

## Loglinear models & mosaic displays



Michael Friendly

Psych 6136

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

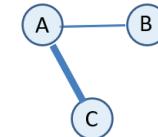
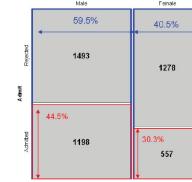


## Mosaic displays

- 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

## Today's topics

- Mosaic displays: basic ideas
- Models for count data
  - Fitting loglinear models
- Two-way tables
- Fitting & graphing LLMs
- Three-way tables: different kinds of independence
- Sequential plots & models
- Marginal & partial displays



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## Mosaic displays: basic ideas

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

UCB Admissions: Gender frequencies



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:  $V_3 | V_1, V_2 = n_{ikj} / n_{i++}$

→ Area ~ cell frequency,  $n_{ijk}$

# Mosaic displays: basic ideas

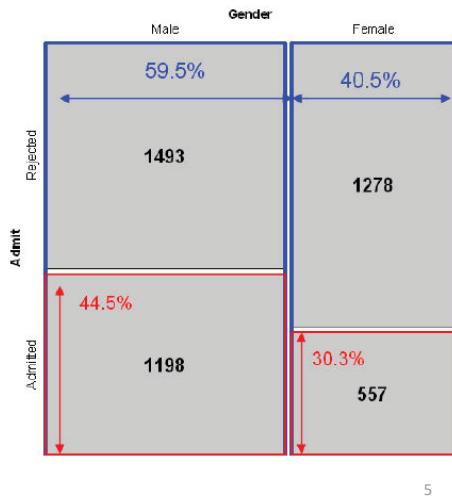
UCB Admissions: Gender x Admit

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,  $n_{ijk}$



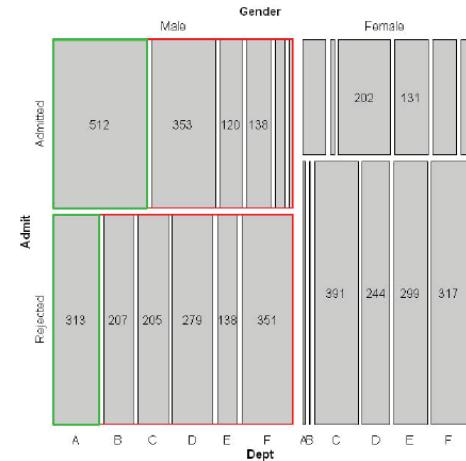
Gender x Admit x Dept frequencies

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,  $n_{ijk}$



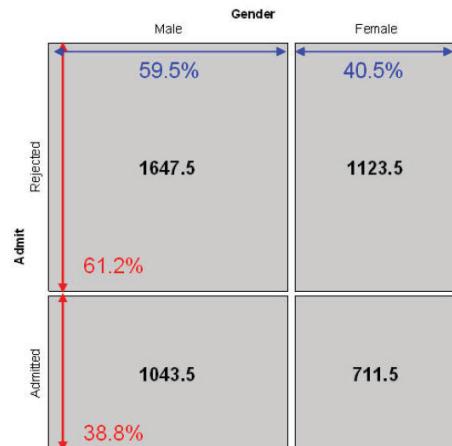
# Mosaic displays: Independence

Expected frequencies if Admit  $\perp$  Gender

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

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

→ Row and col tiles align when variables are independent



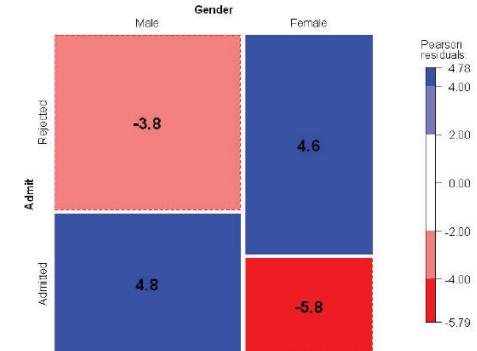
# Mosaic displays: Residuals & shading

- Pearson residuals:

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

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

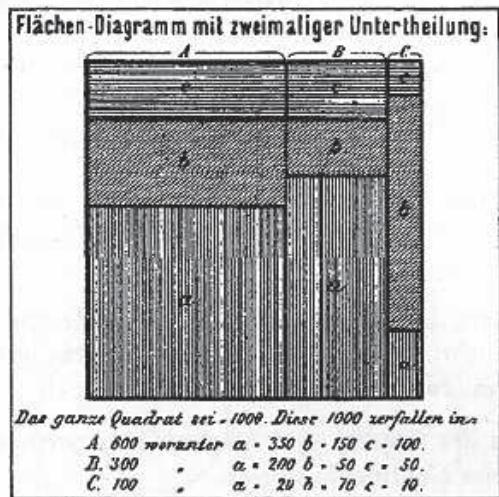
UCB Admissions:  $\sim$  Admit + Gender



## History corner: von Mayr



Georg von Mayr (1877) was the first to suggest an area-proportional display for two categorical variables



Total count = 1000

Divided into (cows, pigs,  
sheep?)

$$A = 600, B = 300, C = 100)$$

Each of these sub-divided by a 2<sup>nd</sup> variable (region: a, b, c)

The name: “bottle diagram with double divisions” suggests further splits

See: Friendly (2002), "A Brief History of the Mosaic Display", *JCGS*, 11:1,89-107,  
<http://dx.doi.org/10.1198/106186002317375631>

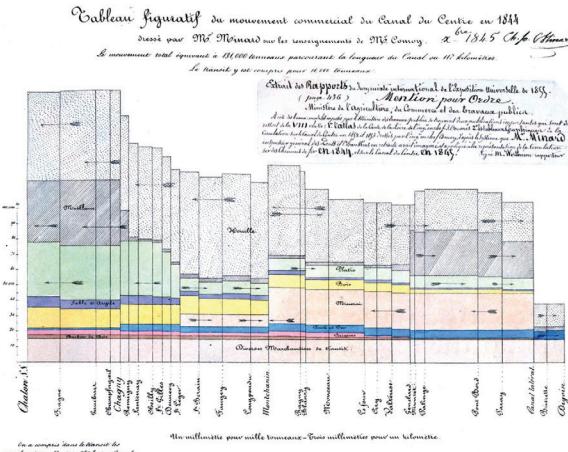
○

## History corner: Minard

Charles Joseph Minard used an early form of an area-proportional plot to show the value of transport of goods along the Canal du Centre, from Chalon to Dijon.

