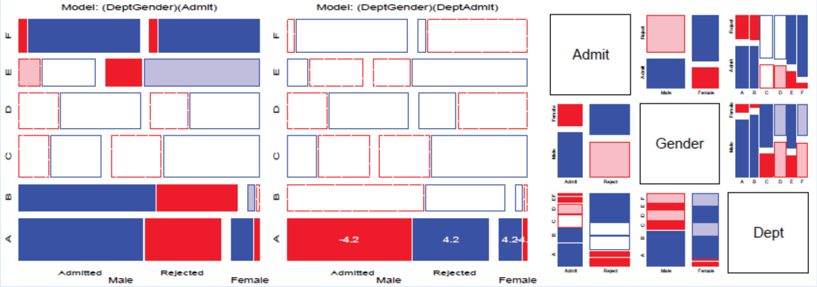


Loglinear models & mosaic displays

Psy 6136 Categorical Data Analysis

Michael Friendly

Psych 6136

http://friendly.github.io/psy6136

Psy 6136 Categorical Data Analysis

Today's topics

- Mosaic displays: basic ideas
- Models for count data
  - Fitting loglinear models
- Two-way tables
- Three-way tables
- Sequential plots & models
- Marginal & partial displays

Mosaic displays

- Similar to sieve plot, tile plot, using area ~ frequency
- Mosaic plots generalize more readily to *n*-way tables (subject to resolution of the display)
- Intimately connected to loglinear & generalized linear models
  - Can fit sequential models as variables are entered
  - Show the pattern of association not accounted for in a given model

Mosaic displays: basic ideas

Mosaic displays theory: Hartigan & Kleiner (1981); Friendly (1994, 1999)

Area proportional display for an n-way table

Tiles: recursive splits of a unit square, alternating H, V

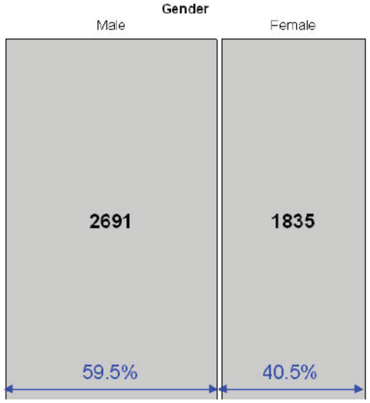
V_1: width ~ marginal frequencies, n_{i++}

V_2: height ~ cond freq: $V_2 | V_1 = n_{ij} / n_{i++}$

V_3: width ~ cond freq: $V_3 | V_1, V_2 = n_{ikj} / n_{ij+}$

→ Area ~ cell frequency, n_{ijk}

UCB Admissions: Gender frequencies



Mosaic displays: basic ideas

Area proportional display for an n-way table

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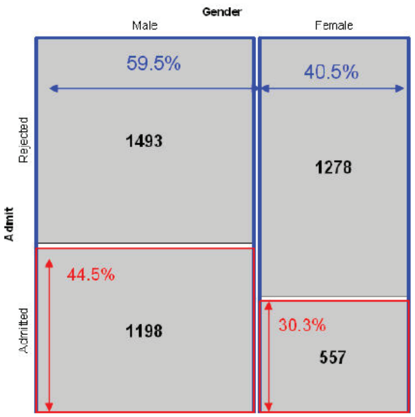
→ Area ~ cell frequency, n_{ijk}

UCB Admissions: Gender x Admit



Mosaic displays: basic ideas

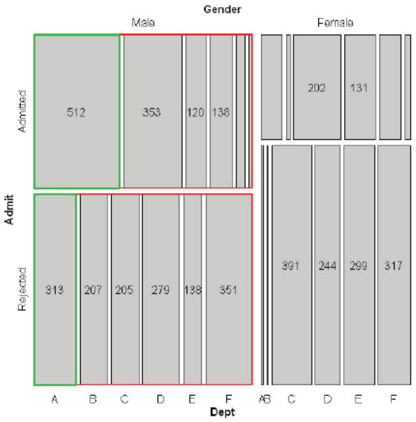
Area proportional display for an n-way table

Tiles: recursive splits of a unit square, alternating H, V

V_1: width ~ marginal frequencies, n_{i++}
V_2: height ~ cond freq: $V_2 | V_1 = n_{ij} / n_{i++}$
V_3: width ~ cond freq: $V_3 | V_1, V_2 = n_{ikj} / n_{ij+}$

→ Area ~ cell frequency, n_{ijk}

Gender x Admit x Dept frequencies



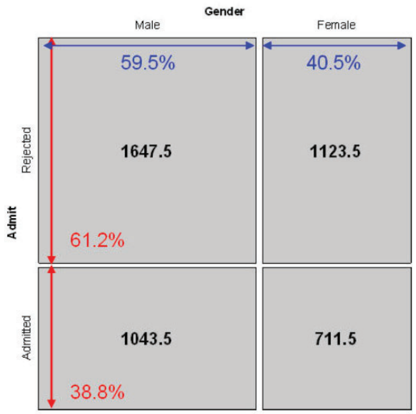
Mosaic displays: Independence

Expected frequencies under independence are products of the row / col margins

$$\widehat{m}_{ij} = \frac{n_{i+} n_{+j}}{n_{++}} = n_{++} \text{row } \% \text{col } \%$$

→ Row and col tiles align when variables are independent

Expected frequencies if Admit ⊥ Gender



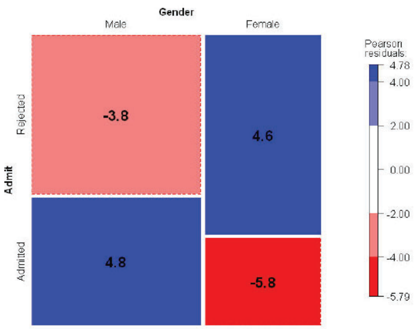
Mosaic displays: Residuals & shading

- Pearson residuals:

$$d_{ij} = \frac{n_{ij} - \widehat{m}_{ij}}{\sqrt{\widehat{m}_{ij}}}$$

- Pearson $\chi^2 = \Sigma\Sigma d_{ij}^2 = \Sigma\Sigma \frac{(n_{ij} - \hat{m}_{ij})^2}{\hat{m}_{ij}}$
- Other residuals: deviance (LR), Freeman-Tukey (FT), adjusted (ADJ), ...
- Shading:
  - Sign: − negative in red; + positive in blue
  - Magnitude: intensity of shading: $|d_{ij}| > 0, 2, 4, \ldots$
- ⇒ Independence: rows align, or cells are empty!

UCB Admissions: ~ Admit + Gender



Loglinear models: Perspectives

Loglinear models grew up and developed from three different ideas and ways of thinking about notions of independence in frequency data

- **Loglinear approach**: analog of ANOVA; associations are interactions
- **glm() approach**: analog of general regression model, for log(Freq), with Poisson distn of errors
- **Logit models**: Loglinear simplified for a binary response

Loglinear approach

First developed as analog of classical ANOVA models, where multiplicative relations are re-expressed in additive form as models for log(Freq)

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

- This expresses the independence model for a 2-way table as no A*B association
- Short-hand notations: [A][B] = A ⊥ B = ~ A + B
- Fit by simple iterative proportional scaling: MASS::loglm()

```
loglm(Freq ~ A + B + C)        # [A][B][C]
loglm(Freq ~ A * B + C )       # [A B][C]
loglm(Freq ~ A * B * C)        # [A B C]
```

glm() approach

Extension of classical linear models recognized loglinear models as a model for log(Freq), with Poisson dist^n for cell counts

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

- Looks like std ANOVA/regression model, but for log(Freq)
- This allows quantitative predictors and special ways to treat ordinal factors
- Fit by maximum likelihood using glm(…, family=poisson)
- Standard diagnostic methods available

```
glm( Freq ~ A + B + C, family = poisson      # [A] [B] [C]
glm( Freq ~ A * B + C, family = poisson)     # [A B] [C]
```

Logit models

When one variable is a binary response, a logit model is a simpler way to specify a loglinear model

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

- $\log(m_{1jk}/m_{2jk})$ is the log odds of response 1 vs 2
- The model only includes terms for the effect of A on B & C
- Equivalent loglinear model: [AB][AC][BC]
- The logit models assumes the [BC] association;

$$[AB] \rightarrow \beta_j^B \quad [AC] \rightarrow \beta_k^C$$

- Fit using family=binomial

```
glm(outcome=="survived" ~ B + C, family = binomial)
```

Two-way tables: loglinear approach

For two discrete variables, A and B, suppose a multinomial sample of total size n over the IJ cells of a two-way $I \times J$ contingency table, with cell frequencies n_{ij}, and cell probabilities $\pi_{ij} = n_{ij}/n$.

