# Two-way tables: Independence and association

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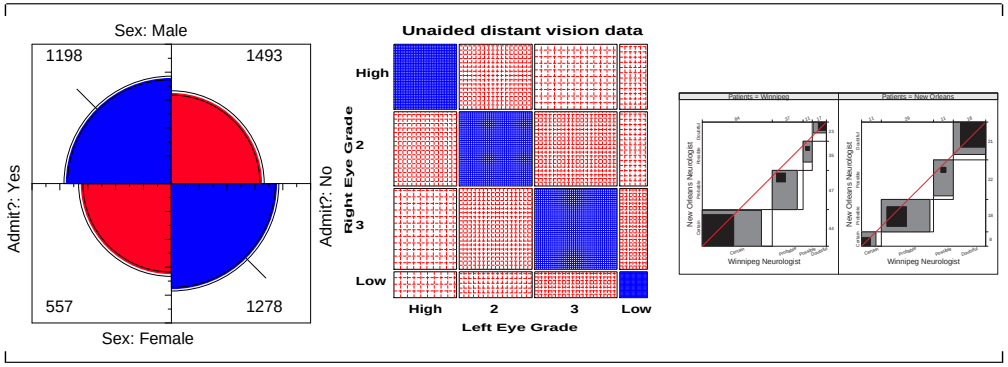





## Two-way tables: Overview

Two-way contingency tables are a convenient and compact way to represent a data set cross-classified by two discrete variables, *A* and *B*.

**Special cases:**

- $2 \times 2$ tables: two binary factors (e.g., gender, admitted?, died?, ...)
- $2 \times 2 \times k$ tables: a collection of $2 \times 2$s, stratified by another variable
- $r \times c$ tables
- $r \times c$ tables, with ordered factors

**Questions:**

- Are *A* and *B* statistically independent? (vs. associated)
- If associated, what is the strength of association?
- Measures: $2 \times 2$— odds ratio; $r \times c$— Pearson $\chi^2$, LR $G^2$
- How to understand the pattern or nature of association?





## Two-way tables: Examples

$2 \times 2$ table: Admissions to graduate programs at U. C. Berkeley

Table: Admissions to Berkeley graduate programs

| | Admitted | Rejected | Total | % Admit | Odds(Admit) |
|---|---|---|---|---|---|
| Males | 1198 | 1493 | 2691 | 44.52 | 0.802 |
| Females | 557 | 1278 | 1835 | 30.35 | 0.437 |
| Total | 1755 | 2771 | 4526 | 38.78 | 0.633 |

Males were nearly twice as likely to be admitted.

- Association between gender and admission?
- If so, is this evidence for gender bias?
- How do characterise strength of association?
- How to test for significance?
- How to visualize?





## $2 \times 2$ tables: UCB data

In R, the data is contained in `UCBAdmissions`, a $2 \times 2 \times 6$ table for 6 departments. Collapse over department:

```
data(UCBAdmissions)
UCB <- margin.table(UCBAdmissions, 2:1)
UCB

##          Admit
## Gender    Admitted Rejected
##   Male        1198     1493
##   Female       557     1278
```

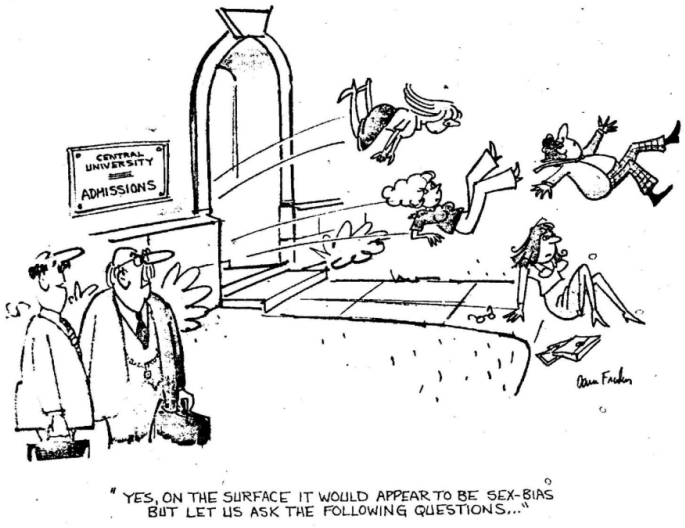
Association between gender and admit can be measured by the odds ratio, the ratio of odds of admission for males vs. females. Details later.

```
oddsratio(UCB, log=FALSE)

##  odds ratios for Gender and Admit
##
## [1] 1.8411

confint(oddsratio(UCB, log=FALSE))

##                                 2.5 % 97.5 %
## Male:Female/Admitted:Rejected 1.6244 2.0867
```




- How to analyse these data?
- How to visualize & interpret the results?
- Does it matter that we collapsed over Department?