- Width  $\sim$  distance
  - Height  $\sim$  amount of good

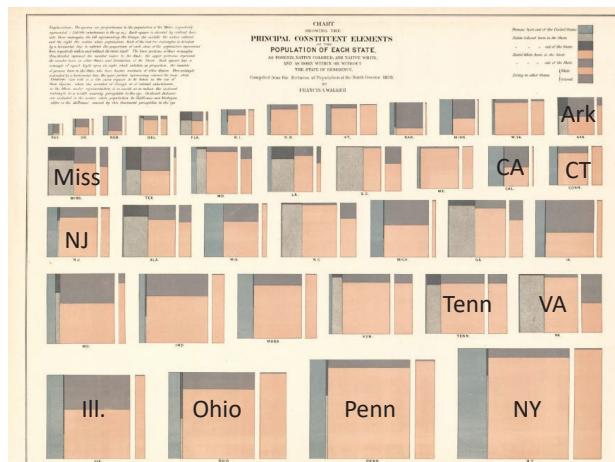
→ Value = distance × amount



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# History corner: Francis Walker

In the 1870 *Statistical Album of the US Census*, Francis Walker wanted to show the populations of the states as comprised of {foreign, native colored, native white} and born {within, outside} their state of residence.



States are ordered by total pop, shown by area

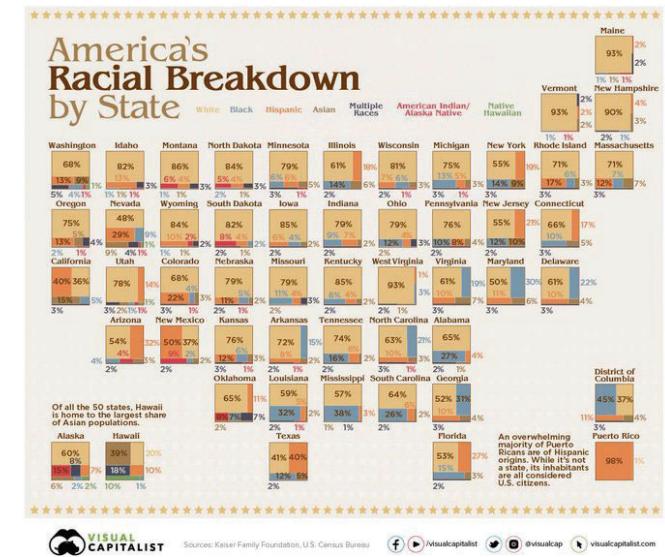
For each state, a small mosaic, supplemented by a marginal one (w/in, outside)

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# Mosaic cartograms

US map provides a spatial framework for showing the distribution of categorical data

Each mosaic is positioned as in a schematic US map



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## 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** dist<sup>n</sup> of errors
- **Logit models:** Loglinear, simplified for a **binary** response

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## 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()**
  - Parameters aren't estimated; only fitted frequencies.

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

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## glm() approach

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

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

- 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)`
  - Can estimate parameters; do structured tests
- Standard diagnostic methods available

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

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## 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 A1 vs A2
- 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;  
 $[AB] \rightarrow \beta_j^B$     $[AC] \rightarrow \beta_k^C$
- Fit using **family=binomial**

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

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## 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  $\log m_{ij}$ ,

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

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## Two-way tables: loglinear approach

### Independence model

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

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

- $\mu$  is the grand mean of  $\log m_{ij}$
- the parameters  $\lambda_i^A$  and  $\lambda_j^B$  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

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## Two-way tables: loglinear approach

### Saturated model

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

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

- The saturated model fits the table perfectly ( $\hat{m}_{ij} = n_{ij}$ ): there are as many parameters as cell frequencies. Residual df = 0.
- A global test for association tests  $H_0 : \lambda_{ij}^{AB} = 0$ .
- If reject  $H_0$ , which  $\lambda_{ij}^{AB} \neq 0$ ?
- For **ordinal** variables, the  $\lambda_{ij}^{AB}$  may be structured more simply, giving tests for ordinal association.

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## 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:

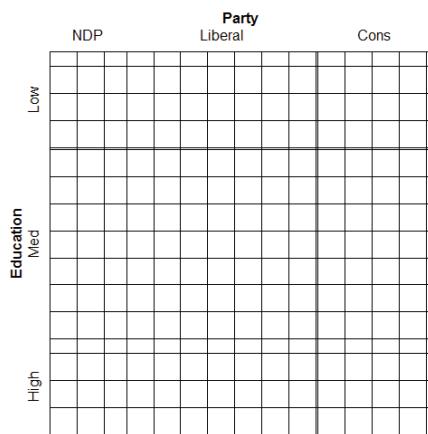
	X^2	df	P(> X^2)
Likelihood Ratio	0	4	1
Pearson	0	4	1



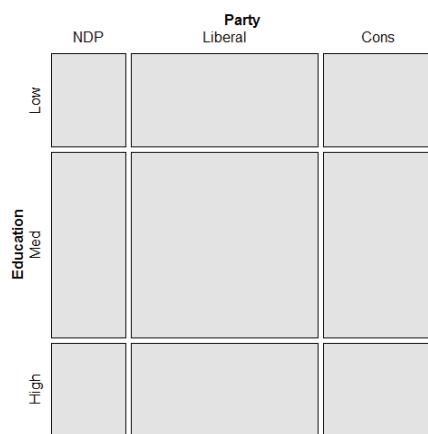
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Both sieve diagrams and mosaic plots show what independence “looks like”

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



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



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## Two-way tables: glm approach

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

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

- $\mathbf{X}$  is a known design (model) matrix, expressing the table factors
- $\beta$  is a column vector containing the unknown  $\lambda$  parameters.
- This is the same as the familiar matrix formulation of ANOVA/regression, except that
  - The response,  $\log \mathbf{m}$  makes multiplicative relations additive
  - The distribution is taken as Poisson rather than Gaussian (normal)

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### Example: 2 x 2 table

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

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

- 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  $\lambda_{11}^{AB}$
- 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  $G^2$ ,

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

or the Pearson  $X^2$ ,

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

with degrees of freedom  $df = \# \text{ cells} - \# \text{ estimated parameters}$ .

- 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)

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

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# Degrees of freedom

Q: Why do degrees of freedom for an  $r \times c$  table =  $(r-1) * (c-1)$ ?