- The table variables are statistically independent when the cell (joint) probability equals the product of the marginal probabilities, $\Pr(A = i \,\&\, B = j) = \Pr(A = i) \times \Pr(B = j)$, or,

$$\pi_{ij} = \pi_{i+}\pi_{+j} \ .$$

- An equivalent model in terms of expected frequencies, $m_{ij} = n\pi_{ij}$ is

$$m_{ij} = (1/n)\ m_{i+}\ m_{+j} \ .$$

- This multiplicative model can be expressed in additive form as a model for $\log m_{ij}$,

$$\log m_{ij} = -\log n + \log m_{i+} + \log m_{+j} \ . \qquad (1)$$

Two-way tables: loglinear approach

Independence model

By anology with ANOVA models, the independence model (1) can be expressed as

$$\log m_{ij} = \mu + \lambda_i^A + \lambda_j^B \ , \qquad (2)$$

- μ is the grand mean of $\log m_{ij}$
- the parameters λ_i^A and λ_j^B express the marginal frequencies of variables A and B — "main effects"
- typically defined so that $\sum_i \lambda_i^A = \sum_j \lambda_j^B = 0$ as in ANOVA

Two-way tables: loglinear approach

Saturated model

Dependence between the table variables is expressed by adding association parameters, λ_{ij}^{AB}, giving the *saturated model*,

$$\log m_{ij} = \mu + \lambda_i^A + \lambda_j^B + \lambda_{ij}^{AB} \equiv [AB] \equiv \sim A * B \ . \qquad (3)$$

- The saturated model fits the table perfectly ($\widehat{m}_{ij} = n_{ij}$): there are as many parameters as cell frequencies. Residual df = 0.
- A global test for association tests $H_0 : \boldsymbol{\lambda}_{ij}^{AB} = \mathbf{0}$.

- If reject H_0, which $\lambda_{ij}^{AB} \neq 0$?
- For ordinal variables, the λ_{ij}^{AB} may be structured more simply, giving tests for ordinal association.

Example: Independence

Generate a table of Education by Party preference, strictly independent

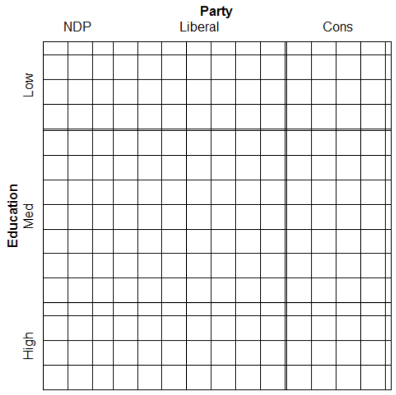
```
> educ <- c(50, 100, 50)                           # marginal frequencies
> names(educ) <- c("Low", "Med", "High")
> party <- c(20, 50, 30)                           # marginal frequencies
> names(party) <- c("NDP", "Liberal", "Cons")
> table <- outer(educ, party) / sum(party)         # cell = row * col / n
> names(dimnames(table)) <- c("Education", "Party")
> table
         Party
Education NDP Liberal Cons
     Low   10      25   15
     Med   20      50   30
     High  10      25   15
```

Perfect fit:

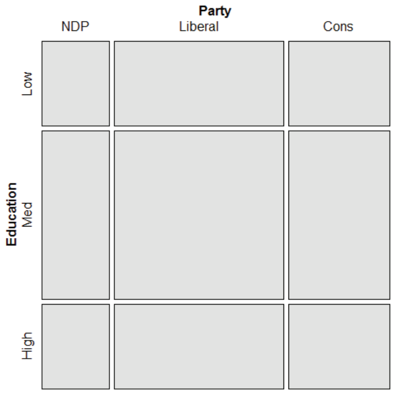
```
> MASS::loglm(~ Education + Party, table)
Call:
MASS::loglm(formula = ~Education + Party, data = table)

Statistics:
                 X^2 df P(> X^2)
Likelihood Ratio   0  4        1
Pearson            0  4        1
```

Both sieve diagrams and mosaic plots show what independence “looks like”

```
> sieve(table, shade=TRUE)
```



```
> mosaic(table, shade=TRUE)
```



Two-way tables: glm approach

In the GLM approach, the vector of cell frequencies, $\boldsymbol{n} = \{n_{ij}\}$ is specified to have a Poisson distribution with means $\boldsymbol{m} = \{m_{ij}\}$ given by

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

- $\boldsymbol{X}$ is a known design (model) matrix, expressing the table factors
- β is a column vector containing the unknown λ parameters.

- This is the same as the familiar matrix formulation of ANOVA/regression, except that
  - The response, $\log \boldsymbol{m}$ makes multiplicative relations additive
  - The distribution is taken as Poisson rather than Gaussian (normal)

Example: 2 x 2 table

For a 2 × 2 table, the saturated model (3) with the usual zero-sum constraints can be represented as

$$\log \begin{pmatrix} m_{11} \\ m_{12} \\ m_{21} \\ m_{22} \end{pmatrix} = \begin{bmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & -1 & -1 \\ 1 & -1 & 1 & -1 \\ 1 & -1 & -1 & 1 \end{bmatrix} \begin{pmatrix} \mu \\ \lambda_1^A \\ \lambda_1^B \\ \lambda_{11}^{AB} \end{pmatrix} \begin{array}{l} \text{total n} \\ \text{margin A} \\ \text{margin B} \\ \text{association} \end{array}$$

- only the linearly independent parameters are represented. $\lambda_2^A = -\lambda_1^A$, because $\lambda_1^A + \lambda_2^A = 0$, and so forth.
- association is represented by the parameter λ_{11}^{AB}
- can show that $\lambda_{11}^{AB} = \frac{1}{4}\log(\theta)$ (log odds ratio)

- Advantages of the GLM formulation: easier to express models with ordinal or quantitative variables, special terms, etc. Can also allow for *over-dispersion*.

Assessing goodness of fit

Goodness of fit of a specified model may be tested by the likelihood ratio G^2,

$$G^2 = 2 \sum_i n_i \log \left(\frac{n_i}{\widehat{m}_i} \right) , \qquad (4)$$

or the Pearson X^2,

$$X^2 = \sum_i \frac{(n_i - \widehat{m}_i)^2}{\widehat{m}_i} , \qquad (5)$$

with degrees of freedom df = # cells - # estimated parameters.

- E.g., for the model of independence, $[A][B]$, df = $IJ - [(I-1) + (J-1)] = (I-1)(J-1)$
- The terms summed in (4) and (5) are the squared *cell residuals*
- Other measures of balance goodness of fit against parsimony, e.g., *Akaike's Information Criterion* (smaller is better)

$$AIC = G^2 - 2df \text{ or } AIC = G^2 + 2 \text{ \# parameters}$$

R functions for loglinear models

- `vcd::assocstats()` – only χ2 tests for two-way tables; not a model (no parameters; no residuals)
- `MASS::loglm()` – general loglinear models for *n*-way tables

  `loglm(formula, data, subset, na.action, …)`
- `glm()` – all generalized linear models; loglinear with family = poisson

  `glm(formula, data, weights, subset, …)`
- Formulas have the form:
  - table form: ~ A + B + … (independence);
  - ~ A * B + C (allow A*B association)
  - frequency data frame: Freq ~ A * B + C

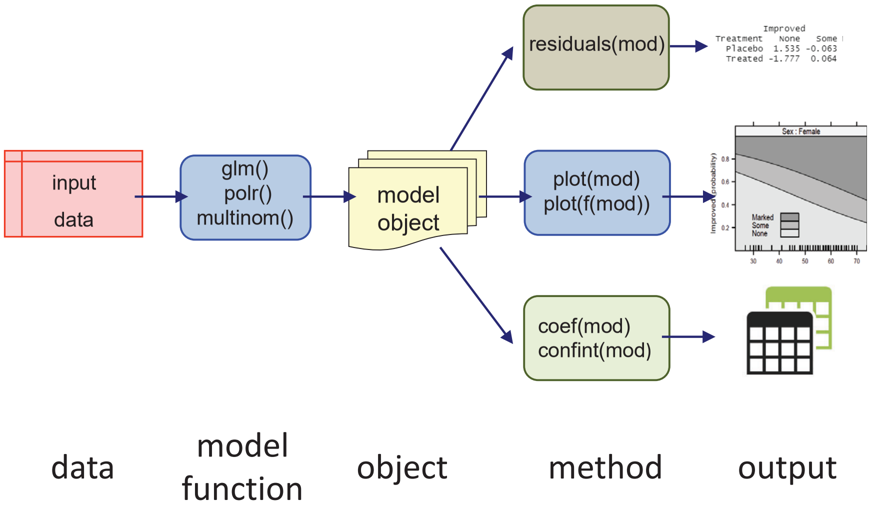
R functions

- `loglm()` and `glm()` return an R object with named components and with a `class()`

```
> arth.mod <- loglm(~Treatment+Improved, data=arth.tab, fitted=TRUE)
> names(arth.mod)
> names(arth.mod)
 [1] "lrt"         "pearson"     "df"          "margin"      "fitted"      "param"
 [7] "call"        "formula"     "frequencies" "deviance"    "nobs"        "terms"

class(arth.mod)
 [1] "loglm"
```

