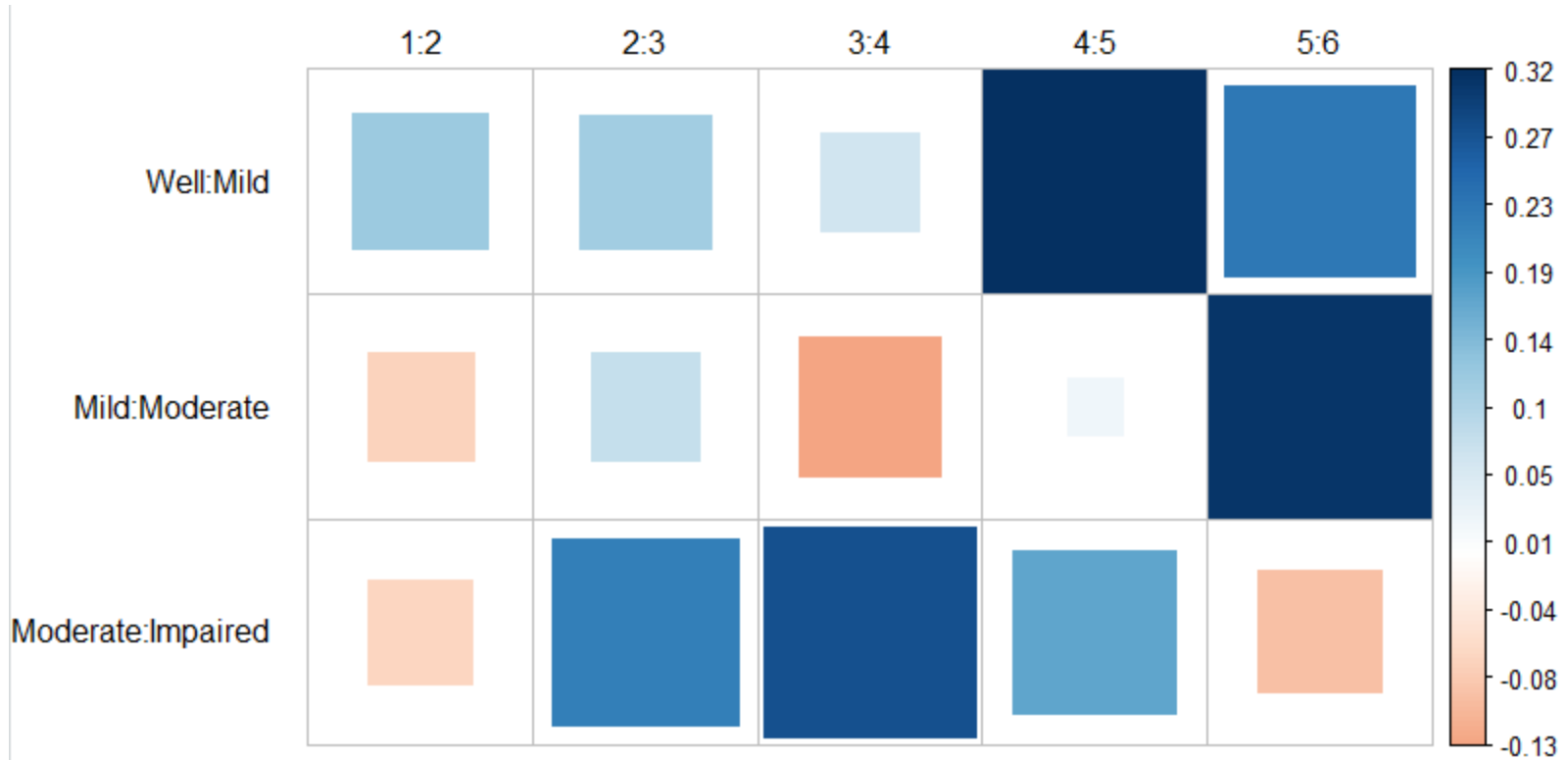
```
> mean(LMT$coefficients)
[1] 0.103
> mean(LMT$coefficients) |> exp()
[1] 1.11
```

On average, a one-unit step down the SES scale multiplies the odds of one worse mental health classification by $\exp(0.103) = 1.11$ (11% increase)

Local odds ratios

We can plot these as area- and color-proportional shaded squares using `corrplot()`

```
corrplot(as.matrix(LMT), method="square", is.corr = FALSE,  
         tl.col = "black", tl.srt = 0, tl.offset=1)
```



Fitting ordinal models

To fit ordinal models, use `as.numeric()` on a factor variable to assign integer scores (or other numeric scores)

```
Cscore <- as.numeric(Mental$ses)
Rscore <- as.numeric(Mental$mental)
```

Then, add the appropriate $L \times L$, R, or C terms to the independence model:

```
linlin <- update(indep, . ~ . + Rscore:Cscore)
roweff <- update(indep, . ~ . + mental:Cscore)
coleff <- update(indep, . ~ . + Rscore:ses)
```


Comparing models

```
LRstats(indep, linlin, roweff, coleff, sortby="AIC")

## Likelihood summary table:
##           AIC    BIC LR Chisq Df Pr(>Chisq)
## indep  209.6  220.2   47.42 15  3.16e-05 ***
## coleff 179.0  195.5    6.83 10    0.741
## roweff 174.4  188.6    6.28 12    0.901
## linlin 174.1  185.8    9.90 14    0.770
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- All ordinal models are acceptable by LR tests
- The $L \times L$ model is judged the best by both AIC and BIC.
- This has only 1 more parameter than the independence model

Comparing models

When overall tests are unclear, you can carry out tests of nested sets of models using `anova()`, giving tests of ΔG^2 .

The indep, linlin and row effect models are one nested set:

```
anova(indep, linlin, roweff, test="Chisq")

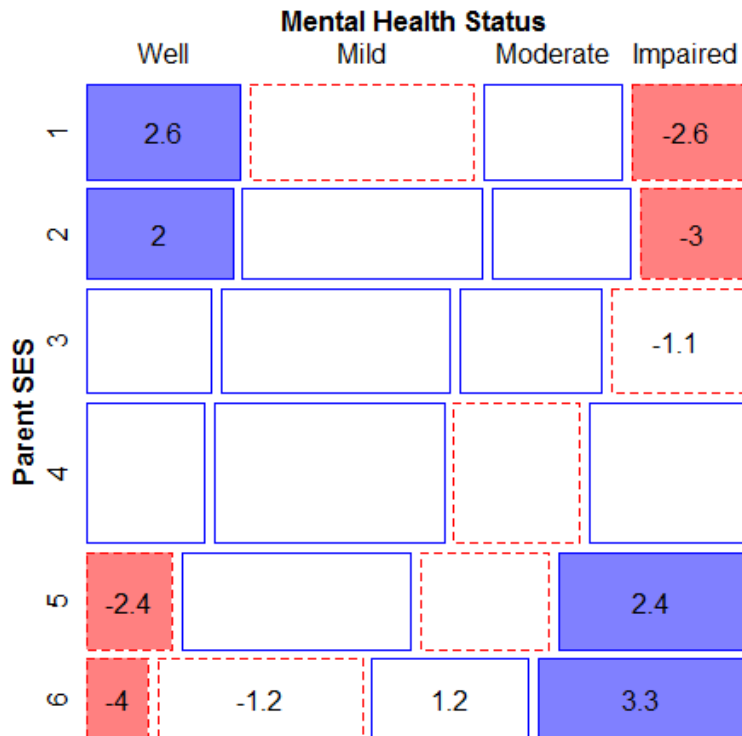
## Analysis of Deviance Table
##
## Model 1: Freq ~ mental + ses
## Model 2: Freq ~ mental + ses + Rscore:Cscore
## Model 3: Freq ~ mental + ses + mental:Cscore
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      15      47.4
## 2      14       9.9  1    37.5    9e-10 ***
## 3      12       6.3  2     3.6    0.16
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The $L \times L$ model is a signif. improvement; the R model is not

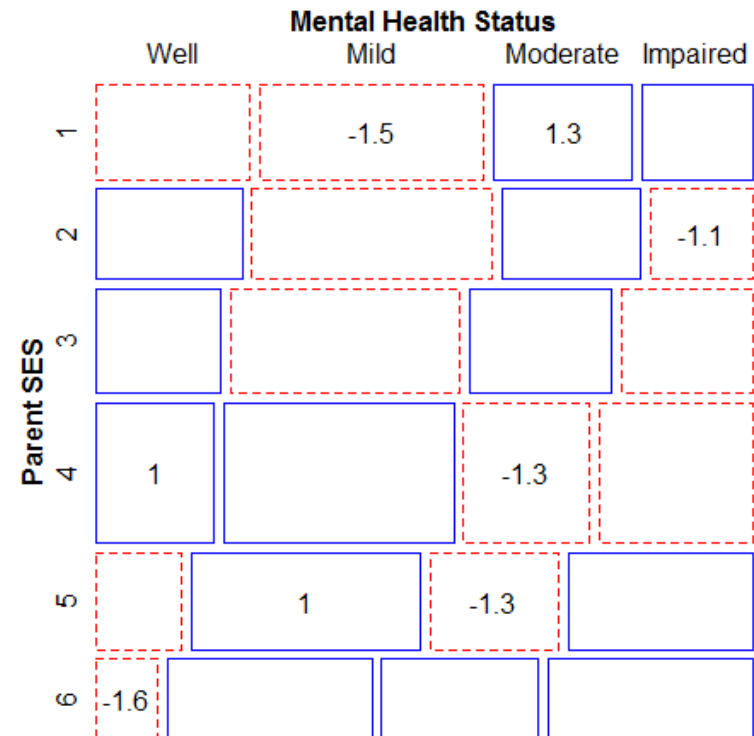
Comparing models: Mosaic plots

Beyond statistical tests, mosaic plots show the remaining structure in the residuals, unaccounted for in a given model.