A: Because the row & column totals are used to calculate expected frequencies  
→ Only  $(r-1)$  independent parameters for each column  
→ Only  $(c-1)$  independent parameters for each row

```
> addmargins(HE) |> knitr::kable()
```

	Black	Brown	Red	Blond	Sum
Black	68	119	26	7	220
Brown	20	84	17	94	215
Hazel	15	54	14	10	93
Green	5	29	14	16	64
Sum	108	286	71	127	592

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# R functions for loglinear models

- **vcg::assocstats()** – only  $\chi^2$  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, ...)`
- Model formulas have the form:
  - **table** form:  $\sim A + B + \dots$  (independence);
  - $\sim A * B + C$  (allow  $A*B$  association)
  - **frequency** data frame: `Freq ~ A * B + C`

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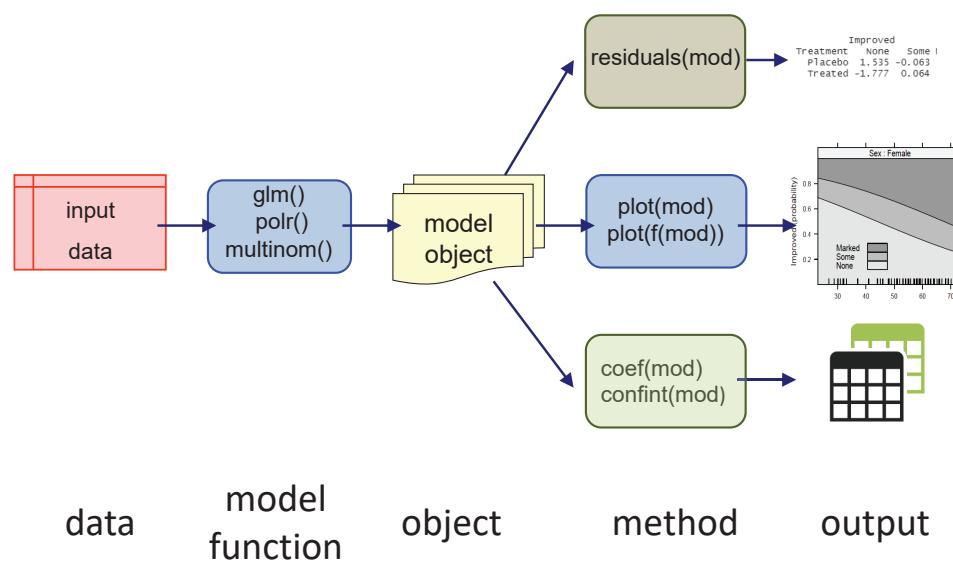
# R functions & methods

- **loglm()** and **glm()** return an R object with named components and with a `class()` – here “**loglm**”

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

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

# Model-based methods: Fitting & graphing



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## 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  $2 \times 3$  table of Treatment x Improved

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

arth.tab is a "table" object  
print.table() gives this output

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## Arthritis treatment

Fit the independence model,  $\sim$  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
```

The method print.loglm() gives this output

Some methods: residuals(), deviance(), coef(), ...

```
> 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
0.0238 -0.0238
```

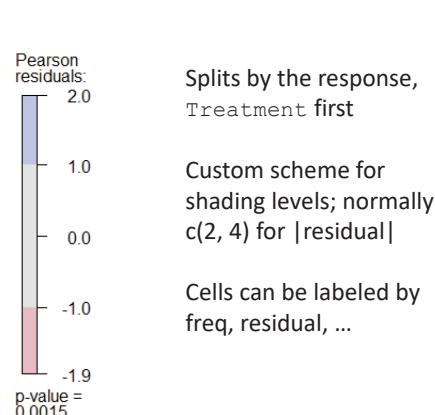
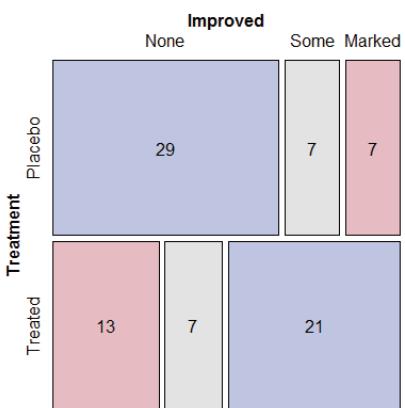
```
$Improved
None      Some      Marked
0.5014 -0.5972  0.0959
```

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## 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)
```



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## Arthritis treatment: glm()

glm() for loglinear models easiest w/ the data as a data.frame in **frequency** form, **family=poisson**

```
> 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

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## 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

```

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## 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

```

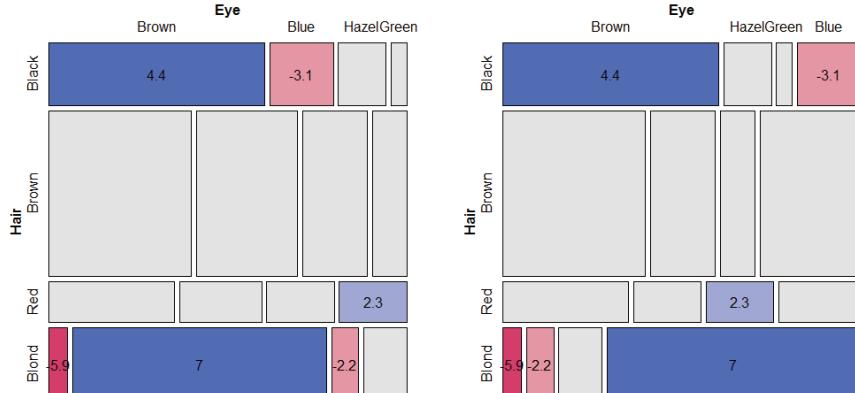
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## Mosaic displays: Seeing patterns

```

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

```



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

```

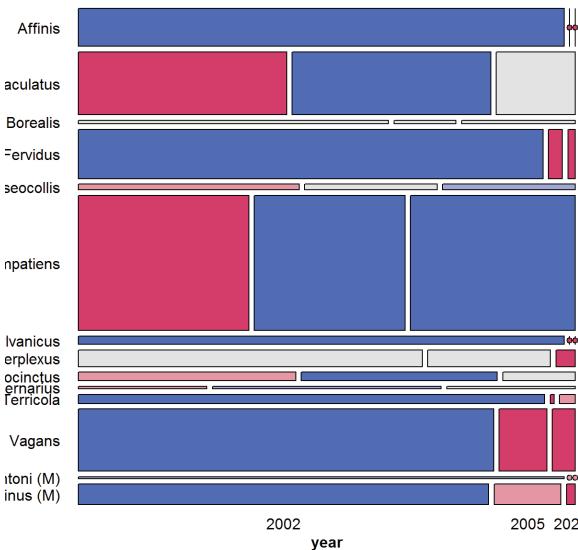
species	2002	2005	2021
<chr>	<dbl>	<dbl>	<dbl>
1 Affinis	508	0	0
2 Bimaculatus	362	345	137
3 Borealis	30	6	11
4 Fervidus	634	19	10
5 Griseocollis	35	21	21
6 Impatiens	638	564	616
7 Pensylvanicus	112	0	0
8 Perplexus	160	57	9
9 Rufocinctus	51	46	17
10 Ternarius	9	16	9
11 Terricola	119	1	4
12 Vagans	713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

How to understand the pattern of association?