- They have methods: `print()`, `summary`, `coef()`, `residuals()`, `plot()` and other methods
  - Methods are specific to the class of the object
  - E.g., `residuals(arth.mod)` → `residuals.loglm(arth.mod)`

Model-based methods: Fitting & graphing



Example: Arthritis treatment

Data on effects of treatment for rheumatoid arthritis (in case form)

```
> data(Arthritis, package="vcd")
> str(Arthritis)
'data.frame':       84 obs. of  5 variables:
 $ ID       : int  57 46 77 17 36 23 75 39 33 55 ...
 $ Treatment: Factor w/ 2 levels "Placebo","Treated": 2 2 2 2 2 2 2 2 2 2 ...
 $ Sex      : Factor w/ 2 levels "Female","Male": 2 2 2 2 2 2 2 2 2 2 ...
 $ Age      : int  27 29 30 32 46 58 59 59 63 63 ...
 $ Improved : Ord.factor w/ 3 levels "None"<"Some"<..: 2 1 1 3 3 3 1 3 1 1 ...
```

For now, ignore Age; consider the 2 x 3 table of Treatment x Improved

```
> arth.tab <- with(Arthritis, table(Treatment, Improved))
> arth.tab
         Improved
Treatment None Some Marked
  Placebo   29    7      7
  Treated   13    7     21
```

Arthritis treatment

Fit the independence model, ~ `Treatment + Improved`

```
> (arth.mod <- loglm(~Treatment + Improved, data = arth.tab, fitted=TRUE))
Call:
loglm(formula = ~Treatment + Improved, data = arth.tab, fitted = TRUE)

Statistics:
                  X^2 df P(> X^2)
Likelihood Ratio 13.53  2 0.001154
Pearson          13.06  2 0.001463
```

Some methods:

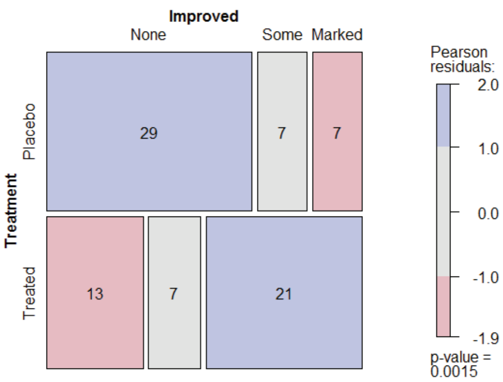
```
> round(residuals(arth.mod), 3)
         Improved
Treatment   None   Some Marked
  Placebo  1.535 -0.063 -2.152
  Treated -1.777  0.064  1.837

# Likelihood ratio chisquare
> deviance(arth.mod)
[1] 13.53
```

```
> coef(arth.mod)
$`(Intercept)`
[1] 2.543

$Treatment
 Placebo  Treated
 0.02381 -0.02381

$Improved
    None     Some   Marked
 0.50136 -0.59725  0.09589
```

Arthritis treatment: Plots

Visualization: `mosaic()` or `plot()` the model *or* table

```
> mosaic(arth.mod, shade=TRUE, gp_args=list(interpolate=1:4),
                  labeling = labeling_values)
```



Splits by the response, `Treatment` first

Custom scheme for shading levels; normally c(2, 4) for |residual|

Cells can be labeled by freq, residual, …

Arthritis treatment: glm()

glm() for loglinear models easiest with the data as a data.frame in frequency form

```
> arth.df <- as.data.frame(xtabs(~ Treatment + Improved,
                                   data=Arthritis))
> arth.df
  Treatment Improved Freq
1   Placebo     None   29
2   Treated     None   13
3   Placebo     Some    7
4   Treated     Some    7
5   Placebo   Marked    7
6   Treated   Marked   21
```

```
> arth.glm <- glm(Freq ~ Treatment + Improved, data = arth.df,
                  family = poisson)
```

More on `glm()` models later

Example: Hair color & Eye color

```
> haireye <- margin.table(HairEyeColor, 1:2)
> (HE.mod <- loglm(~ Hair + Eye, data=haireye))
Call:
loglm(formula = ~Hair + Eye, data = haireye)

Statistics:
                   X^2 df P(> X^2)
Likelihood Ratio 146.4  9        0
Pearson          138.3  9        0

> round(residuals(HE.mod), 2)
Re-fitting to get frequencies and fitted values
       Eye
Hair    Brown  Blue Hazel Green
  Black  4.00 -3.39 -0.49 -2.21
  Brown  1.21 -2.02  1.31 -0.35
  Red   -0.08 -1.85  0.82  2.04
  Blond -7.33  6.17 -2.47  0.60
```

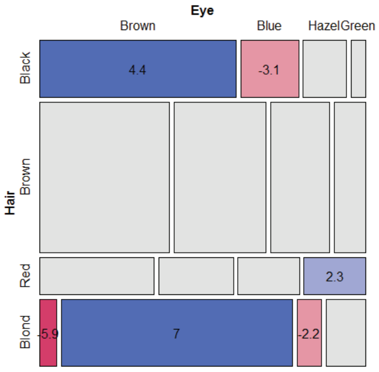
Mosaic displays: Seeing patterns

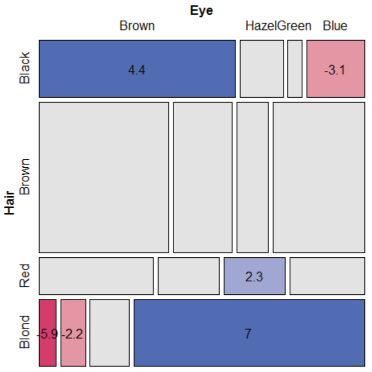
- In two-way models, residuals contain the info on lack of independence
  - Equivalently: help to understand the pattern of association
  - Effect ordering: permuting the rows / cols often makes the pattern more apparent
- Correspondence analysis: → reorder by scores on Dim 1
  - seriation::permute(order="CA") does this for two-way tables

```
> haireye
       Eye
Hair    Brown Blue Hazel Green
  Black    68   20    15     5
  Brown   119   84    54    29
  Red      26   17    14    14
  Blond     7   94    10    16
```

```
> library(seriation)
> permute(haireye, "CA")
       Eye
Hair    Brown Hazel Green Blue
  Black    68    15     5   20
  Brown   119    54    29   84
  Red      26    14    14   17
  Blond     7    10    16   94
```

```
mosaic(haireye,              shade=TRUE, labeling=labeling_residuals)
mosaic(permute(haireye, "CA"), shade=TRUE, labeling=labeling_residuals)
```





Bee abundance data

A study by Taylor Kerekes examined the abundance of bee species in Ontario over three periods of time.

Q: Does relative abundance of species differ over years?

A: Do a chi-square test

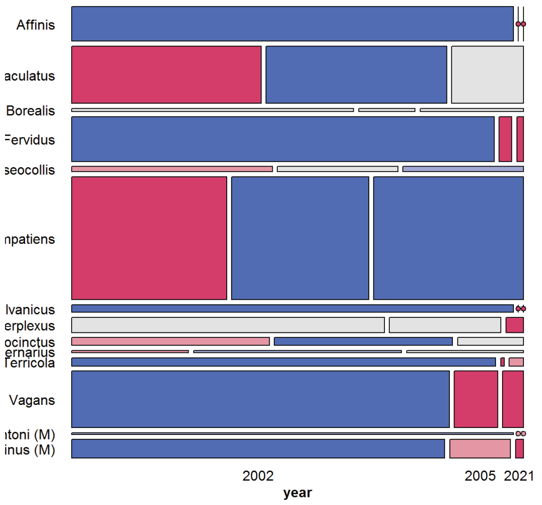
```
chisq.test(bees[,-1])
Pearson's Chi-squared test

data:  bees[, -1]
X-squared = 1981, df = 26, p-value <2e-16
```

```
# A tibble: 14 x 4
   species         `2002` `2005` `2021`
   <chr>            <dbl>  <dbl>  <dbl>
 1 Affinis            508      0      0
 2 Bimaculatus        362    345    137
 3 Borealis            30      6     11
 4 Fervidus           634     19     10
 5 Griseocollis        35     21     21
 6 Impatiens          638    564    616
 7 Pensylvanicus      112      0      0
 8 Perplexus          160     57      9
 9 Rufocinctus         51     46     17
10 Ternarius            9     16      9
11 Terricola          119      1      4
12 Vagans             713     82     39
13 Ashtoni  (M)        27      0      0
14 Citrinus  (M)      234     38      5
```

How to understand the pattern of association?

mosaic(bees.mat, shade=TRUE, …)