Mental health data: Independence



Mental health data: Linear x Linear



Interpreting the $L \times L$ model

In the $L \times L$ model, the parameter γ is the constant local odds ratio. e^γ is the multiplier of the odds for a one-step change in mental or ses

```
> coef(linlin) [ ["Rscore:Cscore" ] ]  
[1] 0.09069
```

```
> exp(coef(linlin) [ ["Rscore:Cscore" ] ] )  
[1] 1.095
```

- $\hat{\gamma} = 0.0907 \implies$ local odds ratio, $\hat{\theta}_{ij} = \exp(0.0907) = 1.095$.
- each step down the SES scale increases the odds of being classified one step poorer in mental health by 9.5%.
- a very simple interpretation of association!

Log-multiplicative (RC) models

- The $L \times L$, R, and C models are all simpler to interpret than the saturated model
- But, all depend on assigning **fixed** scores to the categories
- The **row-and-column effects model** (RC(1)) makes these **parameters**

$$\log(m_{ij}) = \mu + \lambda_i^A + \lambda_j^B + \gamma \alpha_i \beta_j \quad \text{or, } \lambda_{ij}^{AB} = \gamma \alpha_i \beta_j$$

where γ , α and β comprise additional parameters to be estimated beyond the independence model.

- γ here is \sim to γ in the $L \times L$ model
- The ordering and spacing of the categories is **estimated** from the data (as in CA)
- Requires some constraints to be identifiable: e.g., unweighted solution—

$$\sum_i \alpha_i = \sum_j \beta_j = 0$$

$$\sum_i \alpha_i^2 = \sum_j \beta_j^2 = 1$$

Log-multiplicative (RC) models

- This generalizes to multiple bilinear terms, the RC(M) model

$$\lambda_{ij}^{AB} = \sum_{k=1}^M \gamma_k \alpha_{ik} \beta_{jk} \quad M = \min(I - 1, J - 1)$$

- e.g., the RC(2) model has **two** bilinear terms (like a 2D CA solution)

$$\lambda_{ij}^{AB} = \gamma_1 \alpha_{i1} \beta_{j1} + \gamma_2 \alpha_{i2} \beta_{j2}$$

- RC models are **not** loglinear– contain multiplicative terms
 - Can't use `glm()`
 - The `gnm()` function in `gnm` fits a wide variety of such **generalized nonlinear models**
 - The `rc()` function in `logmult` uses `gnm()` and makes plotting easier.

Generalized *nonlinear* models

The `gnm` package provides fully general ways to specify nonlinear GLMs

- Basic nonlinear functions: `Exp()`, `Inv()`, `Mult()`
- The RC(1) model: `gnm(Freq ~ A + B + Mult(A, B))`
- The RC(2) model:
`gnm(Freq ~ A + B + instances(Mult(A, B), 2))`
- Models for mobility tables—the UNIDIFF model

$$\log m_{ijk} = \alpha_{ik} + \beta_{jk} + \exp(\gamma_k)\delta_{ij}$$

the exponentiated multiplier is specified as `Mult(Exp(C), A:B)`

- User-defined functions allow further extensions

Example: Mental impairment & SES

Fit the RC(1) and RC(2) model by adding terms using Mult() to the independence model

```
> library(gnm)
> indep <- gnm(Freq ~ mental + ses,
               family = poisson, data = Mental, verbose=FALSE)
> RC1 <- update(indep, . ~ . + Mult(mental, ses))
> RC2 <- update(indep, . ~ . + instances(Mult(mental, ses), 2))
```

Compare models with GOF tests and AIC, BIC

```
> vcdExtra::LRstats(indep, linlin, roweff, coleff, RC1, RC2)
Likelihood summary table:
      AIC BIC LR Chisq Df Pr(>Chisq)
indep  210 220    47.4  15  3.2e-05 ***
linlin  174 186    9.9  14    0.77
roweff  174 189    6.3  12    0.90
coleff  179 196    6.8  10    0.74
RC1     180 199    3.6   8    0.89
RC2     187 211    0.5   3    0.91
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Comparing models

anova() again gives tests of $\Delta\chi^2$ for nested models

- Are estimated RC scores better than integer scores in the L x L model?
- If so, do we need more than one dimension?

```
> anova(linlin, RC1, RC2, test="Chisq")
Analysis of Deviance Table

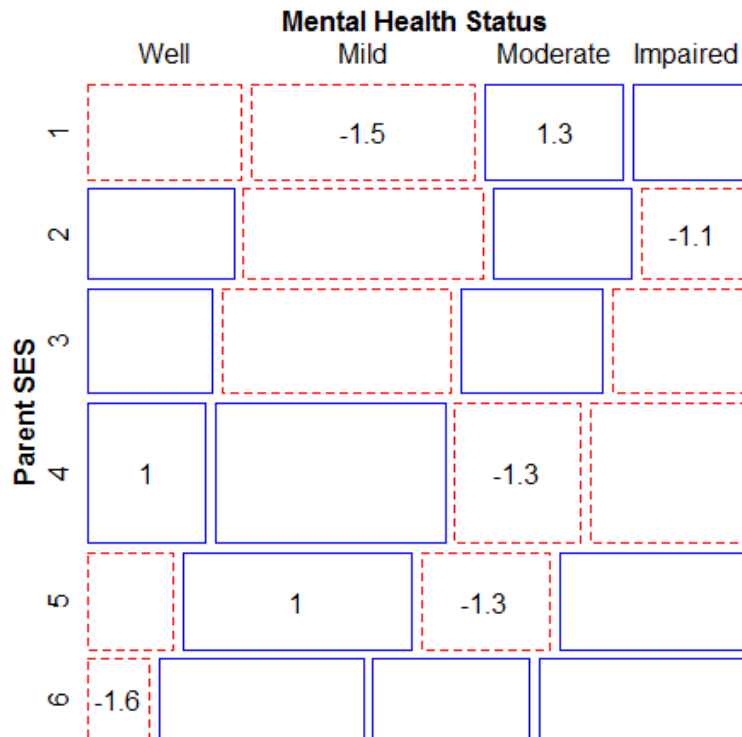
Model 1: Freq ~ mental + ses + Rscore:Cscore
Model 2: Freq ~ mental + ses + Mult(mental, ses)
Model 3: Freq ~ mental + ses + Mult(mental, ses, inst = 1) +
      Mult(mental, ses, inst = 2)