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```
mosaic(bees.mat, shade=TRUE, ...)
```

Bees Abundance Data

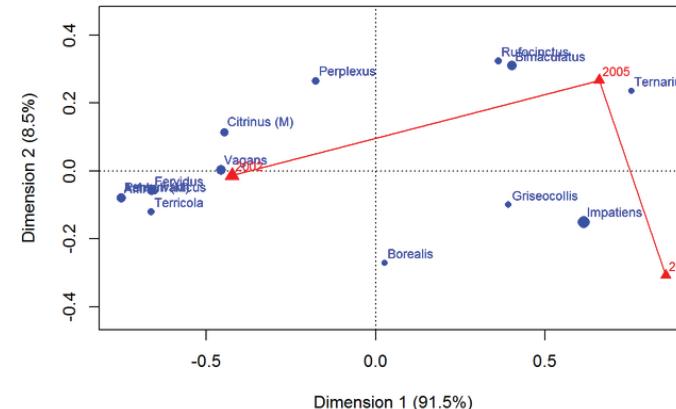


Alphabetic order of species:  
No clear pattern

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**Correspondence analysis** finds scores for the row & col categories to account for maximum  $\chi^2$

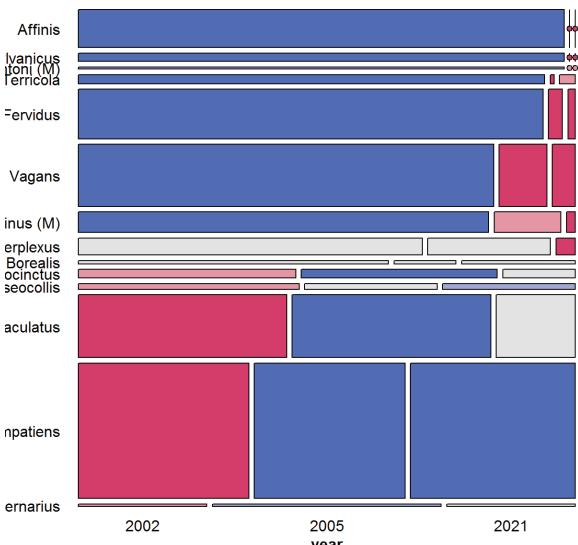
```
bees.ca <- ca(bees.mat)
plot(bees.ca,
     lines=c(FALSE, TRUE),      # join years with lines
     mass = c(TRUE, TRUE))     # symbol size ~ marginal frequency
```



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```
mosaic(permute(bees.mat, "CA"), shade=TRUE, ...)
```

Bees Abundance Data



One main cluster was very prevalent in 2002

A few species became prominent in later years

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## 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,  $\lambda_{ijk}^{ABC}$

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

- 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,  $\lambda_{ijk}^{ABC}$  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!

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## Reduced models

- Goal: fit the **smallest** model sufficient to explain/describe the observed frequencies
  - Similar to Anova models, e.g.,  $\sim(A + B + C)^3$  with all interactions
  - Do we need all those interaction terms?
- Hierarchical** models
  - Most loglinear models are taken to be hierarchical:
  - A high-order term, like  $\lambda_{ijk}^{ABC} \rightarrow$  all **lower order terms** included
    - Why: principle of **marginality**—hard to interpret w/o low order relatives
- Thus, a shorthand notation for a loglinear model lists only the **high-order** terms. For example:
  - $[ABC] \rightarrow A + B + C + AB + AC + BC + ABC$
  - $[AB][AC] \rightarrow A + B + C + AB + AC$

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## 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:
 
$$[A][B] \equiv A \perp B \equiv A \text{ independent of } B$$
- 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	$[AB][C]$	$(AB) \perp C$
Conditional independence	$[AC][BC]$	$(A \perp B)   C$
All two-way associations	$[AB][AC][BC]$	homogeneous assoc.
Saturated model	$[ABC]$	ABC interaction

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## 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  $C$

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

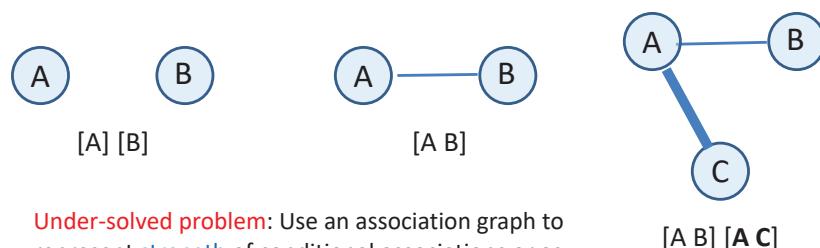
- Homogeneous association:** All two-way, but each two-way is the *same* over the other factor

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

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## Association graphs

- An association graph represents variables in an  $n$ -way frequency table by an **undirected graph**
  - Nodes are the variables
  - Edges are first-order (2-way) **associations**
  - two variables are **independent** if not joined by an edge



**Under-solved problem:** Use an association graph to represent **strength** of conditional associations or as a widget for model fitting

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# Model types & association graphs

Hypothesis	Fitted margins	Model symbol	Independence interpretation	Association graph
$H_1$	$n_{i++}, n_{+j+}, n_{++k}$	$[A][B][C]$	$A \perp B \perp C$	
$H_2$	$n_{ij+}, n_{++k}$	$[AB][C]$	$(A, B) \perp C$	
$H_3$	$n_{i+k}, n_{+jk}$	$[AC][BC]$	$A \perp B   C$	
$H_4$	$n_{ij+}, n_{i+k}, n_{+jk}$	$[AB][AC][BC]$	NA	

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# 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]
```

e.g., Berkeley data

```
loglm(~ (Admit + Gender) * Dept)
loglm(~ Admit*Dept + Gender * Dept)
```

Association graph



$\rightarrow A \perp G | D$

(just put your finger over D)

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## 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
  - Conditional association [Admit, Gender | Dept]  $\neq$  marginal [A, G]
- Three-way tables: The AB marginal and  $AB | C$  conditional associations are the same, if either:
  - A & C are conditionally independent,  $A \perp C | B = [AB][CB]$
  - B & C are conditionally independent,  $B \perp C | A = [AB][AC]$
  - $\rightarrow$  no three-way association

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## Higher-way tables

DaytonSurvey data: A  $2^5$  table

2,276 HS seniors asked if they had ever used cigarettes, alcohol, or marijuana

sex	race	cigarette		alcohol		marijuana			
		Yes	No	Yes	No	Yes	No	Yes	No
female	white	405	268	1	17	13	218	1	117
	other	23	23	0	1	2	19	0	12
male	white	453	228	1	17	28	201	1	133
	other	30	19	1	8	1	18	0	17

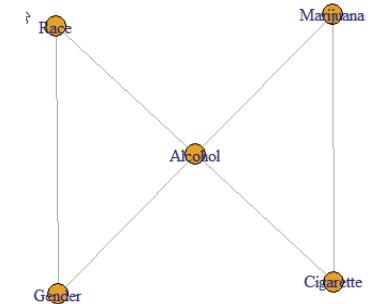
Suppose we wish to fit the model:

$[A M] [A C] [M C] [A R] [A G] [R G]$

The association graph implies:

$\{\text{race, gender}\} \perp \{\text{marijuana, cigarette}\} | \text{alcohol}$

If it fits, we can collapse the table over {race, gender} to study associations among A, M & C.



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## Response vs. Association models

- In association models, the interest is just on *which* variables are associated, and *how*
  - Hair-eye data: [Hair Eye]? [Hair Sex]? [Eye Sex]
  - $\Rightarrow$  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  $\Rightarrow$  associations [Admit Gender] and/or [Admit Dept]

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## 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  $X^2$ ,

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

with residual degrees of freedom  $\nu = \# \text{ cells} - \# \text{ estimated parameters}$ .

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

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## 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/  $v_2$  df) fits a subset of the parameters of  $M_1$  (w/  $v_1$  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  $\chi^2$  distribution with  $df = v_2 - v_1$

$$\Delta G^2 \equiv G^2(M_2 | M_1) = G^2(M_2) - G^2(M_1) = 2 \sum_i n_i \log(\hat{m}_{i1}/\hat{m}_{i2}) \quad (7)$$

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## 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  $G^2$  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?
- Absolute fit of all 2-way model is not terrible. Investigate this further!

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# Fitting these in R

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

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

## glm() - data in frequency form

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

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# 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
```