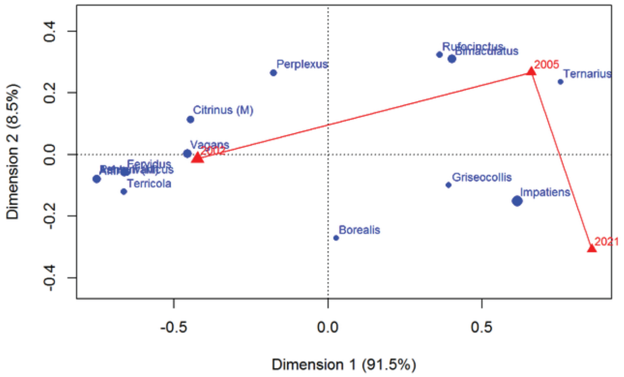
Bees Abundance Data



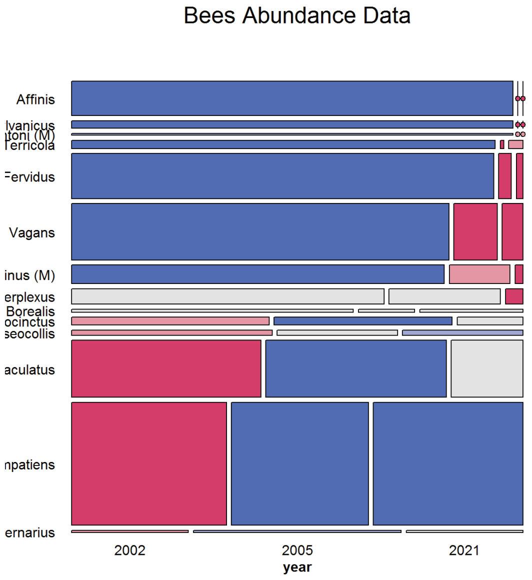
Alphabetic order of species:
No clear pattern

Correspondence analysis finds scores for the row & col categories to account for maximum χ^2

```
bees.ca <- ca(bees.mat)
plot(bees.ca,
     lines=c(FALSE,TRUE),     # join years with lines
     mass = c(TRUE, TRUE))    # symbol size ~ marginal frequency
```



mosaic(permute(bees.mat, “CA”), shade=TRUE, …)



Three-way tables

Saturated model

For a 3-way table, of size $I \times J \times K$ for variables A, B, C, the saturated loglinear model includes associations between all pairs of variables, as well as a 3-way association term, λ_{ijk}^{ABC}

$$\log m_{ijk} = \mu + \boxed{\lambda_i^A + \lambda_j^B + \lambda_k^C} + \boxed{\lambda_{ij}^{AB} + \lambda_{ik}^{AC} + \lambda_{jk}^{BC}} + \boxed{\lambda_{ijk}^{ABC}} . \quad (6)$$

- One-way terms ($\lambda_i^A, \lambda_j^B, \lambda_k^C$): differences in the *marginal frequencies* of the table variables.
- Two-way terms ($\lambda_{ij}^{AB}, \lambda_{ik}^{AC}, \lambda_{jk}^{BC}$) pertain to the *partial association* for each pair of variables, *controlling* for the remaining variable.

- The three-way term, λ_{ijk}^{ABC} allows the partial association between any pair of variables to vary over the categories of the third variable.
- Fits perfectly, but doesn't *explain* anything, so we hope for a simpler model!

Reduced models

- Goal: fit the smallest model sufficient to explain/describe the observed frequencies
  - Similar to Anova models, ~(A + B + C)^3 with all interactions
- Hierarchical models
  - A high-order term, like $\lambda_{ijk}{}^{ABC}$ → all lower order terms included
  - E.g. [ABC] → A + B + C + AB + AC + BC
  - [AB][AC] → A + B + C + AB + AC
- Thus, a shorthand notation for a loglinear model lists only the high-order terms

Reduced models

- For a three-way table there is a range of models between mutual independence, [A][B][C], and the saturated model, [ABC]
- Each model has an independence interpretation:

  [A][B] ≡ A ⊥ B ≡ A independent of B
- Special names for various submodels

Table: Log-linear Models for Three-Way Tables

Model	Model symbol	Interpretation
Mutual independence	$[A][B][C]$	$A \perp B \perp C$
Joint independence	$[AB][C]$	$(A\, B) \perp C$
Conditional independence	$[AC][BC]$	$(A \perp B) \mid C$
All two-way associations	$[AB][AC][BC]$	homogeneous assoc.
Saturated model	$[ABC]$	ABC interaction

Model types

- **Joint independence**: $(AB) \perp C$, allows A*B association, but asserts no A*C and B*C associations

$$[AB][C] \equiv \log\, m_{ijk} = \mu + \lambda_i^A + \lambda_j^B + \lambda_k^C + \lambda_{ij}^{AB}$$

- **Conditional independence**: $A \perp B$, controlling for C

$$[AC][BC] \equiv \log\, m_{ijk} = \mu + \lambda_i^A + \lambda_j^B + \lambda_k^C + \lambda_{ik}^{AC} + \lambda_{jk}^{BC}$$

- **Homogeneous association**: All two-way, but each two-way is the *same* over the other factor

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

Model types: loglm()

Each of these have simple translations into the model formulae for loglm()

```
loglm(~ A + B + C)        # mutual independence      [A][B][C]
loglm(~ A * B + C)        # joint independence       [AB][C]
loglm(~ A*C + B*C)        # conditional independence [AC][BC]
loglm(~ (A + B + C)^2)    # homogeneous, all 2-way   [AB][AC][BC]
loglm(~ A * B * C)        # saturated model          [ABC]
```

Collapsibility: Marginal & conditional associations

- Q: When can we legitimately collapse a table, ABC over some variable (C)?
- A: When the marginal association of AB is the same as the conditional association, AB | C
- Recall the Berkeley data
  - Margin of Admit, Gender ignoring Dept showed strong association
  - The partial assoc. within Dept were mostly NS
  - This is an example of Simpson's paradox
- Three-way tables: The AB marginal and AB | C conditional associations are the same, if either:
  - A & C are conditionally independent, A ⊥ C| B = [AB][CB]
  - B & C are conditionally independent, B ⊥ C | A = [AB][AC]
  - → no three-way association

Response vs. Association models

- In association models, the interest is just on *which* variabels are associated, and *how*
  - Hair-eye data: [Hair Eye]? [Hair Sex]? [Eye Sex]
  - ⟹ fit the homogeneous association model (or the saturated model)
  - Test the individual terms, delete those which are NS
- In response models, the interest is on which predictors are associated with the response
  - The minimal (null or baseline) model is the model of joint independence of the response (say, A) from all predictors, [A] [B C D . . .]
  - Associations among the predictors are fitted exactly (not analyzed)
  - Similar to regression, where predictors can be arbitrarily correlated
  - e.g., Berkeley data: fit the baseline model [Admit] [Gender Dept]
  - lack-of-fit ⟹ associations [Admit Gender] and/or [Admit Dept]

Goodness of fit tests

As noted earlier, overall goodness of fit of a specified model may be tested by the likelihood ratio G^2, or the Pearson X^2,

$$G^2 = 2 \sum_i n_i \log \left(\frac{n_i}{\widehat{m}_i} \right) \qquad X^2 = \sum_i \frac{(n_i - \widehat{m}_i)^2}{\widehat{m}_i} ,$$

with residual degrees of freedom ν = # cells − # estimated parameters.

- These measure the lack of fit of a given model— a large value ⟹ a poor model
- Both are distributed as $\chi^2(\nu)$ (in large samples: all $\widehat{m}_i > 5$)
- $\mathcal{E}(\chi^2(\nu)) = \nu$, so G^2/ν (or X^2/ν) measures lack of fit per degree of freedom (overdispersion)
- But: how to compare or test competing models?

Nested models & ANOVA-type tests

Two models, M_1 and M_2 are nested when one (say, M_2) is a special case of the other

- Model M_2 (w/ ν_2 df) fits a subset of the parameters of M1 (w/ ν_1 df)
- M_2 is more restrictive – cannot fit better than M_1: $G^2(M_2) \geq G^2(M_1)$
- The least restrictive model is the saturated model [ABC …], w/ $G^2 = 0$

Therefore, we can test the difference in G^2 as a specific test of the added restrictions in M_2 compared to M_1.

- This test has a χ^2 distribution with df = ν_2 - ν_1

$$\begin{aligned} \Delta G^2 \equiv G^2(M_2 \mid M_1) &= G^2(M_2) - G^2(M_1) \qquad (7) \\ &= 2 \sum n_i \log(\widehat{m}_{i1} / \widehat{m}_{i2}) \end{aligned}$$

Example: Berkeley admissions

For the UC Berkeley data, with table variables [A]dmit, [D]ept and [G]ender the following models form a nested chain

$$[A][D][G] \subset [A][DG] \subset [AD][AG][DG] \subset [ADG]$$

Table: Hierarchical G^2 tests for loglinear models fit to the UC Berkeley data

Type	LLM terms	G^2	df	$\Delta(G^2)$	$\Delta(df)$	$Pr(> \Delta(G^2))$
Mutual ind	[A][D][G]	2097.67	16			
Joint	[A][DG]	877.06	11	1220.62	5	0.0000
All 2-way	[AD][AG][DG]	20.20	5	1128.70	5	0.0000
Saturated	[ADG]	0.0	0	20.20	5	0.0011

- Only testing the decrease in G2 from one model to the next
- Here, each model is significantly better than the previous
- Joint vs. all two-way: Does Admit depend on Dept and/or Gender?
- Absolut fit of all 2-way model is not terrible. Investigate this further!