  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1      14      9.90
2       8      3.57  6    6.32    0.39
3       3      0.52  5    3.05    0.69
```

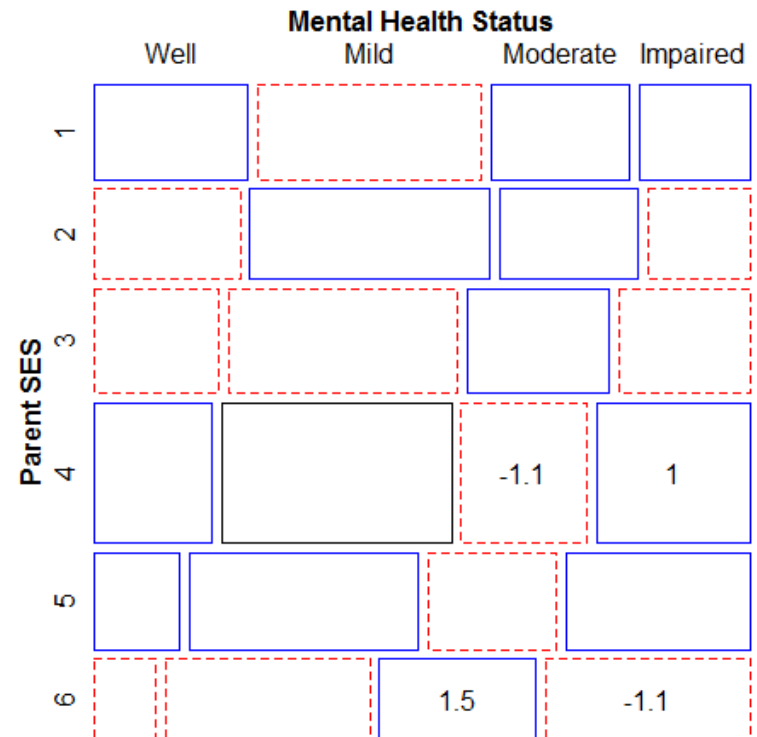
Neither RC model shows a significant advantage over the L x L model

Comparing models: Mosaic plots

Mental health data: Linear x Linear

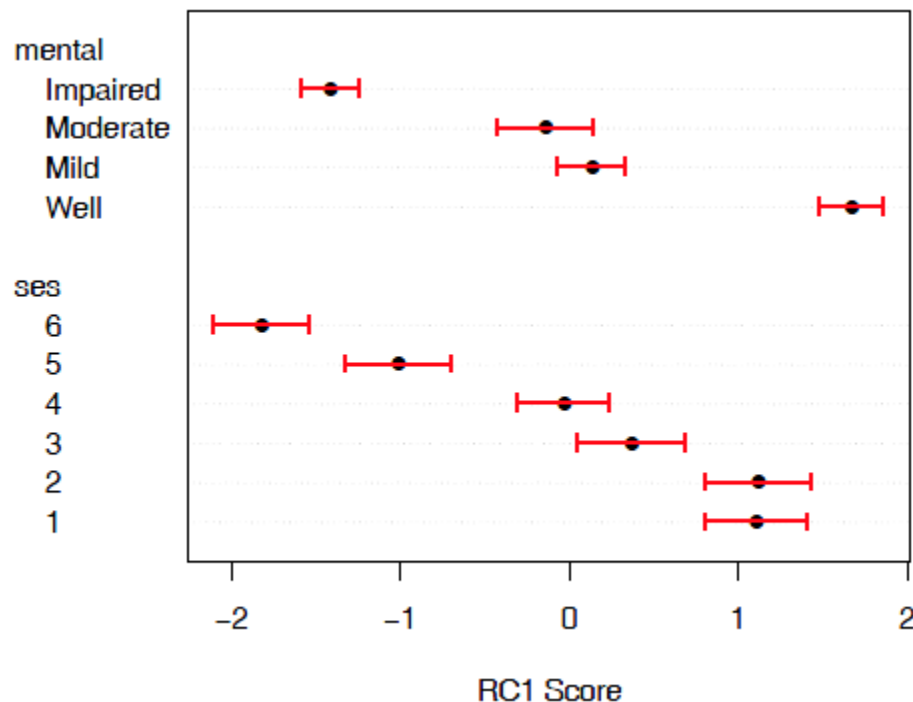


Mental health data: RC(1) model



Visualizing RC scores

- The RC(1) model can be interpreted visually using a dotplot of the scaled category scores together with error bars.
- This allows you to see where this model differs from the $L \times L$ model with integer spacing



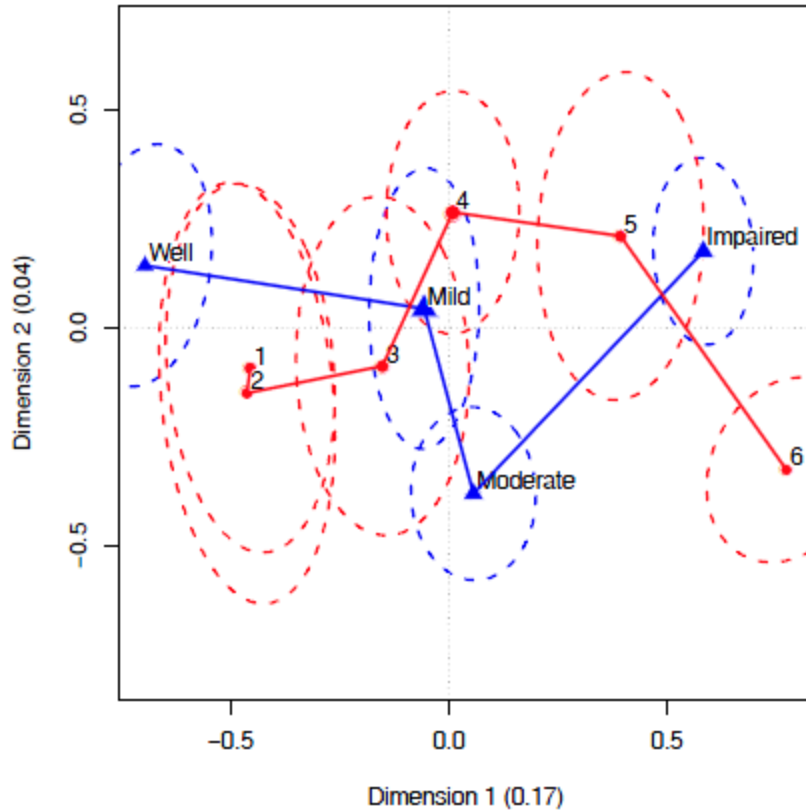
mental: mild & moderate not that different, but ordered correctly

ses: approx. linear, except for ses = (1,2), which don't differ

Similar to what we saw in CA

When this matters, RC models provide the statistical machinery for inference

Visualizing RC scores

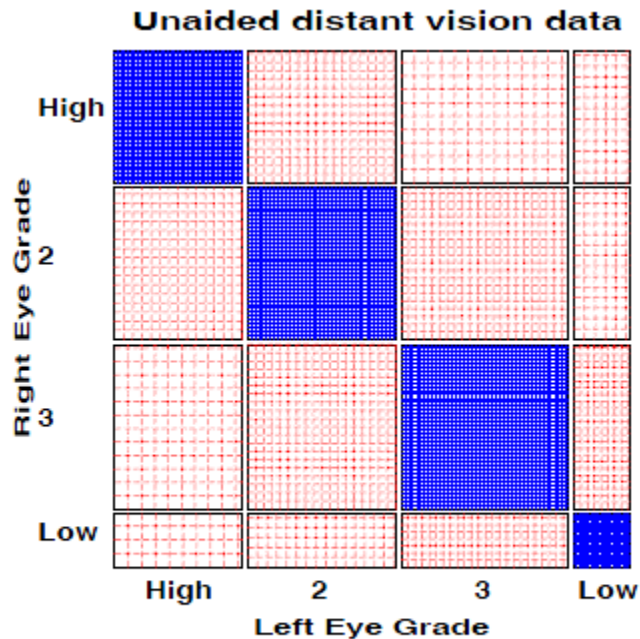


- For the RC(2) model, plot the category scores for dim. 1 and 2
- The `logmult` package makes these plots much easier
- Also, provides bivariate confidence ellipses

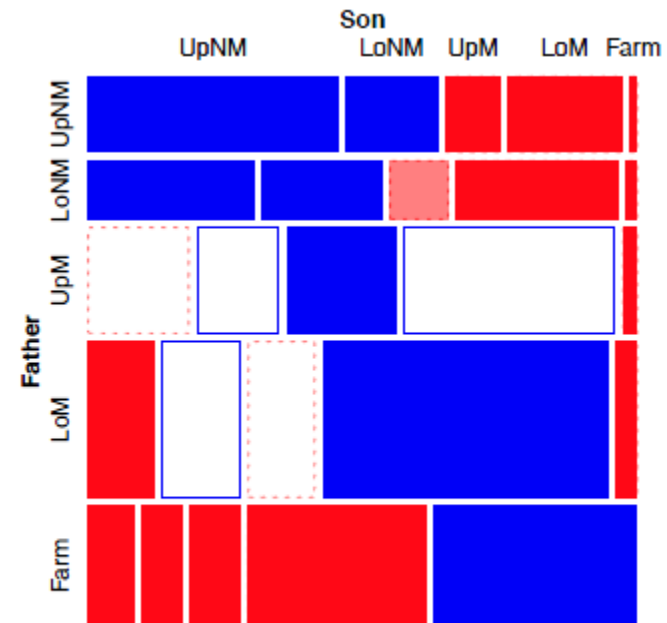
Square tables

Square tables arise when the row and column variables have the **same** categories, often **ordered**

Special loglinear models allow us to tease apart different **reasons** for association



Visual acuity data



Hauser social mobility data

Square tables: Models

In such cases, general association is a given, because of the diagonal cells
More interesting models concern the nature of association in off-diagonal cells

- **Quasi-independence:** ignore the diagonal cells

$$\log m_{ij} = \mu + \lambda_i^A + \lambda_j^B + \delta_i I(i = j) .$$

This model adds one parameter, δ_i , for each diagonal cell, which fits those frequencies perfectly.

- **Symmetry:** $\pi_{ij} = \pi_{ji}$, but this implies marginal homogeneity, $\pi_{i+} = \sum_j \pi_{ij} = \sum_j \pi_{ji} = \pi_{+i}$ for all i .
- **Quasi-symmetry:**

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

- It can be shown that

$$\begin{aligned} \text{symmetry} &= \text{quasi-symmetry} + \text{marginal homogeneity} \\ G^2(S) &= G^2(QS) + G^2(MH) \end{aligned}$$

Square tables: Models

For these models, the essential idea is to construct factor levels corresponding to the unique parameters representing association

$$\text{Diag}_{4 \times 4} = \begin{bmatrix} 1 & \cdot & \cdot & \cdot \\ \cdot & 2 & \cdot & \cdot \\ \cdot & \cdot & 3 & \cdot \\ \cdot & \cdot & \cdot & 4 \end{bmatrix} \quad \text{Symm}_{4 \times 4} = \begin{bmatrix} 11 & 12 & 13 & 14 \\ 12 & 22 & 23 & 24 \\ 13 & 23 & 33 & 34 \\ 14 & 24 & 34 & 44 \end{bmatrix}$$

Diag adds k parameters to fit **diagonal cells**, beyond independence

Symm adds $k \times (k+1)$ parameters to fit a **symmetric pattern** of association

More general **topological** models allow an **arbitrary** pattern of association, but more parsimonious than the independence model

$$\text{Topo}_{4 \times 4} = \begin{bmatrix} 2 & 3 & 4 & 4 \\ 3 & 3 & 4 & 4 \\ 4 & 4 & 5 & 5 \\ 4 & 4 & 5 & 1 \end{bmatrix}$$

Square tables: Using gnm()

Some models for structured associations in square tables:

- quasi-independence (ignore diagonals)