# Two-way tables: Examples

$r \times c$ table: Hair color and eye color— Students in a large statistics class.

Table: Hair-color eye-color data

| Eye Color | Hair Color Black | Brown | Red | Blond | Total |
|---|---|---|---|---|---|
| Brown | 68 | 119 | 26 | 7 | 220 |
| Blue | 20 | 84 | 17 | 94 | 215 |
| Hazel | 15 | 54 | 14 | 10 | 93 |
| Green | 5 | 29 | 14 | 16 | 64 |
| Total | 108 | 286 | 71 | 127 | 592 |

- Association between hair color and eye color?
- How do characterise strength of association?
- How to test for significance?
- How to visualize?
- How to interpret the pattern of association?





# $r \times c$ tables: HEC data

In R, the data is contained in `HairEyeColor`, a $4 \times 4 \times 2$ table for males and females. Collapse over gender:

```
data(HairEyeColor)
HEC <- margin.table(HairEyeColor, 2:1)
```

Association between hair and eye color can be tested by the standard Pearson $\chi^2$ test. Details later.

```
chisq.test(HEC)

##
##  Pearson's Chi-squared test
##
## data:  HEC
## X-squared = 138, df = 9, p-value <2e-16
```





# Two-way tables: Examples

$r \times c$ table with ordered categories: Mental health and parents' SES

Table: Mental impairment and parents' SES

| SES | Mental impairment Well | Mild | Moderate | Impaired |
|---|---|---|---|---|
| 1 | 64 | 94 | 58 | 46 |
| 2 | 57 | 94 | 54 | 40 |
| 3 | 57 | 105 | 65 | 60 |
| 4 | 72 | 141 | 77 | 94 |
| 5 | 36 | 97 | 54 | 78 |
| 6 | 21 | 71 | 54 | 71 |

- Mental impairment is the response, SES is the predictor
- How do characterise strength of association?
- How to interpret the pattern of association?
- How to take ordinal nature of the variables into account?

# ordered $r \times c$ tables: Mental data I

In R, the data is contained in `Mental` in vcdExtra, a frequency data frame.

```
data(Mental, package="vcdExtra")
str(Mental)

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

Convert to a contingency table using **`xtabs()`**, and test association:

```
mental.tab <- xtabs(Freq ~ ses + mental, data=Mental)
chisq.test(mental.tab)

##
##  Pearson's Chi-squared test
##
## data:  mental.tab
## X-squared = 46, df = 15, p-value = 5.3e-05
```





# ordered $r \times c$ tables: Mental data II

For ordinal factors, more powerful tests are available with Cochran-Mantel-Haenszel tests:

```
CMHtest(mental.tab)

## Cochran-Mantel-Haenszel Statistics for ses by mental
##
##                  AltHypothesis Chisq Df     Prob
## cor         Nonzero correlation  37.2  1 1.09e-09
## rmeans  Row mean scores differ  40.3  5 1.30e-07
## cmeans  Col mean scores differ  40.7  3 7.70e-09
## general    General association  46.0 15 5.40e-05
```

Details later, but $\chi^2/df$ gives a useful comparison.