Fitting these in R

`loglm()` - data in contingency table form (MASS package)

```
data(UCBAdmissions)
  ## conditional independence (AD, DG) in Berkeley data
mod.1 <- loglm(~ (Admit + Gender) * Dept, data=UCBAdmissions)
  ## all two-way model (AD, DG, AG)
mod.2 <- loglm(~ (Admit + Gender + Dept)^2, data=UCBAdmissions)
```

`glm()` - data in frequency form

```
berkeley <- as.data.frame(UCBAdmissions)
mod.3 <- glm(Freq ~ (Admit + Gender) * Dept, data=berkeley,
                family='poisson')
```

- `loglm()` simpler for nominal variables
- `glm()` allows a wider class of models and quantitative predictors (covariates)
- `gnm()` fits models for structured association and generalized *non-linear* models
- vcdExtra package provides visualizations for all.

Example: Berkeley admissions

Fit the model of mutual independence, using loglm()

```
> berk.loglm0 <- loglm(~ Admit + Dept + Gender, data=UCBAdmissions)
> berk.loglm0
Call:
loglm(formula = ~Admit + Dept + Gender, data = UCBAdmissions)

Statistics:
                    X^2 df P(> X^2)
Likelihood Ratio 2097.7 16        0
Pearson          2000.3 16        0
```

Conditional independence [AD] [AG]

```
> berk.loglm1 <- loglm(~ Admit * (Dept + Gender), data=UCBAdmissions)
> berk.loglm1
Call:
loglm(formula = ~Admit * (Dept + Gender), data = UCBAdmissions)

Statistics:
                    X^2 df P(> X^2)
Likelihood Ratio 1148.9 10        0
Pearson          1015.7 10        0
```

Conditional independence, [AD] [AG]

```
> berk.loglm2 <- loglm(~ Admit + (Dept * Gender), data=UCBAdmissions)
> berk.loglm2
Call:
loglm(formula = ~Admit + (Dept * Gender), data = UCBAdmissions)

Statistics:
                    X^2 df P(> X^2)
Likelihood Ratio 877.06 11        0
Pearson          797.70 11        0
```

All two-way model, [AD] [AG] [DG]

```
> berk.loglm3 <-loglm(~(Admit+Dept+Gender)^2, data=UCBAdmissions)
> berk.loglm3
Call:
loglm(formula = ~(Admit + Dept + Gender)^2, data = UCBAdmissions)

Statistics:
                    X^2 df   P(> X^2)
Likelihood Ratio 20.204  5 0.0011441
Pearson          18.823  5 0.0020740
```

ANOVA tests

These are nested. Compare with `anova()`

```
> aov1 <- anova(berk.loglm0, berk.loglm1, berk.loglm3, test="Chisq")
> aov1
LR tests for hierarchical log-linear models

Model 1:
 ~Admit + Dept + Gender
Model 2:
 ~Admit * (Dept + Gender)
Model 3:
 ~(Admit + Dept + Gender)^2

          Deviance df Delta(Dev) Delta(df) P(> Delta(Dev)
Model 1   2097.671 16
Model 2   1148.901 10    948.770         6        0.00000
Model 3     20.204  5   1128.697         5        0.00000
Saturated    0.000  0     20.204         5        0.00114
```

These are tests of relative fit, $\Delta G^2 = G^2 (M_i \mid M_{i-1})$

LRstats

`vcdExtra::LRstats()` gives one-line summaries of a collection of models
These are tests of absolute goodness of fit

```
> LRstats(berk.loglm0, berk.loglm1, berk.loglm2, berk.loglm3)
Likelihood summary table:
             AIC  BIC LR Chisq Df Pr(>Chisq)
berk.loglm0 2273 2282     2098 16     <2e-16 ***
berk.loglm1 1336 1352     1149 10     <2e-16 ***
berk.loglm2 1062 1077      877 11     <2e-16 ***
berk.loglm3  217  240       20  5     0.0011 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

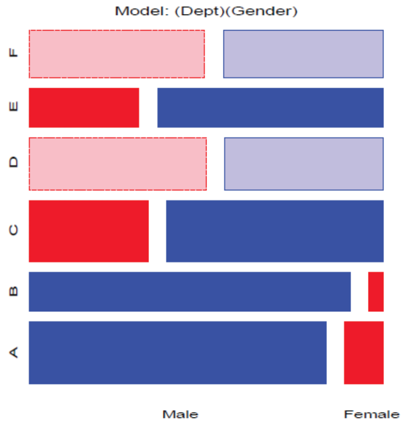
- AIC and BIC are GOF measures adjusted for model parsimony
- Not not significance tests, but smaller is better
- Also apply to non-nested models

$$
\begin{aligned}
AIC &= G^2 + 2 \times \#\text{ parameters} \\
BIC &= G^2 + 2\log(n) \times \#\text{ parameters}
\end{aligned}
$$

Mosaic displays: Predictor variables

Berkeley data: Departments × Gender (ignoring Admit):

- Did departments differ in the total number of applicants?
- Did men and women apply differentially to departments?



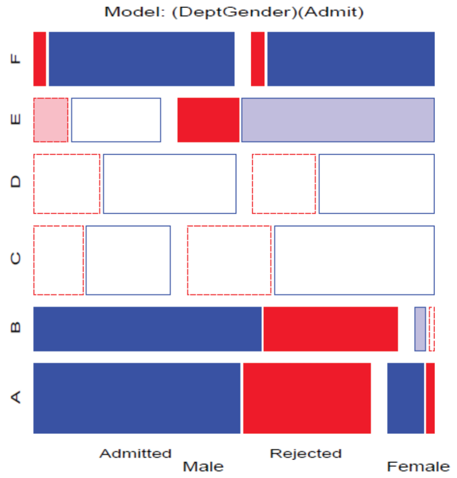
In response models, the mosaic of the predictors gives a graphic summary of background variables

- Model [Dept] [Gender]: $G^2_{(5)} =$ 1220.6.
- *Note*: Departments ordered A–F by overall rate of admission.
- Men more likely to apply to departments A,B; women more likely in depts C–F

Mosaic displays: Visual fitting

- Each mosaic shows:
  - The DATA – size of tiles
  - (some) marginal frequencies – initial splits (visual grouping)
  - RESIDUALS (shading) – what associations have been omitted?
- Visual fitting
  - Start with a simple model: mutual independence or joint independence for response models
  - Pattern of residuals: suggest a better model → smaller residuals
  - Add terms: → smaller residuals, less shading: "cleaning the mosaic"
  - Good fitting model will have mostly unshaded tiles

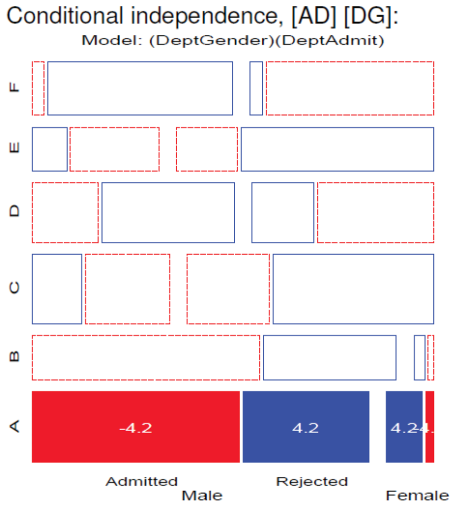
For the Berkeley data, start with the model of joint independence, [A][DG]
Fits badly: $G^2_{(11)} = 877.1$



This is the null, or baseline model when Admit is the response variable.

Allows assoc. of [Dept Gender], not shown in shading

Remaining shading suggests:
[AD] : Admit varies w/ Dept
[AG] : Admit varies w/ Gender

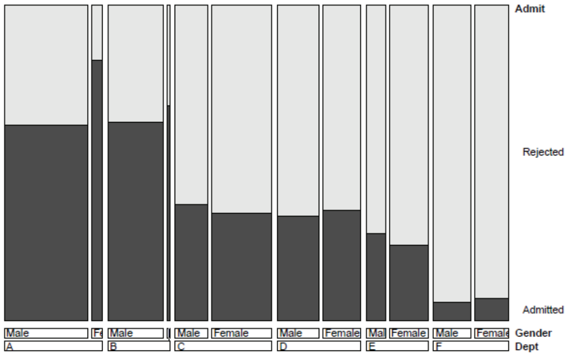


- E.g., Add [Admit Dept] association → Conditional independence:
  - Fits poorly: ($G^2_{(6)}$ = 21.74)
  - But, only in Department A!
- GLM approach allows fitting a special term for Dept. A
- Note: These displays use *standardized residuals*: better statistical properties.

Double decker plots

Visualize dependence of one response variable (typically binary) on combinations of predictors
Formally: mosaic plots with vertical splits for all predictors, highlighting the response by shading