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## 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
```

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# 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**,  $\Delta G^2 = G^2(M_i | M_{i-1})$

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## LRstats: AIC & BIC

`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 significance tests, but **smaller** is better
- Also apply to **non-nested** models

$$AIC = G^2 + 2 \times \# \text{ parameters}$$

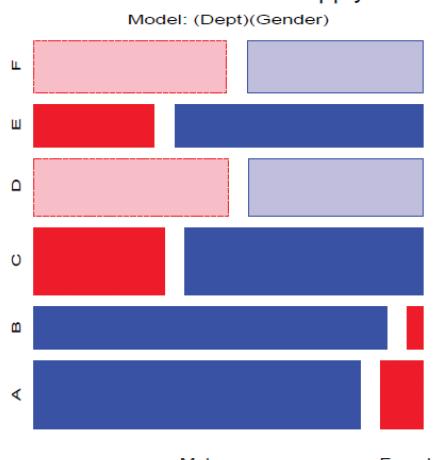
$$BIC = G^2 + 2 \log(n) \times \# \text{ parameters}$$

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## Mosaic displays: Predictor variables

Berkeley data: Departments  $\times$  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

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## Mosaic displays: Visual fitting

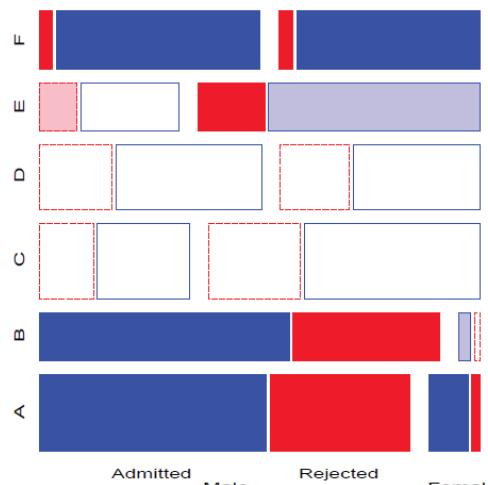
- Each mosaic shows:
  - The DATA – size of tiles
  - (some) marginal frequencies – initial splits (visual grouping)
  - RESIDUALS (shading) – what associations have been omitted?
- Visual fitting
  - Start with a simple model: mutual independence or joint independence for response models
  - Pattern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

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## Baseline response model

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

Model: (DeptGender)(Admit)



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

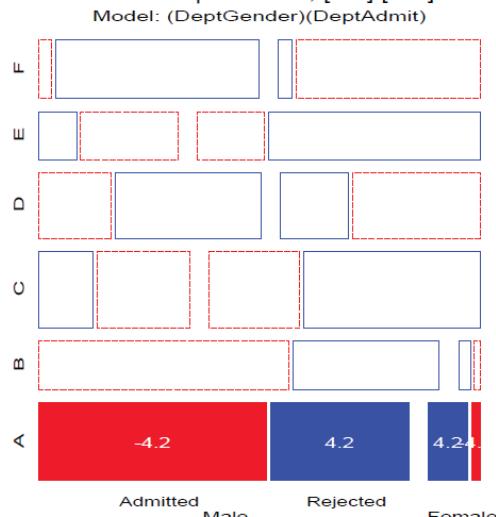
Allows/fits assoc. of [Dept Gender], not shown in shading

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

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## Add an association term...

Conditional independence, [AD] [DG]:



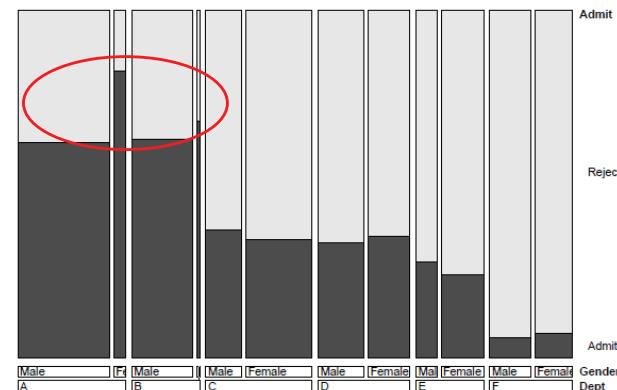
- E.g., Add [Admit Dept] association → Conditional independence:
  - Fits poorly: ( $G^2_{(6)} = 21.74$ )
  - But, only in Department A!
- GLM approach allows fitting a special term for Dept. A
- Note: These displays use *standardized residuals*: better statistical properties.

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## 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

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



An exploratory plot

Highlights the M-F diff<sup>ce</sup> in Admit for Dept A

DDAR Fig 5.34, p 211

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## Survival on the *Titanic*

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## 4-way tables: Survival on the *Titanic*

Data on the fate of passengers & crew on the HMS Titanic: a  $4 \times 2 \times 2 \times 2$  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
```

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## 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:

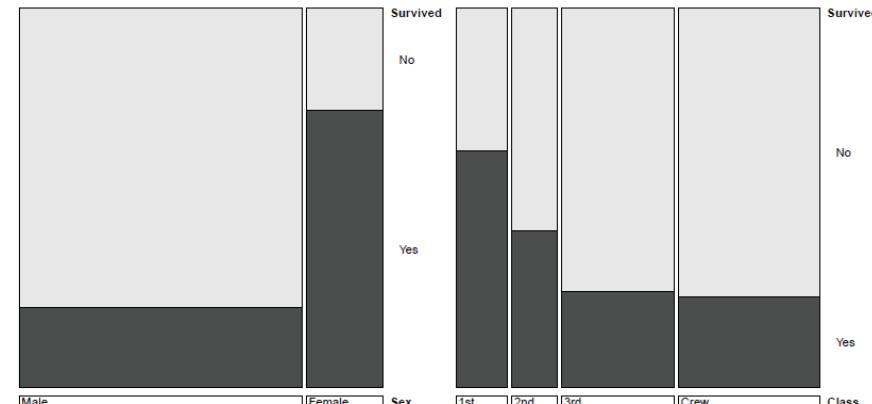
- **Structural zeros**: could not occur (children in crew)
- **Sampling zeros**: did not happen to occur (children in 1<sup>st</sup> & 2<sup>nd</sup> who died)
- Beware: zeros can cause problems:
  - Loss of df
  - 0/0 → NaN in  $\chi^2$  tests