```
##     cor  rmeans  cmeans general
##   37.16    8.06   13.56    3.06
```





# 2 by 2 tables: Notation

| Row | Column 1 | Column 2 | Total |
|---|---|---|---|
| 1 | $n_{11}$ | $n_{12}$ | $n_{1+}$ |
| 2 | $n_{21}$ | $n_{22}$ | $n_{2+}$ |
| Total | $n_{+1}$ | $n_{+2}$ | $n_{++}$ |

| Gender | Admit | Reject | Tot |
|---|---|---|---|
| Male | 1198 | 1493 | 2691 |
| Female | 557 | 1278 | 1835 |
| Total | 1755 | 2771 | 4526 |

- $\boldsymbol{N} = \{n_{ij}\}$ are the observed frequencies.
- $+$ subscript means sum over: row sums: $n_{i+}$; col sums: $n_{+j}$; total sample size: $n_{++} \equiv n$
- Similar notation for:
  - Cell joint population probabilities: $\pi_{ij}$; also use $\pi_1 = \pi_{1+}$ and $\pi_2 = \pi_{2+}$
  - Population marginal probabilities: $\pi_{i+}$ (rows), $\pi_{+j}$ (cols)
  - Sample proportions: use $p_{ij} = n_{ij}/n$, etc.





# Independence

Two categorical variables, *A* and *B* are statistically independent when:

- The conditional distributions of B given A are the same for all levels of A

$$\boldsymbol{\pi_{1j} = \pi_{2j} = \cdots = \pi_{rj}}$$

- Joint cell probabilities are the product of the marginal probabilities

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

For $2 \times 2$ tables, this gives rise to tests and measures based on

- Difference in row marginal probabilities: test $H_0 : \pi_1 = \pi_2$
- Odds ratio
- Standard $\chi^2$ tests also apply for large $n$
- Fisher's exact test or simulation required in small samples.

# Independence: Example I

In the Arthritis data, people are classified by `Sex`, `Treatment` and `Improved`. Are `Treatment` and `Improved` independent?

- → row proportions are the same for Treated and Placebo
- → cell frequencies ∼ row total × column total

```
data(Arthritis, package="vcd")
arth.tab <- xtabs( ~ Treatment + Improved, data=Arthritis)
round(prop.table(arth.tab, 1), 3)

##           Improved
## Treatment  None  Some Marked
##   Placebo 0.674 0.163  0.163
##   Treated 0.317 0.171  0.512
```

More people given the Placebo show No improvement; more people Treated show Marked improvement





# Independence: Example II

Frequencies, if `Treatment` and `Improved` were independent:

```
row.totals <- margin.table(arth.tab, 1)
col.totals <- margin.table(arth.tab, 2)
round(outer(row.totals, col.totals)/ sum(arth.tab), 1)

##           Improved
## Treatment None Some Marked
##   Placebo 21.5  7.2   14.3
##   Treated 20.5  6.8   13.7
```

These are the expected frequencies, under independence.

```
chisq.test(arth.tab)

##
##  Pearson's Chi-squared test
##
## data:  arth.tab
## X-squared = 13.1, df = 2, p-value = 0.0015
```





# Sampling models: Poisson, Binomial, Multinomial

Some subtle distinctions arise concerning whether the row and/or column marginal totals of a contingency table are fixed by the sampling design or random.

- Poisson: each $n_{ij}$ is regarded as an independent Poisson variate; nothing fixed
- Binomial: each row (or col) is regarded as an independent binomial distribution, with one fixed margin (group total), other random (response)
- Multinomial: only the total sample size, $n_{++}$, is fixed; frequencies $n_{ij}$ are classified by $A$ and $B$
- These make a difference in how hypothesis tests are derived, justified and explained.
- Happily, for most inferential methods, the same results arise under Poisson, binomial and multinomial sampling

Q: What is an appropriate sampling model for the UCB admissions data? For the Hair-Eye color data? For the Mental impairment data?





# Odds and odds ratios

For a binary response where $\pi = \Pr(\text{success})$, the ***odds*** of a success is

$$\text{odds} = \frac{\pi}{1-\pi} \ .$$

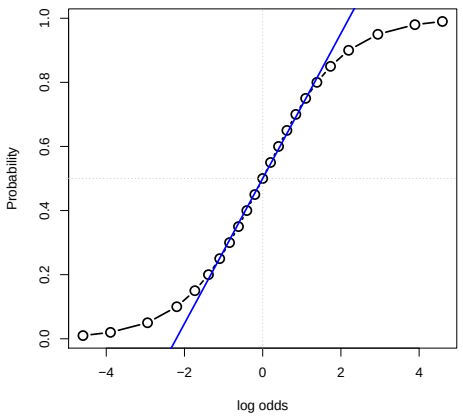
- Odds vary multiplicatively around 1 ("even odds", $\pi = \frac{1}{2}$)
- Taking logs, the log(odds), or ***logit*** varies symmetrically around 0,

$$\text{logit}(\pi) \equiv \log(\text{odds}) = \log\left(\frac{\pi}{1-\pi}\right) \ .$$

```
p <- c(.1, .25, .50, .75, .9)
odds <- p / (1-p)
logodds <- log(odds)
(odds.df <- data.frame(p, odds, logodds))