```
doubledecker(Admit ~ Dept + Gender, data = UCBAdmissions[2:1, ,])
```



An exploratory plot

Highlights the M-F diff^{ce} in Admit for Dept A

DDAR Fig 5.34, p 211

Survival on the *Titanic*

4-way tables: Survival on the *Titanic*

Data on the fate of passengers & crew on the HMS Titanic: a 4 × 2 × 2 × 2 table

```
> data(Titanic, package="datasets")
> str(Titanic)
 'table' num [1:4, 1:2, 1:2, 1:2] 0 0 35 0 0 0 17 0 118 154 ...
 - attr(*, "dimnames")=List of 4
  ..$ Class   : chr [1:4] "1st" "2nd" "3rd" "Crew"
  ..$ Sex     : chr [1:2] "Male" "Female"
  ..$ Age     : chr [1:2] "Child" "Adult"
  ..$ Survived: chr [1:2] "No" "Yes"
```

What proportion survived? Ans: 711/2201 = 32.3%

```
> addmargins(margin.table(Titanic, 4))
Survived
  No  Yes  Sum
1490  711 2201
> margin.table(Titanic, 4) / sum(Titanic)
Survived
   No   Yes
0.677 0.323
```

Zero cells

```
> structable(Titanic)
            Sex      Male      Female
            Survived   No Yes    No Yes
Class Age
1st   Child             0   5     0   1
      Adult           118  57     4 140
2nd   Child             0  11     0  13
      Adult           154  14    13  80
3rd   Child            35  13    17  14
      Adult           387  75    89  76
Crew  Child             0   0     0   0
      Adult           670 192     3  20
```

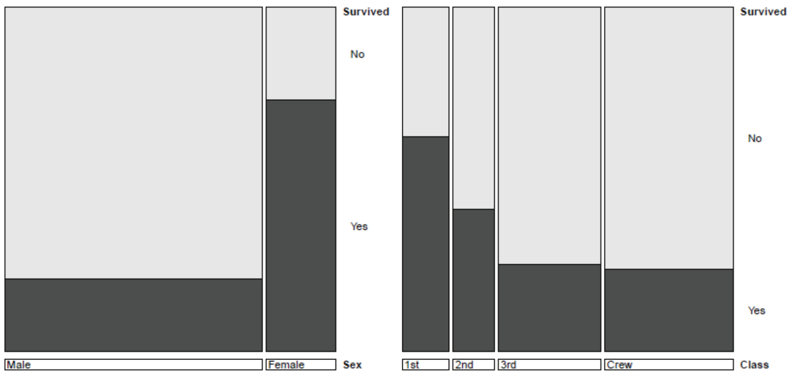
Two types of zero cells:

- Structural zeros: could not occur (children in crew)
- Sampling zeros: did not happen to occur (children in 1st & 2nd who died)
- Beware: zeros can cause problems:
  - Loss of df
  - 0/0 → NaN in $\chi 2$ tests

Exploratory plots

One-way doubledecker plots against survival show what might be expected:

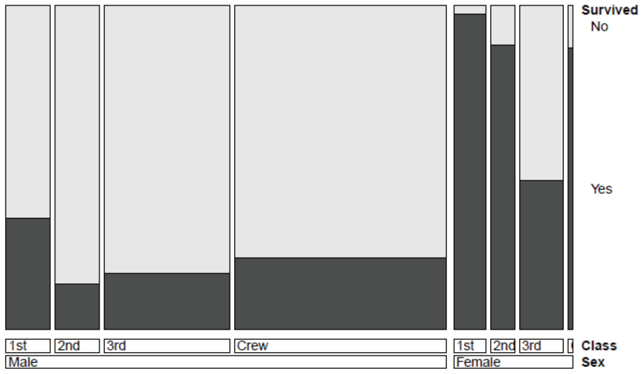
```
doubledecker(Survived ~ Sex, data=Titanic)
doubledecker(Survived ~ Class, data=Titanic)
```



Exploratory plots

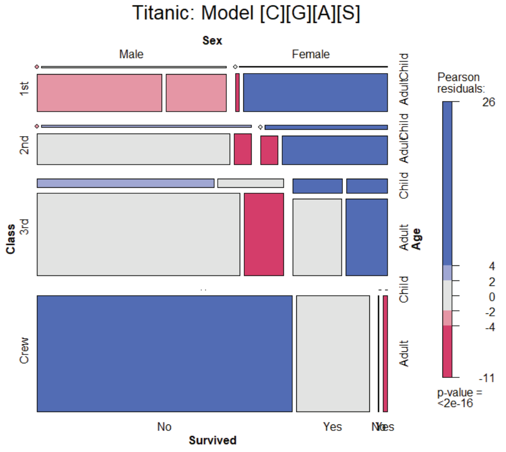
Two-way doubledecker plot against survival shows different effects of `Class` for men and women:

```
doubledecker(Survived ~ Sex + Class, data=Titanic)
```



Fitting & visualizing models

```
mod0 <- loglm(~ 1 + 2 + 3 + 4, data=Titanic)
mosaic(mod0, main="Titanic: Model [C][G][A][S]")
```



In the model formulas, I'm using variable numbers 1-4 for Class, Gender, Age and Survived

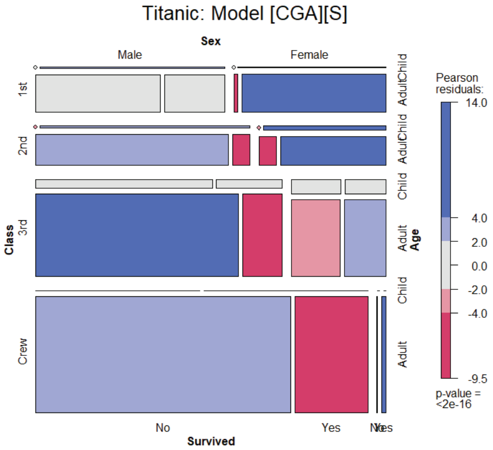
The independence model serves only as a background for the total associations in the table

Let's clean this mosaic!!

Note the scale of residuals: +26 -- -11

Baseline model for Survived

```
mod1 <- loglm(~ 1*2*3 + 4, data=Titanic)
mosaic(mod1, main="Titanic: Model [CGA][S]")
```



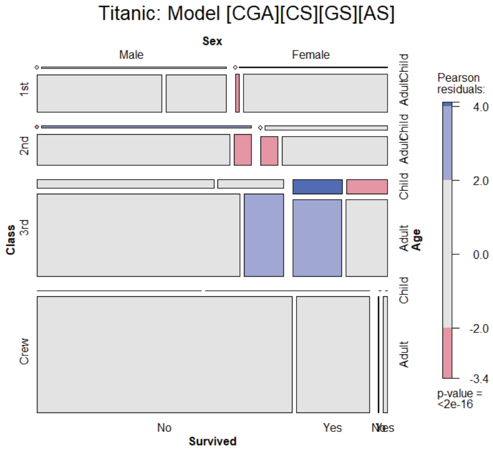
With *S* as response, the baseline model includes all association s among [CGA]

But this model asserts survival is independent of all of these

G^2 (15) = 671.96, a very poor fit

Adding associations: Main effects

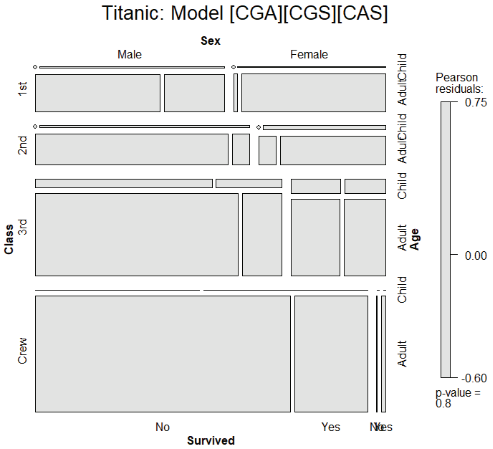
```
mod2 <- loglm(~ 1*2*3 + (1+2+3)*4, data=Titanic)
mosaic(mod2, main="Titanic: Model [CGA][CS][GS][AS]")
```



- This model allows associations of each of C, G, A with Survived
- $G^2(10) = 112.57$, still not good
- Pattern of residuals suggests 2-way interactions (3-way terms):
- "Women & children first": suggests a term [GAS]
- Allow interactions of Class with Gender [CGS] and Class with Age [CAS]

Final model

```
mod3 <- loglm(~ 1*2*3 + (1*2)*4 + (1*3)*4, data=Titanic)
mosaic(mod3, main="Titanic: Model [CGA][CGS][CAS]")
```



Nice & clean!

$G^2(4) = 1.69, p=0.79$

Comparing models

As usual, **anova()** give compact relative comparisons of a set of nested models

```
> anova(mod0, mod1, mod2, mod3)
LR tests for hierarchical log-linear models

Model 1:
 ~1 + 2 + 3 + 4
Model 2:
 ~1 * 2 * 3 + 4
Model 3:
 ~1 * 2 * 3 + (1 + 2 + 3) * 4
Model 4:
 ~1 * 2 * 3 + (1 * 2) * 4 + (1 * 3) * 4

          Deviance df Delta(Dev) Delta(df) P(> Delta(Dev)
Model 1    1243.66 25
Model 2     671.96 15     571.70        10          0.000
Model 3     112.57 10     559.40         5          0.000
Model 4       1.69  4     110.88         6          0.000
Saturated     0.00  0       1.69         4          0.793
```

Comparing models

LRstats() gives absolute GOF tests; also provides AIC, BIC stats: model parsimony

```
> LRstats(mod0, mod1, mod2, mod3)
Likelihood summary table:
      AIC  BIC LR Chisq Df Pr(>Chisq)
mod0 1385 1395     1244 25     <2e-16 ***
mod1  833  858      672 15     <2e-16 ***
mod2  284  316      113 10     <2e-16 ***
mod3  185  226        2  4       0.79
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

mod3 [CGA] [CGS] [CAS] wins!