```
gnm(Freq ~ row + col + Diag(row, col), family=poisson)
```

- symmetry ($\lambda_{ij}^{RC} = \lambda_{ji}^{RC}$)

```
gnm(Freq ~ Symm(row, col), family=poisson)
```

- quasi-symmetry = quasi + symmetry

```
gnm(Freq ~ row + col + Symm(row, col), family=poisson)
```

- fully-specified “topological” association patterns

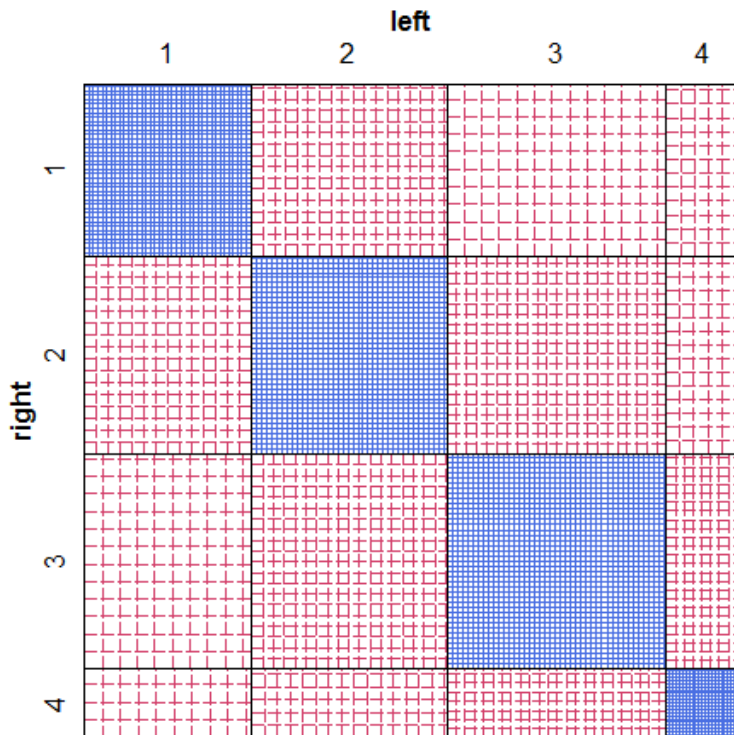
```
gnm(Freq ~ row + col + Topo(row, col, spec=RCmatrix), ...)
```

All of these are actually GLMs, but the `gnm` package provides convenience functions `Diag`, `Symm`, and `Topo` to facilitate model specification.

Example: Visual acuity

```
data("VisualAcuity", package="vcd")
women <- subset(VisualAcuity, gender=="female", select=-gender)
sieve(Freq ~ right + left, data=women, shade = TRUE,
      main = "Unaided distance vision data")
```

Visual acuity data (women)



Diagonal cells clearly dominate

What associations remain, ignoring these?

Is there evidence for quasi-symmetry?

A more complete analysis could examine gender in relation to these associations

Fitting models

Start with the independence model, then update() to add other terms

```
> indep <- glm(Freq ~ right + left, data = women, family = poisson)
> quasi <- update(indep, . ~ . + Diag(right, left))

> symm <- glm(Freq ~ Symm(right, left), data = women, family = poisson)
> qsymm <- update(symm, . ~ right + left + .)
```

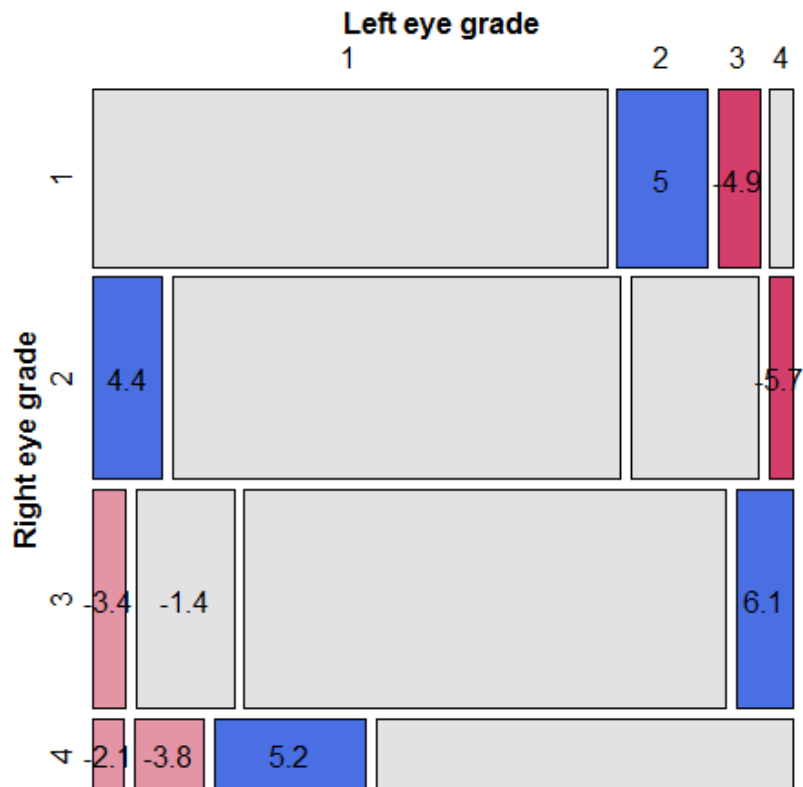
The quasi-symmetry model (qsymm) fits reasonably well; none of the others do by LR G^2 tests or AIC, BIC

```
> vcdExtra::LRstats(indep, quasi, symm, qsymm)
Likelihood summary table:
      AIC  BIC LR Chisq Df Pr(>Chisq)
indep 6803 6808      6672  9    <2e-16 ***
quasi  338  347      199  5    <2e-16 ***
symm   157  164       19  6    0.0038 **
qsymm  151  161        7  3    0.0638 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

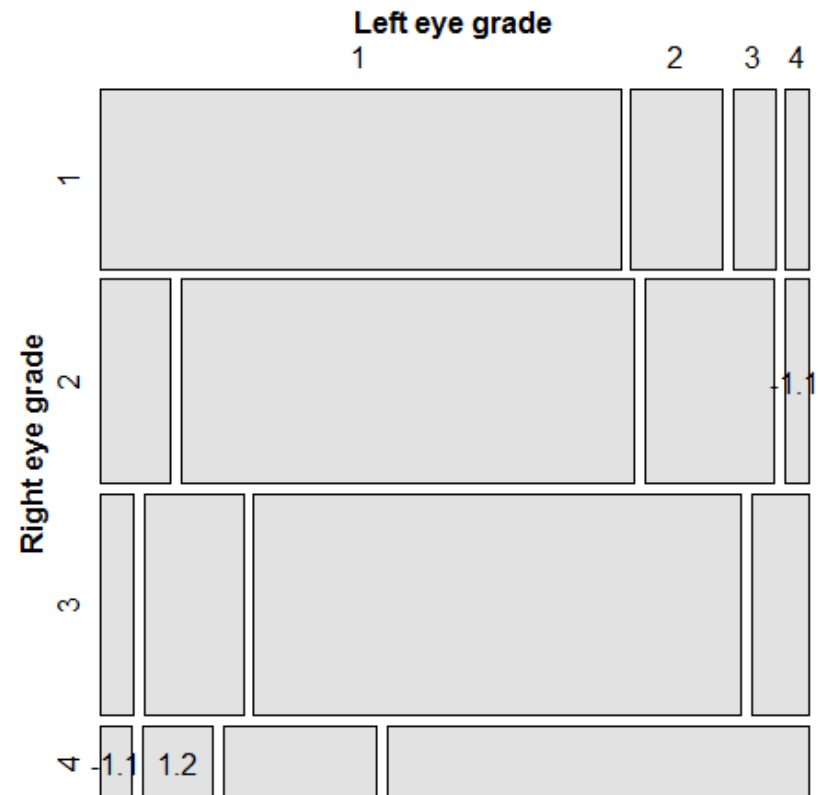
Visualizing model fits

Quasi-independence: The diagonal cells are force to fit *exactly*.
Lack-of-fit appears in the symmetrically opposite cells

Visual Acuity: Quasi Independence



Visual Acuity: Quasi Symmetry



More complex models

- Extensions of these methods occur in a variety of contexts:
 - **Panel surveys**, where attitude items are analyzed over time & space
 - **Social mobility** data, where occupational status of parents and children may admit subtly different models
 - **Migration** data, where geographical & political factors require special treatment (e.g., mover-stayer models)
- These often involve:
 - **ordinal variables**: support for abortion, occupational status
 - **square tables**: husbands/wives, fathers/sons
 - **strata** or layers to control for other factors or analyze change over time or differences over geography

More complex models

- For example, the **log-multiplicative uniform difference** (UNIDIFF) model, for factors R, C, with layer variable L:

$$\log m_{ijk} = \mu + \lambda_i^R + \lambda_j^C + \lambda_k^L + \lambda_{ik}^{RL} + \lambda_{jk}^{CL} + \gamma_k \delta_{ij}^{RC}$$

- The term for the three-way association [RCL] pertains to how the [RC] association varies with layer (L)
 - The UNIDIFF model says there is a multiplier γ_k for a **common** δ_{ij}^{RC} association
 - Special cases: R, C, RC(1) models for the [RC] association;
 - Special cases: **homogeneous associations** ($\gamma_k = 0$) for layers
- **gnm()** notation uses **Exp(L)**, so layer effects are on a log scale.
 - The **logmult** package provides a **unidiff()** function that makes this easier.