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## Exploratory plots

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

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

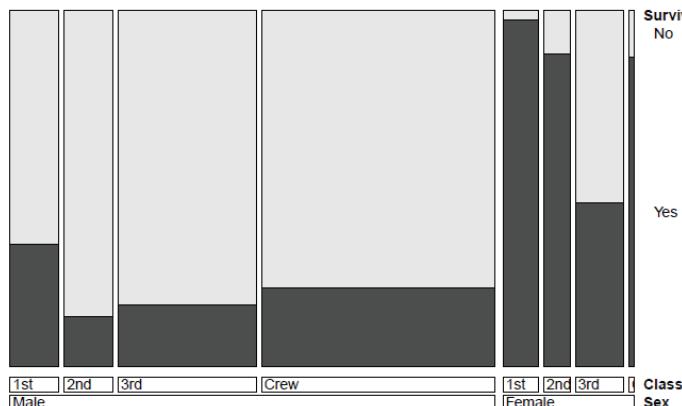


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## Exploratory plots

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

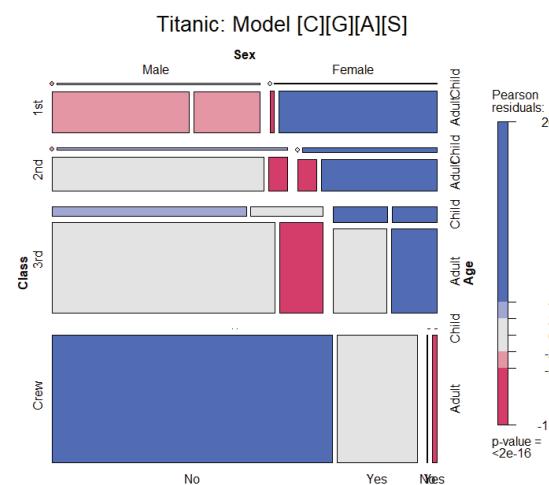
```
doubledecker(Survived ~ Sex + Class, data=Titanic)
```



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## 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

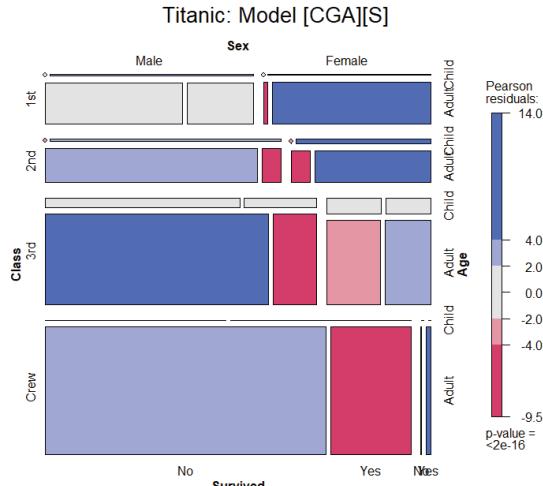
Let's clean this mosaic!!

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

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# Baseline model for Survived

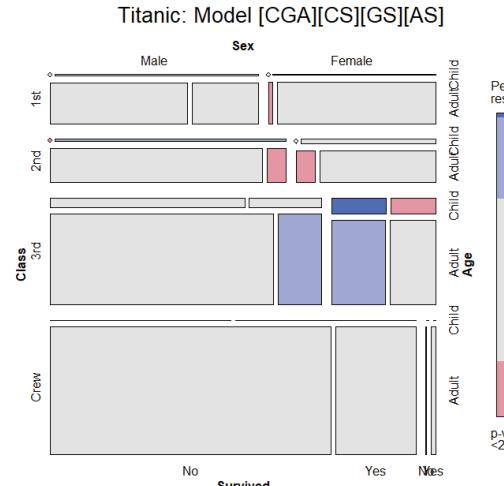
```
mod1 <- loglm(~ 1*2*3 + 4, data=Titanic)
mosaic(mod1, main="Titanic: Model [CGA][S]")
```



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# Adding associations: Main effects

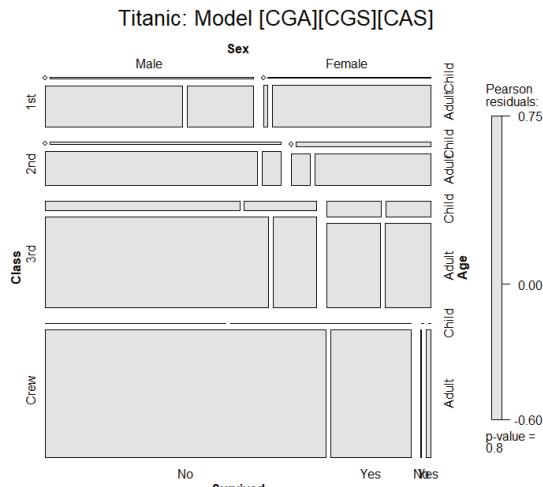
```
mod2 <- loglm(~ 1*2*3 + (1+2+3)*4, data=Titanic)
mosaic(mod2, main="Titanic: Model [CGA][CS][GS][AS]")
```



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# Final model

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



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# 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

Q: Please help me interpret these results 😊

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# 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

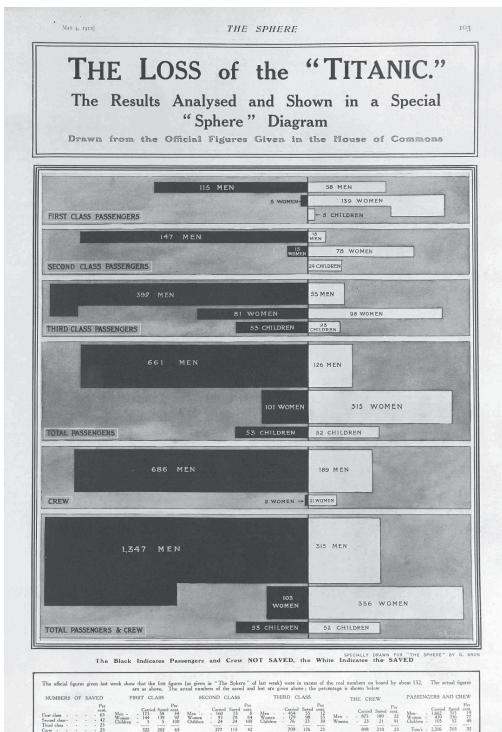
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## Historical note

The *Titanic* sank on Apr. 15, 1912

On May 4, the technical illustrator, G. Bron published this graph in *The Sphere*, a popular magazine.