- Acceptable G^2
- Looks best by AIC & BIC

Model interpretation

Recall that the goal of analysis is to tell a story

- Greatest impact: lower class → decreased survival, regardless of Gender & Age
- Differences in survival by Class were moderated by both Gender & Age
  - Term [CGS]: Women in 3rd class did not have an advantage, while men in 1st class did vs. other classes
  - Term [CAS]: No children in 1st or 2nd class died, but nearly 2/3 in 3rd class did
- Summary:
  - Not so much "women & children first", rather
  - Women & children, ordered by class, and 1st class men!

Sequential plots & models

- Mosaic for an n-way table → hierarchical decomposition of association
- Joint cell probabilities are decomposed as:

$$p_{ijk\ell\cdots} = \underbrace{\overbrace{p_i \times p_{j|i}}^{\{v_1 v_2\}} \times p_{k|ij}}_{\{v_1 v_2 v_3\}} \times p_{\ell|ijk} \times \cdots \times p_{n|ijk\cdots}$$

  - First 2 terms: → mosaic for v_1, v_2
  - First 3 terms: → mosaic for v_1, v_2, v_3
  - … and so on
- Roughly analogous to sequential fitting in regression: X_1 ; $X_2|X_1$; $X_3|X_1,X_2$
- Order of variables matters for interpretation
  - Mosaics: 1st split: easiest to see the marginal proportions
  - Mosaics: 2nd variable seen as conditional proportions, given the 1st

Sequential plots & models

- Sequential models of joint independence
  - Give an additive decomposition of total association – mutual independence $[v_1][v_2]$ … $[v_p]$

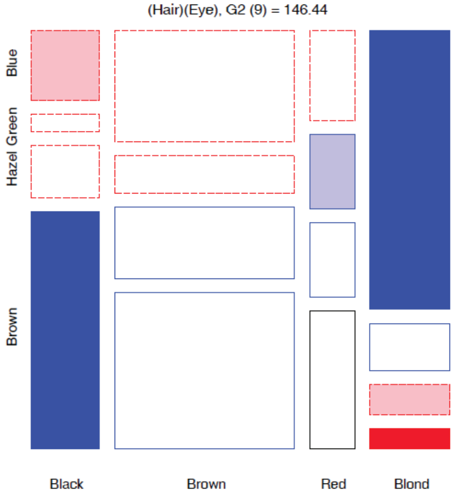
$$G^2_{[v_1][v_2]\ldots[v_p]} = G^2_{[v_1][v_2]} + G^2_{[v_1 v_2][v_3]} + G^2_{[v_1 v_2 v_3][v_4]} + \cdots + G^2_{[v_1 \ldots v_{p-1}][v_p]}$$

- E.g., for Hair Eye color data

Model	Model symbol	df	G^2
Marginal	[Hair] [Eye]	9	146.44
Joint	[Hair, Eye] [Sex]	15	19.86
Mutual	[Hair] [Eye] [Sex]	24	166.30

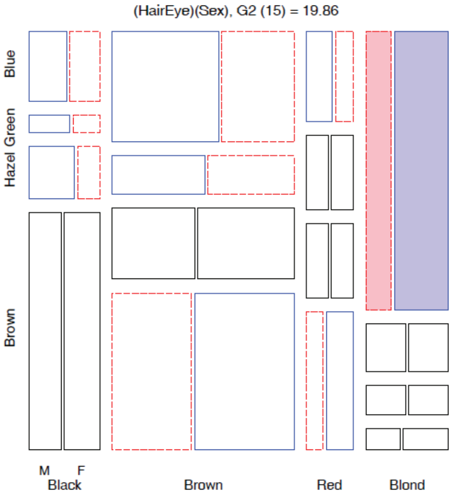
Sequential plots & models

Hair color × Eye color marginal table (ignoring Sex)



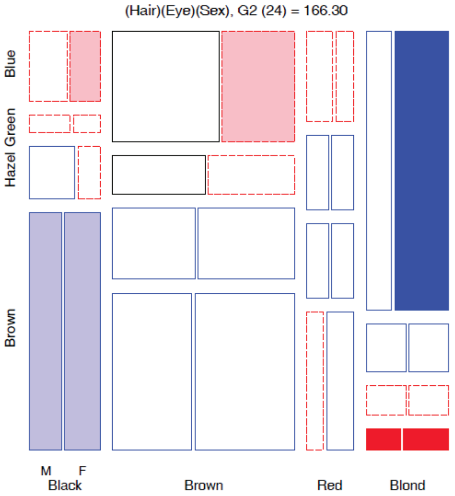
Sequential plots & models

3-way table, Joint independence model [Hair Eye][Sex]



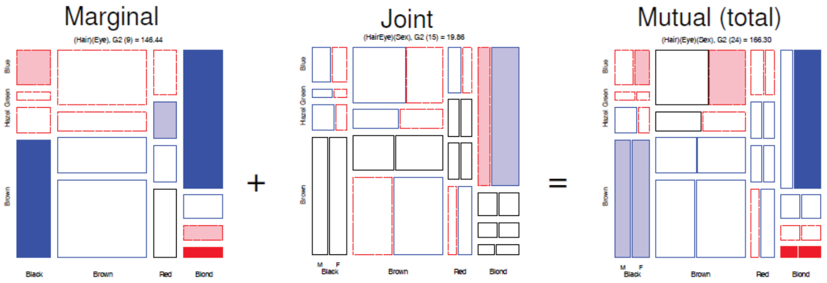
Sequential plots & models

3-way table, Mutual independence [Hair] [Eye][Sex]



Sequential plots & models

Putting these together:



[Hair] [Eye] $G^2_{(9)} = 146.44$

[Hair Eye] [Sex] $G^2_{(15)} = 19.86$

[Hair] [Eye] [Sex] $G^2_{(24)} = 166.30$

Sequential models: Applications

Response models

- When one variable, R, is a response and $E_1, E_2, \ldots$ are explantory, the baseline model is the model of joint independence, $[E_1, E_2, \ldots][R]$
- Sequential mosaics then show the associations among the predictors
- The last mosaic shows all associations with R
- Better-fitting models will need to add associations of the form $[E_i R], [E_i E_j R] \ldots$

Causal models

- Sometimes there is an assumed causal ordering of variables:

$$A \rightarrow B \rightarrow C \rightarrow D$$

- Each path of arrows: $A \rightarrow B$, $A \rightarrow B \rightarrow C$ is a sequential model of joint independence: [A][B], [AB] [C], [ABC] [D].
- Testing these decomposes all joint probabilities

Example: Marital status, pre- & extra-marital sex

Thornes and Collard (1979) studied divorce patterns in relation to premarital and extramarital sex, a 2^4 table, **PreSex** in vcd (G × P × E × M)

```
> data("PreSex", package="vcd")
> structable(Gender + PremaritalSex + ExtramaritalSex ~
             MaritalStatus, data = PreSex)

               Gender           Women              Men
               PremaritalSex      Yes      No      Yes      No
               ExtramaritalSex    Yes  No Yes  No Yes  No Yes  No
MaritalStatus
Divorced                           17  54  36 214  28  60  17  68
Married                             4  25   4 322  11  42   4 130
```

Submodels:

- ❖ [G][P] : Do men & women differ by pre-marital sex?
- ❖ [GP][E]: Given G & P, are there differences in extra-marital sex?
- ❖ [GPE][M]: Are there differences in divorce among the G, P, E groups?