Models for stratified mobility tables

Baseline models:

- Perfect mobility: $\text{Freq} \sim (R+C) * L$
- Quasi-perfect mobility: $\text{Freq} \sim (R+C) * L + \text{Diag}(R, C)$

Layer models:

- Homogeneous: no layer effects— $\gamma_k = 0$
- Heterogeneous: e.g., $\mu_{ijk}^{RCL} = \exp(\gamma_k^L) \delta_{ij}^{RC}$

Extended models: Baseline \oplus Layer model(R:C model)

R:C model	Layer model	
	Homogeneous	log multiplicative
Row effects	$\sim .+ R:j$	$\sim .+ \text{Mult}(R:j, \text{Exp}(L))$
Col effects	$\sim .+ i:C$	$\sim .+ \text{Mult}(i:C, \text{Exp}(L))$
Row+Col eff	$\sim .+ R:j + i:C$	$\sim .+ \text{Mult}(R:j + i:C, \text{Exp}(L))$
RC(1)	$\sim .+ \text{Mult}(R, C)$	$\sim .+ \text{Mult}(R, C, \text{Exp}(L))$
Full R:C	$\sim .+ R:C$	$\sim .+ \text{Mult}(R:C, \text{Exp}(L))$

Example: Social mobility in US, UK & Japan

Data from Yamaguchi (1987): Cross-national comparison of occupational mobility

```
> data(Yamaguchi87, package="vcdExtra")
> Yama.tab <- xtabs(Freq ~ Father + Son + Country, data=Yamaguchi87)
> structable(Country+Son~Father, Yama.tab[, , 1:2])
```

	Country US					Country UK					
	Son	UpNM	LoNM	UpM	LoM	Farm	UpNM	LoNM	UpM	LoM	Farm
Father											
UpNM		1275	364	274	272	17	474	129	87	124	11
LoNM		1055	597	394	443	31	300	218	171	220	8
UpM		1043	587	1045	951	47	438	254	669	703	16
LoM		1159	791	1323	2046	52	601	388	932	1789	37
Farm		666	496	1031	1632	646	76	56	125	295	191

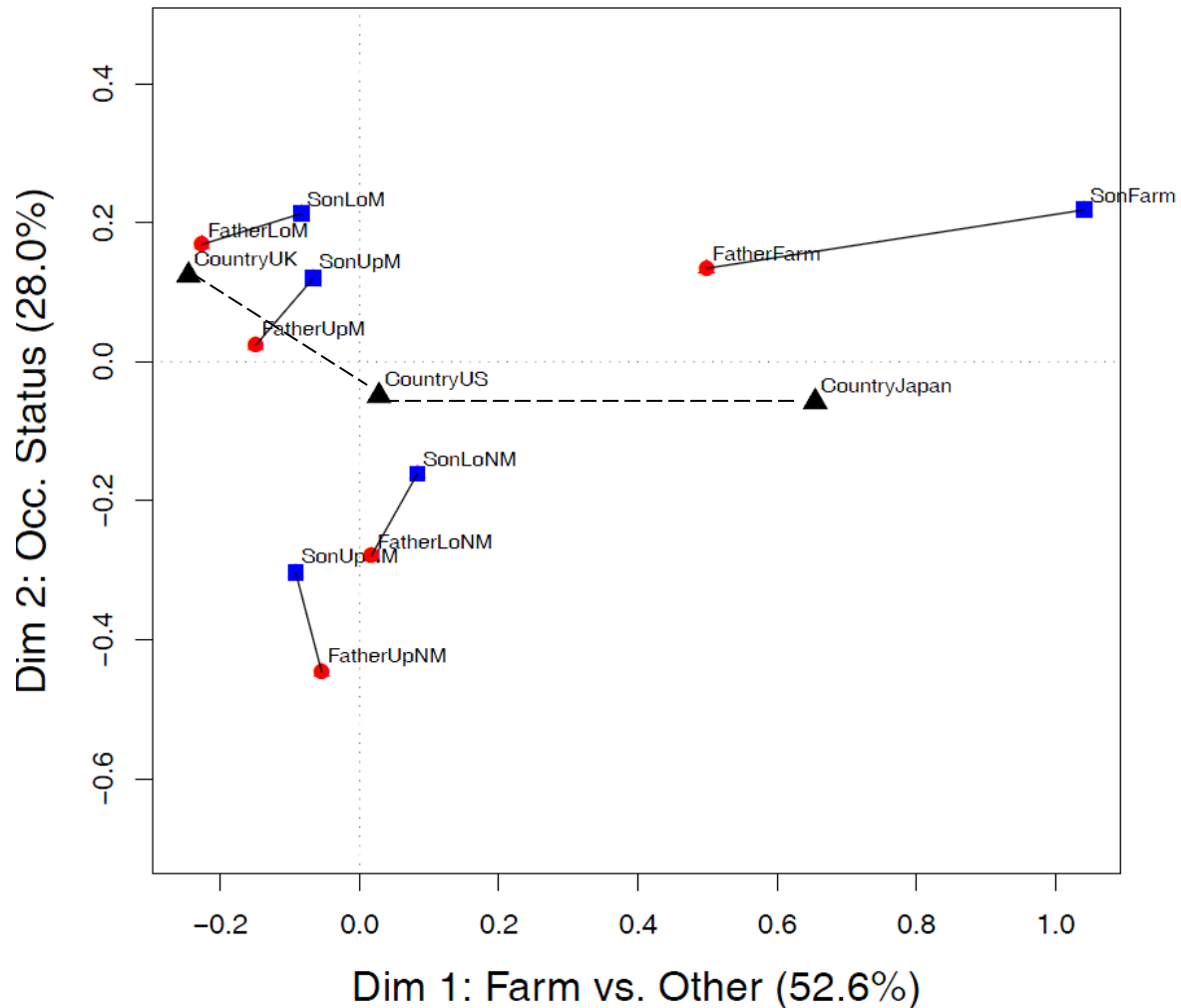
Questions:

- Is occupational mobility the same for all countries? (No layer effects)
- If not, how do they differ?
- Are there simple models that describe mobility?

See: `demo("yamaguchi-xie", package="vcdExtra")`

Explore: Try MCA

Yamaguchi data: Mobility in US, UK and Japan, MCA



```
library(ca)
Yama.dft <- expand.dft(Yamaguchi87)
yama.mjca <- mjca(Yama.dft)
plot(yama.mjca, what=c("none", "all"))
```

Dimensions have reasonable interpretations
Farm differs from others
All sons seem to move up!

How does this relate to theories of mobility?

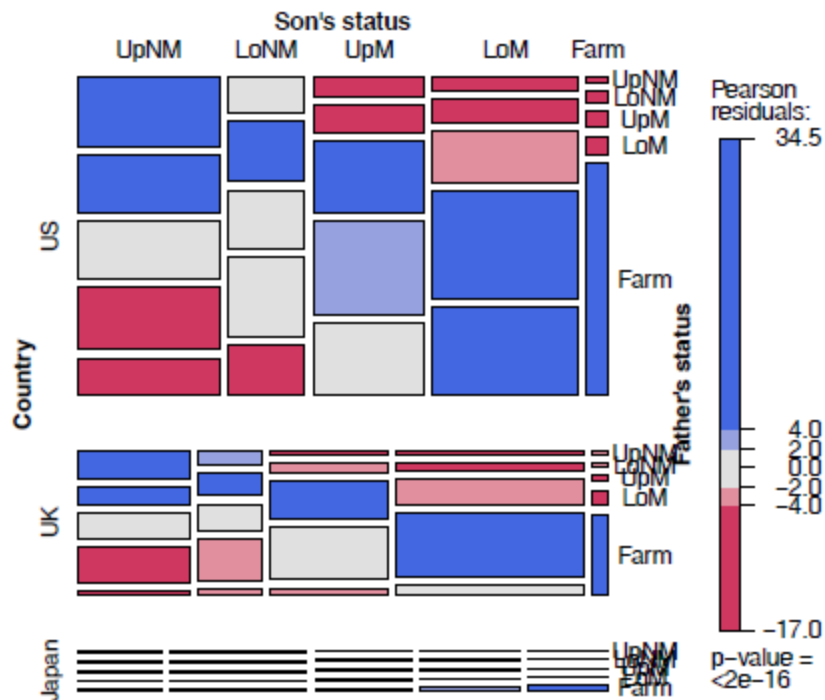
How to understand country effects?