##      p  odds logodds
## 1 0.10 0.111    -2.2
## 2 0.25 0.333    -1.1
## 3 0.50 1.000     0.0
## 4 0.75 3.000     1.1
## 5 0.90 9.000     2.2
```

# Log odds




Log odds:

- Symmetric around $\pi = \frac{1}{2}$: $\text{logit}(\pi) = -\text{logit}(1-\pi)$
- Fairly linear in the middle, $0.2 \leq \pi \leq 0.8$
- The logit transformation of probability provides the basis for logistic regression





# Odds ratio

For two groups, with probabilities of success $\pi_1, \pi_2$, the ***odds ratio***, $\theta$, is the ratio of the odds for the two groups:

$$\text{odds ratio} \equiv \theta = \frac{\text{odds}_1}{\text{odds}_2} = \frac{\pi_1/(1-\pi_1)}{\pi_2/(1-\pi_2)} = \frac{\pi_{11}/\pi_{12}}{\pi_{21}/\pi_{22}} = \frac{\pi_{11}\pi_{22}}{\pi_{12}\pi_{21}}$$

- $\theta = 1 \implies \pi_1 = \pi_2 \implies$ independence, no association
- Same value when we interchange rows and columns (transpose)
- Sample value, $\widehat{\theta}$ obtained using $n_{ij}$.

More convenient to characterize association by ***log odds ratio***, $\psi = \log(\theta)$ which is symmetric about 0:

$$\text{log odds ratio} \equiv \psi = \log(\theta) = \log\left[\frac{\pi_1/(1-\pi_1)}{\pi_2/(1-\pi_2)}\right] = \text{logit}(\pi_1) - \text{logit}(\pi_2) \ .$$





# Odds ratio: Inference and hypothesis tests

Symmetry of the distribution of the log odds ratio $\psi = \log(\theta)$ makes it more convenient to carry out tests independence as tests of $H_0 : \psi = \log(\theta) = 0$ rather than $H_0 : \theta = 1$

- $z = \log(\widehat{\theta})/SE(\log(\theta)) \sim N(0,1)$

`oddsratio()` in vcd uses $\log(\theta)$ by default

```
oddsratio(UCB)

## log odds ratios for Gender and Admit
##
## [1] 0.61035

summary(oddsratio(UCB))

##
## z test of coefficients:
##
##                                Estimate Std. Error z value Pr(>|
## Male:Female/Admitted:Rejected   0.6104     0.0639    9.55   <2e
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```





# Odds ratio: Inference and hypothesis tests

Or, in terms of odds ratios directly:

```
oddsratio(UCB, log=FALSE)

##  odds ratios for Gender and Admit
##
## [1] 1.8411

confint(oddsratio(UCB, log=FALSE))

##                                  2.5 % 97.5 %
## Male:Female/Admitted:Rejected 1.6244 2.0867
```

Males 1.84 times as likely to be admitted, with 95% CI of $1.62 \leq \theta \leq 2.09$.
`chisq.test()` just tests association:

```
chisq.test(UCB)

##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  UCB
## X-squared = 91.6, df = 1, p-value <2e-16
```

# Small sample size

- Pearson $\chi^2$ and LR $G^2$ tests are valid only when most expected frequencies $\geq 5$
- Otherwise, use Fisher's exact test or simulated *p*-values

**Example**

Is there a relation between high cholesterol in diet and heart disease?

```
fat <- matrix(c(6, 2, 4, 11), 2, 2)
dimnames(fat) <- list(cholesterol=c("low", "high"),
                      disease=c("no", "yes"))
fat

##             disease
## cholesterol no yes
##        low   6   4
##        high  2  11
```





# Small sample size

The standard Pearson $\chi^2$ is not significant:

```
chisq.test(fat)

##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  fat
## X-squared = 3.19, df = 1, p-value = 0.074
```

We get a warning message:

```
In chisq.test(fat) : Chi-squared approximation may be incorrect
```





# Small sample size

Using Monte Carlo simulation to calculate the *p*-value:

```
chisq.test(fat, simulate=TRUE)

##
##  Pearson's Chi-squared test with simulated p-value (based on
##  2000 replicates)
##
## data:  fat
## X-squared = 4.96, df = NA, p-value = 0.036
```

This method repeatedly samples cell frequencies from tables with the same margins, and calculates a $\chi^2$ for each.
The $\chi^2$ test is now significant





# Small sample size

Fisher's exact test: calculates probability for all $2 \times 2$ tables as or more extreme than the data.