He used a remarkably modern graph to show the differences in survival by class, gender & age



Read the story:

Friendly, Symanzik,Onder, [Visualizing the Titanic Disaster](#), *Significance*, Feb., 2019

# 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 3<sup>rd</sup> class did not have an advantage, while men in 1<sup>st</sup> class did vs. other classes
  - Term [CAS]: No children in 1<sup>st</sup> or 2<sup>nd</sup> class died, but nearly 2/3 in 3<sup>rd</sup> class did
- Summary:
  - Not so much "women & children first", rather
  - Women & children, ordered by class, and 1<sup>st</sup> class men!

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## Sequential plots & models

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

$$p_{ijkl\ldots} = \underbrace{p_i \times p_{j|i} \times p_{k|ij} \times p_{l|ijk} \times \cdots \times p_{n|ijk\ldots}}_{\{V_1 V_2 V_3\}}$$

- 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: 1<sup>st</sup> split: easiest to see the marginal proportions
  - Mosaics: 2<sup>nd</sup> variable seen as conditional proportions, given the 1<sup>st</sup>

## Sequential plots & models

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

$$G^2_{[v_1][v_2]\dots[v_p]} = G^2_{[v_1][v_2]} + G^2_{[v_1v_2][v_3]} + G^2_{[v_1v_2v_3][v_4]} + \dots + G^2_{[v_1\dots v_{p-1}][v_p]}$$

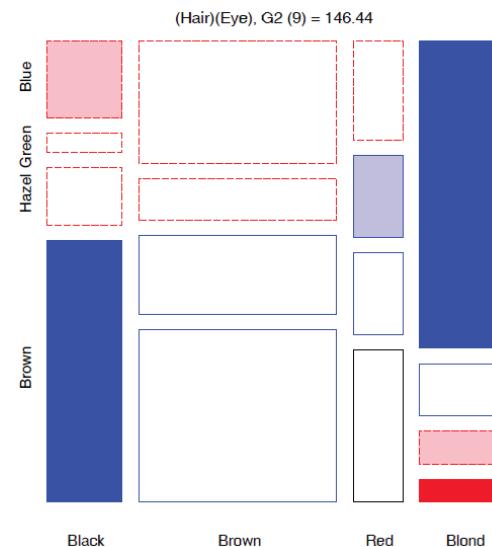
- E.g., for Hair Eye color data

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

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## Sequential plots & models

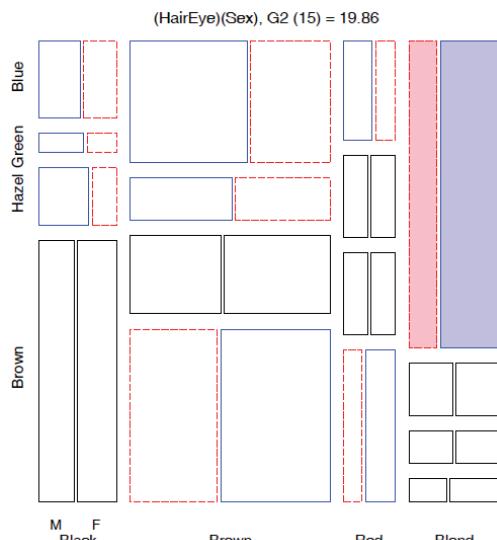
Hair color  $\times$  Eye color marginal table (ignoring Sex)



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## Sequential plots & models

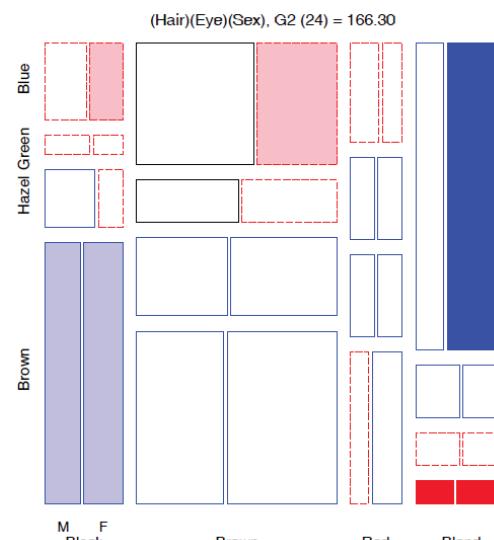
3-way table, Joint independence model [Hair Eye][Sex]



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## Sequential plots & models

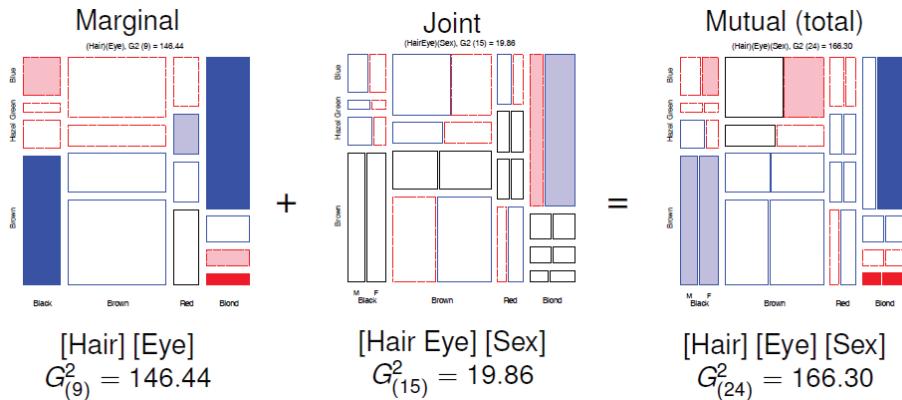
3-way table, Mutual independence [Hair] [Eye][Sex]



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# Sequential plots & models

Putting these together:



TIP: `vcdExtra::seq_loglm()` generates a variety of sequential models

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# Sequential models: Applications

## Response models

- When one variable,  $R$ , is a response and  $E_1, E_2, \dots$  are explanatory, the baseline model is the model of joint independence,  $[E_1, E_2, \dots][R]$
- 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  $[E_i R], [E_i E_j R] \dots$

## 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

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## 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 ( $G \times P \times E \times M$ )

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

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

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?