Yamaguchi data: Baseline models

The minimal, null model asserts $\text{Father} \perp \text{Son} \mid \text{Country} = [\text{FC}][\text{SC}] = (\text{F}+\text{S}) * \text{C}$

```
yamaNull <- gnm(Freq ~ (Father + Son) * Country, data = Yamaguchi87,
  family = poisson)
mosaic(yamaNull, ~Country + Son + Father, condvars = "Country", ...)
```

[FC][SC] Null [FS] association (perfect mobility)



Within country, diagonal cells for F=S dominate

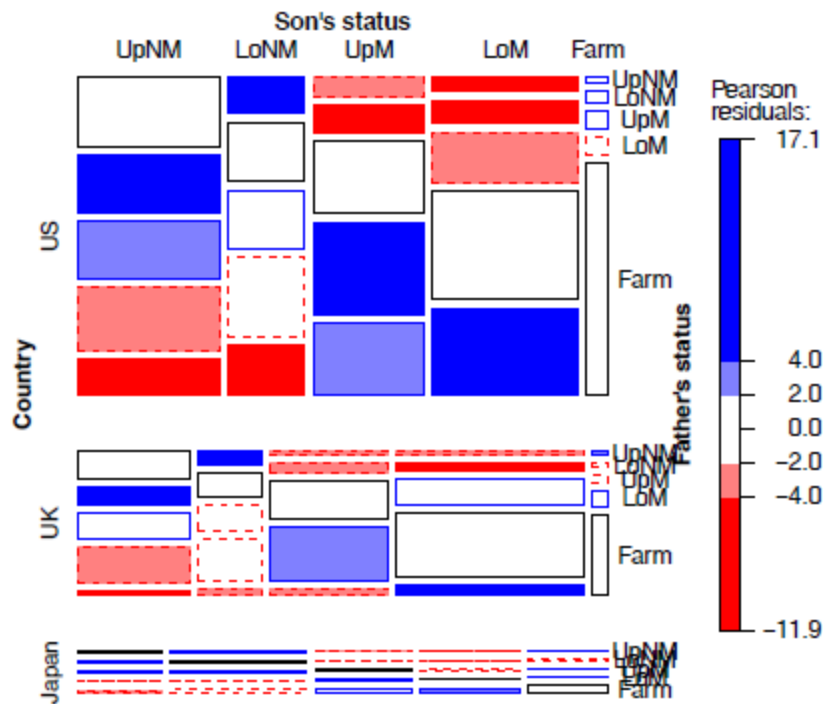
Much more data for US; least for Japan

Yamaguchi data: Baseline models

We expect $F \approx S$. Ignore diagonal cells with quasi-independence \rightarrow Quasi-perfect mobility

```
yamaDiag <- update(yamaNull, ~. + Diag(Father, Son):Country)
mosaic(yamaDiag, ~Country + Son + Father, condvars = "Country", ...)
```

[FC][SC] Quasi perfect mobility, +Diag(F,S)

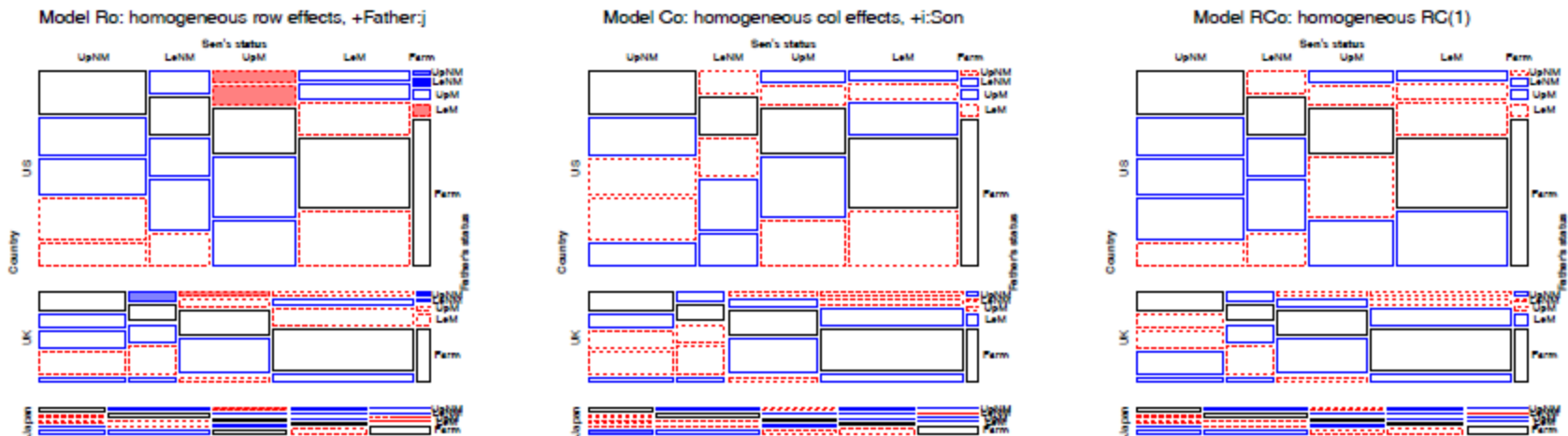


The term $\text{Diag}(F, S):\text{Country}$ fits diagonal cells perfectly w/in each country

Models for homogeneous associations

gnm(): easy to fit collections of models using update() to the yamaDiag model. These have no Country term, so they assert same associations for all countries

```
Rscore <- as.numeric(Yamaguchi87$Father)
Cscore <- as.numeric(Yamaguchi87$Son)
yamaRo <- update(yamaDiag, ~ . + Father:Cscore)
yamaCo <- update(yamaDiag, ~ . + Rscore:Son)
yamaRpCo <- update(yamaDiag, ~ . + Father:Cscore + Rscore:Son)
yamaRCo <- update(yamaDiag, ~ . + Mult(Father, Son))
yamaFIo <- update(yamaDiag, ~ . + Father:Son)
```



Models for heterogeneous associations

Can combine these with models including layer (Country) effects

Log-multiplicative (UNIDIFF) models add a term `Mult(..., Exp(Country))`

```
yamaRx    <- update(yamaDiag, ~ . + Mult(Father:Cscore, Exp(Country)))
yamaCx    <- update(yamaDiag, ~ . + Mult(Rscore:Son, Exp(Country)))
yamaRpCx  <- update(yamaDiag, ~ . + Mult(Father:Cscore +
                                         Rscore:Son, Exp(Country)))
yamaRCx   <- update(yamaDiag, ~ . + Mult(Father, Son, Exp(Country)))
yamaFIx   <- update(yamaDiag, ~ . + Mult(Father:Son, Exp(Country)))
```

We now have quite a collection of alternative models

- How to compare them?
- How to interpret the associations they imply about Father, Son mobility across countries?

Yamaguchi data: Comparing models

LRstats() and related methods facilitate model comparisons

```
> models <- glmlist(yamaNull, yamaDiag,  
                   yamaRo, yamaRx, yamaCo, yamaCx, yamaRpCo,  
                   yamaRpCx, yamaRCo, yamaRCx, yamaFIo, yamaFIx)
```

```
> LRstats(models)
```

Likelihood summary table:

	AIC	BIC	LR	Chisq	Df	Pr(>Chisq)		
yamaNull	6168	6231		5592	48	< 2e-16	***	} Baseline models
yamaDiag	1943	2040		1336	33	< 2e-16	***	
yamaRo	771	877		156	29	< 2e-16	***	} Homogeneous, Father:Son models
yamaRx	766	877		148	27	< 2e-16	***	
yamaCo	682	789		68	29	6.1e-05	***	
yamaCx	677	789		59	27	0.00038	***	
yamaRpCo	659	773		39	26	0.05089	.	} Heterogeneous, Father:Son models
yamaRpCx	658	776		33	24	0.10341		
yamaRCo	658	772		38	26	0.06423	.	
yamaRCx	657	775		32	24	0.12399		
yamaFIo	665	788		36	22	0.02878	*	
yamaFIx	664	791		31	20	0.05599	.	

```
---
```