Example: Marital status, pre- & extra-marital sex

Order the table variables as G → P → E → M

```
> names(dimnames(PreSex))        # table variable names
[1] "MaritalStatus"   "ExtramaritalSex" "PremaritalSex"   "Gender"

> PreSex <- aperm(PreSex, 4:1)   # order variables G, P, E, M
```

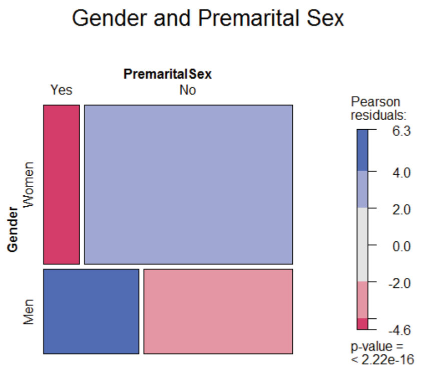
Fit each sequential model to the marginal sub-table. `vcdExtra::seq_loglm()` generates these models of joint independence

```
PreSex.mods <- seq_loglm(PreSex,
                   type="joint",
                   marginals = 2:4)
LRstats(PreSex.mods)
```

Model	df	G^2
[G] [P]	1	75.259
[GP] [E]	3	48.929
[GPE] [M]	7	107.956
[G] [P] [E] [M]	11	232.142

Mosaic plots

```
# (Gender Pre)
mosaic(margin.table(PreSex, 1:2), shade=TRUE,
      main = "Gender and Premarital Sex")
```

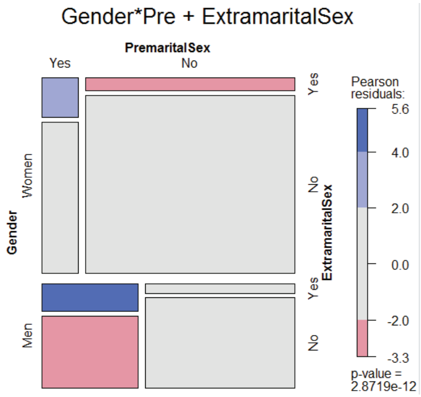


Twice as many women in this sample

Men far more likely to report pre-marital sex than women (odds ratio = 3.7)

Mosaic plots

```
# (Gender Pre)(Extra)
mosaic(margin.table(PreSex, 1:3),
       expected = ~Gender * PremaritalSex + ExtramaritalSex,
       main = "Gender*Pre + ExtramaritalSex")
```

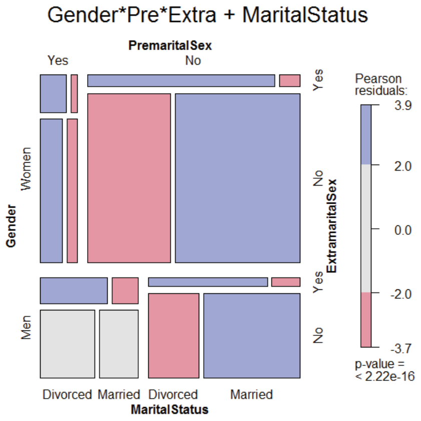


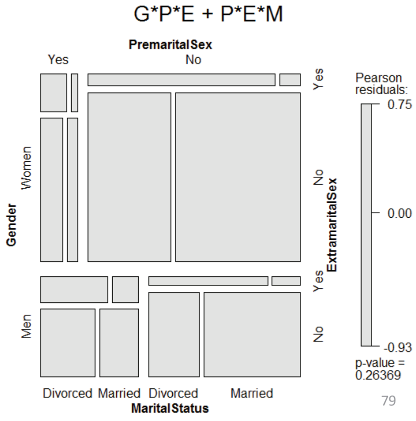
Men & women who reported Pre- far more likely to report Extra- sex

Odds ratio of Extra- given Pre- about the same for men & women (3.61 vs. 3.56)

Mosaic plots

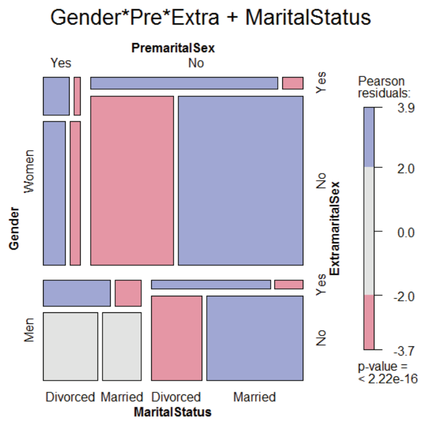
```
mosaic(PreSex,
       expected = ~Gender * PremaritalSex * ExtramaritalSex
       + MaritalStatus,
       main = "Gender*Pre*Extra + MaritalStatus")
# (GPE)(PEM)
mosaic(PreSex,
       expected = ~ Gender * PremaritalSex * ExtramaritalSex
       + MaritalStatus * PremaritalSex * ExtramaritalSex,
       main = "G*P*E + P*E*M")
```





Mosaic plots

```
mosaic(PreSex,
       expected = ~Gender * PremaritalSex * ExtramaritalSex
       + MaritalStatus,
       main = "Gender*Pre*Extra + MaritalStatus")
```



In the model [GPE][M], marital status depends in a complex way

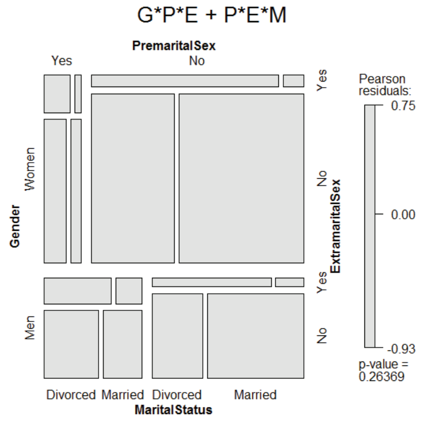
Among women, those reporting Pre- more likely to be divorced

Among men, those reporting Pre- only more likely to be divorced if Extra-

This suggests adding associations of M with P and E: [PEM] term

Mosaic plots

```
# (GPE)(PEM)
mosaic(PreSex,
       expected = ~ Gender * PremaritalSex * ExtramaritalSex
       + MaritalStatus * PremaritalSex * ExtramaritalSex,
       main = "G*P*E + P*E*M")
```



This model fits well, $G^2(4) = 5.26$, p=0.26

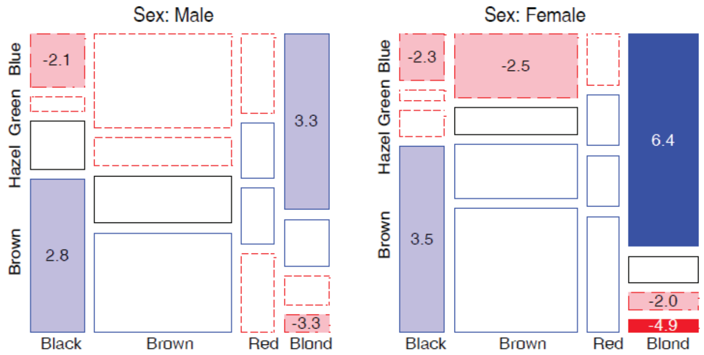
Loglinear thinking: once we take GPE into account, are there simpler models for association with M?

Looking forward: logit models for MaritalStatus often provide an easier path

Partial association, partial mosaics

Sometimes useful to do a stratified analysis

- How does association between two (or more) variables vary over levels of other variables?
- Mosaic plots for main variables show partial association at each level of others
- E.g., Hair color, Eye color, subset by Sex



Partial association, partial mosaics

Stratified analysis: conditional decomposition of G^2

- Fit models of partial (conditional) independence, $A \perp B \,|\, C_k$ at each level of (controlling for) C.
- $\Rightarrow$ partial G^2s add to the overall G^2 for conditional independence, $A \perp B \,|\, C$

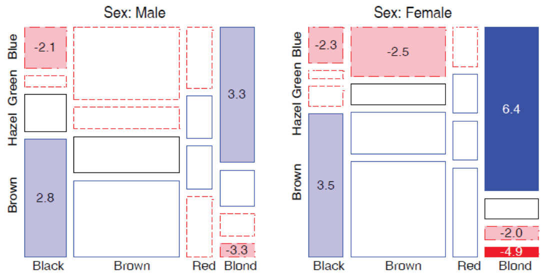
$$G^2_{A \perp B \,|\, C} = \sum_k G^2_{A \perp B \,|\, C(k)}$$

Table: Partial and Overall conditional tests, *Hair* $\perp$ *Eye* | *Sex*

Model	df	G^2	*p*-value
[*Hair*][*Eye*] | Male	9	44.445	0.000
[*Hair*][*Eye*] | Female	9	112.233	0.000
[*Hair*][*Eye*] | Sex	18	156.668	0.000

Partial association: Summary

- Overall, there is a strong association of hair color and eye color, controlling for sex, $G^2(18) = 156.67$
  - For F, $G^2(9) = 112.23$ accounts for 72% of this association
- The pattern of association is similar for M & F
  - The largest difference is for blue-eyed blonds, much more prevalent among F than M. Is there a hair dye effect?



Summary: What we’ve learned