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

Order the table variables as  $G \rightarrow P \rightarrow E \rightarrow M$

```
> 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)
```

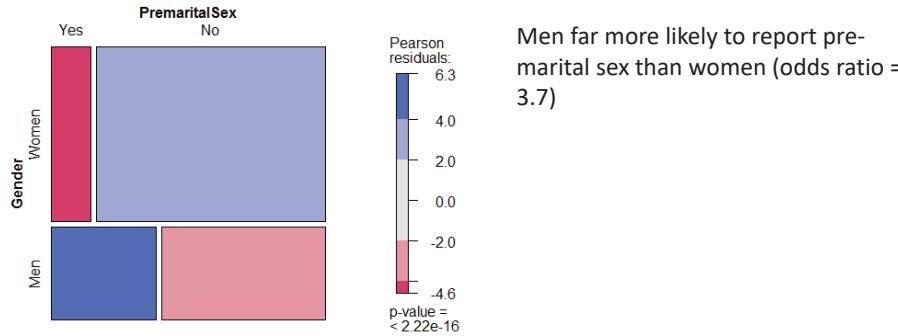
Model	df	$G^2$
[G] [P]	1	75.259
[GP] [E]	3	48.929
[GPE] [M]	7	107.956
[G] [P] [E] [M]	11	232.142

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## Mosaic plots

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

Gender and Premarital Sex

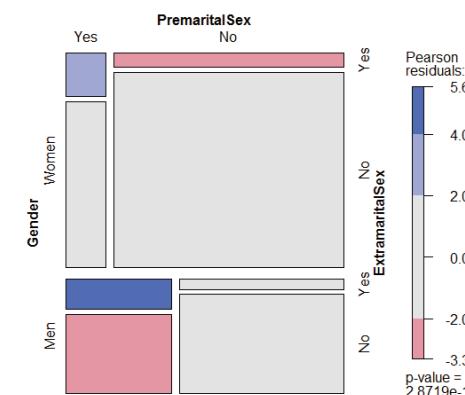


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## Mosaic plots

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

Gender\*Pre + ExtramaritalSex



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

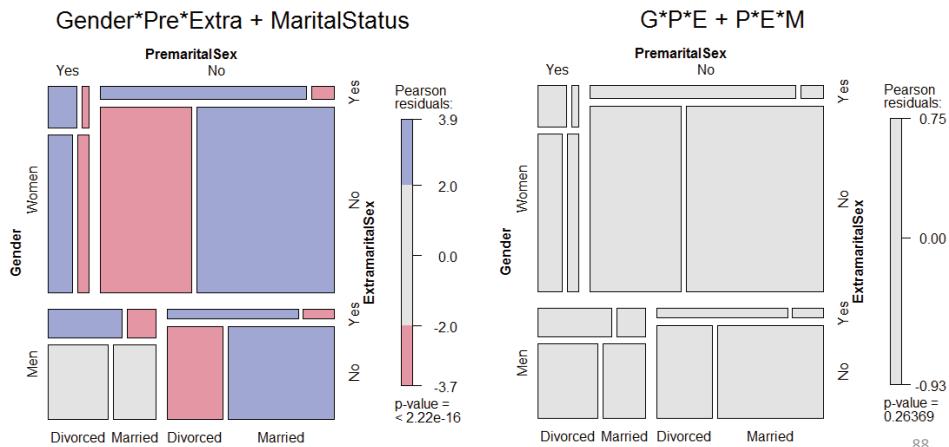
Odds ratio of Extra- given Pre-about the same for men & women (3.61 vs. 3.56)

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## 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")
```

Gender\*Pre\*Extra + MaritalStatus

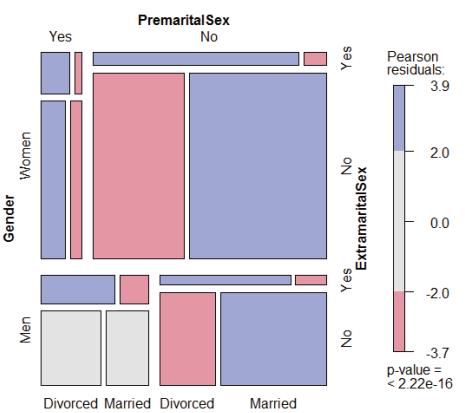


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## Mosaic plots

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

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

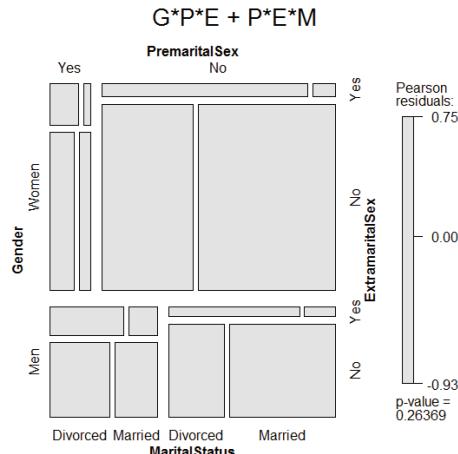
Among men, those reporting Pre-only more likely to be divorced if Extra-

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

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## Mosaic plots

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

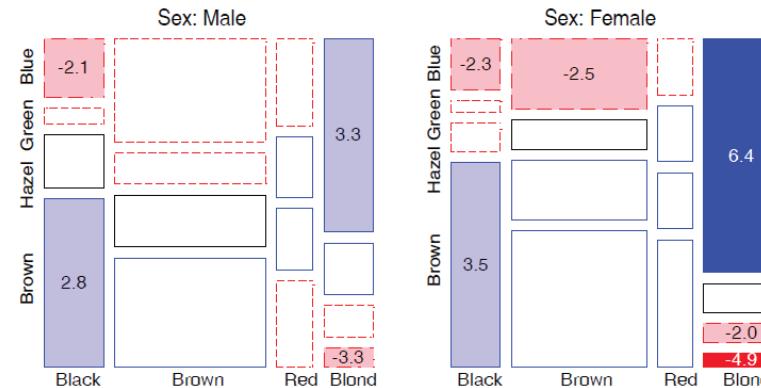


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## Partial association, partial mosaics

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



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## 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  $G^2$ 's 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

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## 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?



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## Summary: What we've learned

- Mosaic plots use sequential splits to show marginal and conditional frequencies in an  $n$ -way table
  - Shading: **sign** and **magnitude** of residuals → contributions to  $\chi^2$
  - Shows the pattern of association not accounted for
  - Permuting rows/cols often helps
- Loglinear models
  - Express associations with ANOVA-like interaction terms: A\*B, A\*C
    - Joint independence:  $[AB][C] \equiv A * B + C$
    - Conditional independence:  $[AC][BC] \equiv A \perp B | C$
  - Fitting models  $\cong$  “cleaning the mosaic”
  - Response models: include all associations among predictors
- Sequential / partial plots & models
  - Sequential: Decompose all associations:  $V_1; V_2|V_1; V_3|\{V_1, V_2\}, \dots$
  - Partial: Decompose conditional associations:  $[V_1, V_2]|\ V_3=\{a, b, \dots\}$