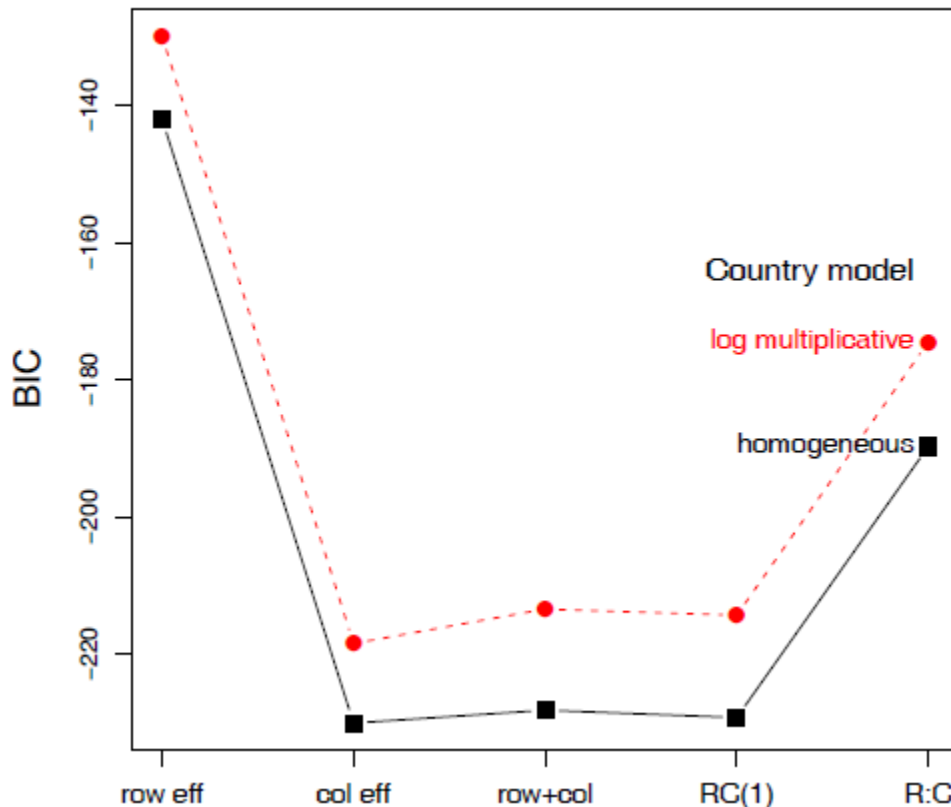
```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Yamaguchi data: Comparing models

Easier to understand by plotting the criteria for these models

```
BIC <- matrix(LRstats(models)$BIC[-(1:2)], 5, 2, byrow=TRUE)
matplot(BIC, ...)
```

Yamaguchi-Xie models: R:C model by Layer model Summary



BIC strongly prefers homogeneous models

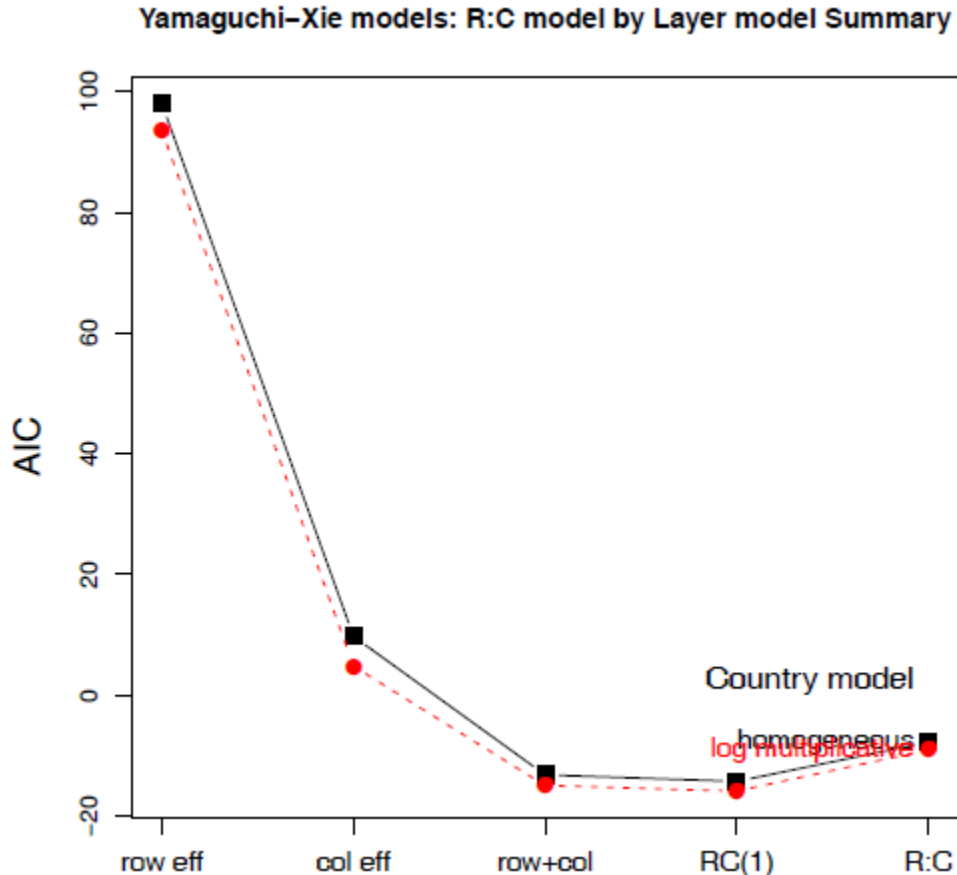
Little difference among Col, Row+Col, RC(1) models

→ R:C association ~ Row scores (fathers' status)

Yamaguchi data: Comparing models

Easier to understand by plotting the criteria for these models

```
AIC <- matrix(LRstats(models)$AIC[-(1:2)], 5, 2, byrow=TRUE)
matplot(AIC, ...)
```



AIC slightly prefers heterogeneous models

Row + Col & RC(1) fit best

→ R:C association ~ ordinal scores

Model summary plots make sense of multiple models

Interpreting associations

logmult::unidiff() uses `gnm()` for fitting, but makes summaries & plotting easier

```
> library(logmult)
> (yamaUni <- unidiff(as.table(Yama.tab)))
```

Layer coefficients:

	US	UK	Japan
	1.000	1.206	0.931

Layer intrinsic association coefficients:

	US	UK	Japan
	0.412	0.497	0.383

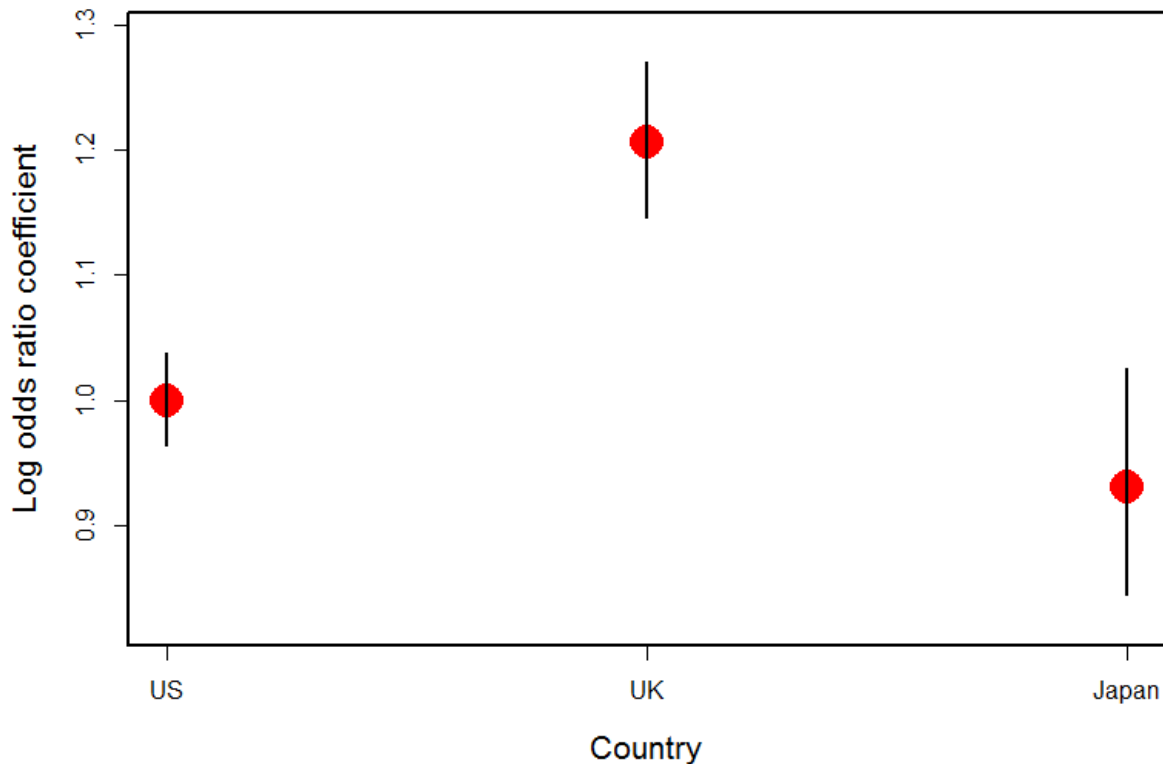
Full two-way interaction coefficients:

		Son				
Father		UpNM	LoNM	UpM	LoM	Farm
	UpNM	1.0063	0.3024	-0.4399	-0.6048	-0.4394
	LoNM	0.4644	0.5228	-0.2547	-0.3856	-0.5121
	UpM	0.0214	-0.0268	0.2557	-0.0972	-0.5828
	LoM	-0.2056	-0.1028	0.0891	0.2632	-0.6504
	Farm	-0.5320	-0.3026	0.0101	0.2592	2.074

Visualizing associations

Plotting the unidiff object plots the layer association coefficients

```
plot(yamaUni, cex=3, col="red", pch=16)
```



Father – Son
association is
ordered UK > US >
Japan

Visualizing associations

The common association parameters, δ_{ij}^{RC} are contained in the unidiff object.
Can extract these and plot in various ways

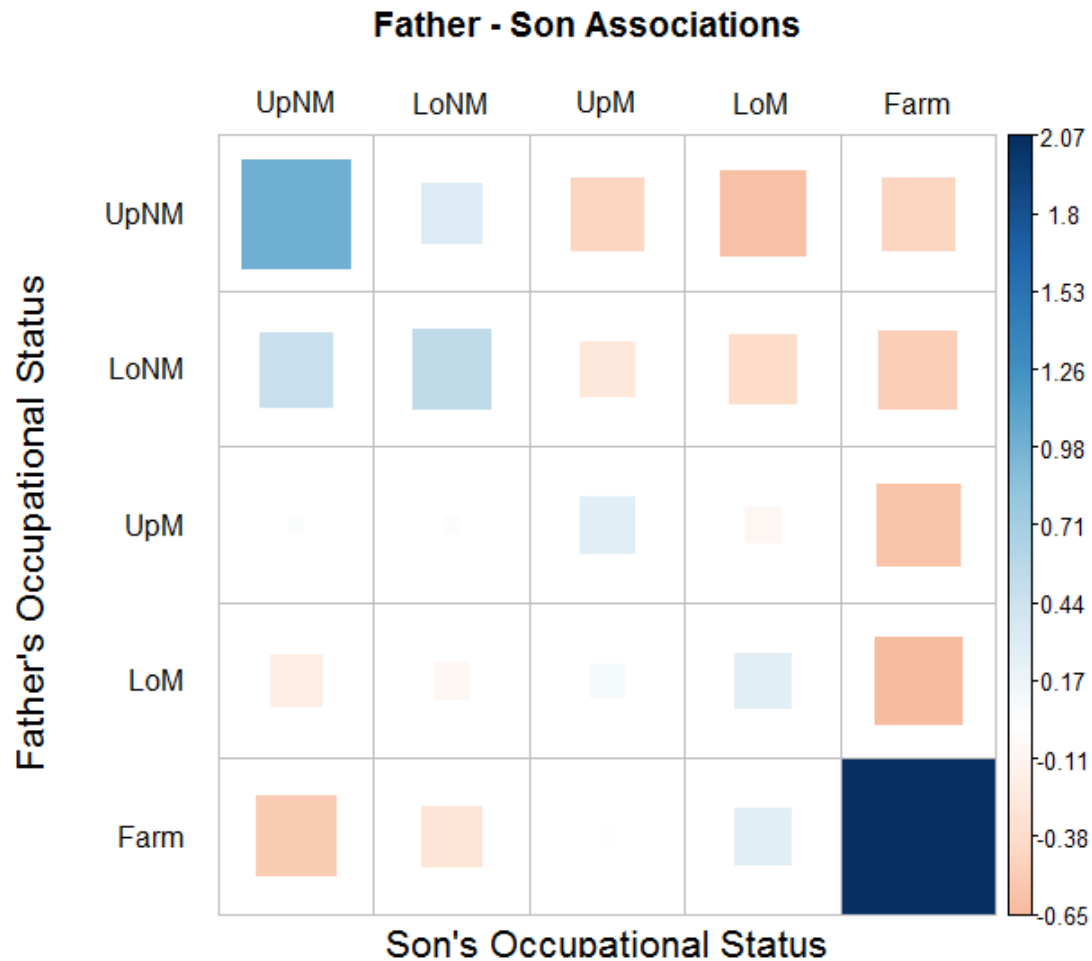
```
> inter <- yamaUni$unidiff$interaction
> names(inter)
[1] "Estimate"      "Std. Error"

> inter.mat <- matrix(inter$Estimate, 5, 5,
                      dimnames=dimnames(Yama.tab)[1:2])

> inter.mat
      Son
Father  UpNM  LoNM  UpM  LoM  Farm
UpNM   1.0063  0.3024 -0.4399 -0.6048 -0.439
LoNM   0.4644  0.5228 -0.2547 -0.3856 -0.512
UpM    0.0214 -0.0268  0.2557 -0.0972 -0.583
LoM   -0.2056 -0.1028  0.0891  0.2632 -0.650
Farm  -0.5320 -0.3026  0.0101  0.2592  2.075
```

Visualizing associations

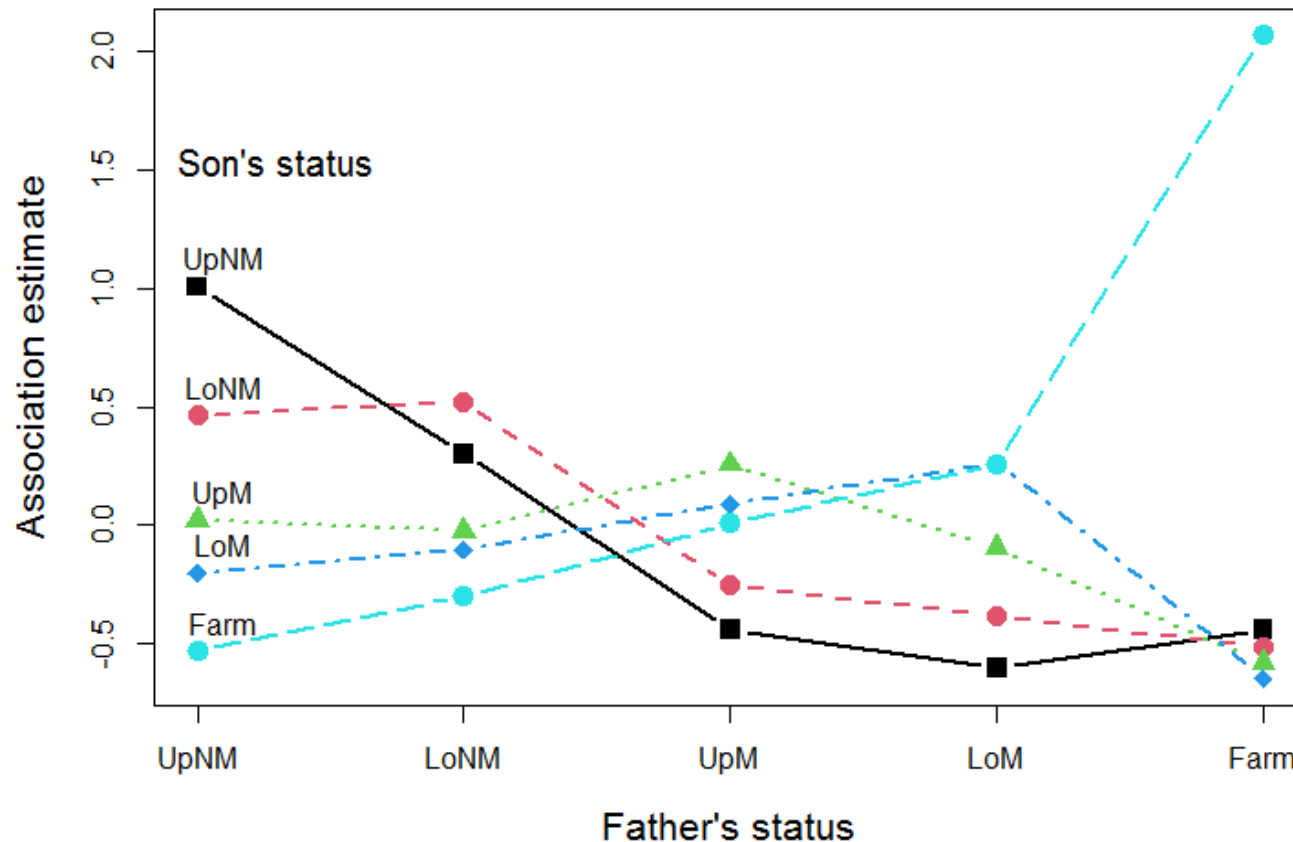
Plot these as shaded squares using `corrplot()`



Visualizing associations

Plot these as a line plot using `matplot()`

```
matplot(t(inter.mat), type="b", pch=15:19, cex=1.5, xaxt="n"  
        xlab="Father's status", ylab="Association estimate" )
```



Summary

- Loglinear models, as originally formulated, were quite general, but treated all table variables as **unordered** factors
 - The GLM perspective is more general, allowing quantitative predictors and handling **ordinal factors**
 - The logit model give a simplified approach when one variable is a **response**
- Models for **ordered factors** give more powerful & focused tests
 - $L \times L$, R, C and R+C models **assign scores** to the factors
 - RC(1) and RC(2) models **estimate** the scores from the data
- Models for **square tables** allow testing structured questions
 - Quasi-independence: ignoring diagonals
 - symmetry & quasi-symmetry
 - theory-specific “topological” models
- These methods can be readily combined to analyze complex tables