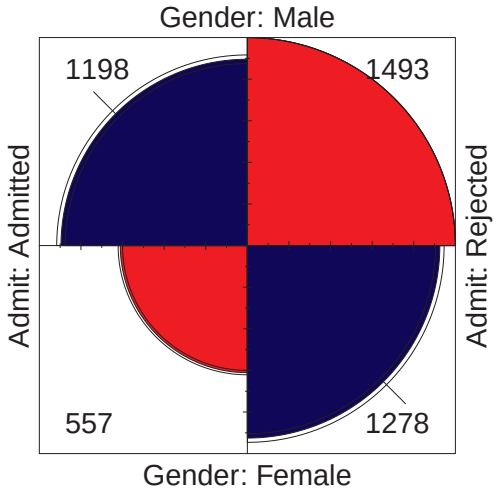
```
fisher.test(fat)

##
##  Fisher's Exact Test for Count Data
##
## data:  fat
## p-value = 0.039
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##    0.86774 105.56694
## sample estimates:
## odds ratio
##     7.4019
```

The *p*-value is similar to the result using simulation.

# Visualizing: Fourfold plots

```
fourfold(UCB, std="ind.max")   # maximum frequency
```




Friendly (1994a):

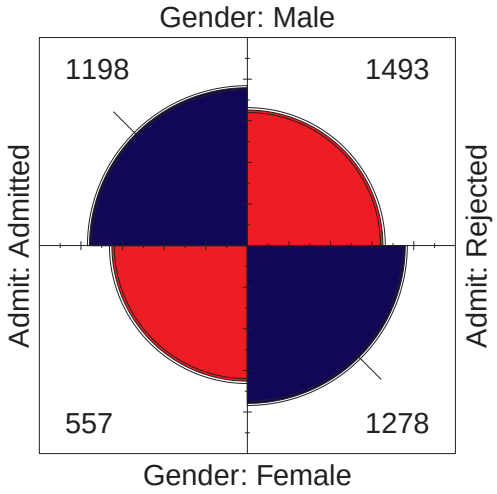
- Fourfold display: area $\sim$ frequency, $n_{ij}$
- Color: blue $(+)$, red$(-)$
- This version: Unstandardized
- Odds ratio: ratio of products of blue / red cells





# Visualizing: Fourfold plots

```
fourfold(UCB)     #standardize both margins
```




Better version:

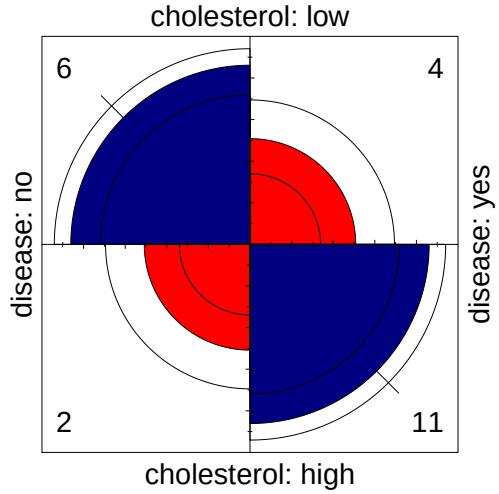
- Standardize to equal row, col margins
- Preserves the odds ratio
- Confidence bands: significance of odds ratio
- If don't overlap $\Longrightarrow$ $\theta \neq 1$





# Cholesterol data

```
fourfold(fat)
```








# Stratified $2 \times 2 \times k$ tables

The UC Berkeley data was collected for 6 graduate departments:

```
ftable(addmargins(UCBAdmissions, 3))

##                   Dept    A    B    C    D    E    F  Sum
## Admit    Gender
## Admitted Male          512  353  120  138   53   22 1198
##          Female         89   17  202  131   94   24  557
## Rejected Male          313  207  205  279  138  351 1493
##          Female         19    8  391  244  299  317 1278
```

**Questions:**

- Does the overall association between gender and admission apply in each department?
- Do men and women apply equally to all departments?
- Do departments differ in their rates of admission?

***Stratified analysis*** tests association between a main factor and a response within the levels of control variable(s)

# Stratified $2 \times 2 \times k$ tables

Odds ratios by department:

```
summary(oddsratio(UCBAdmissions))
```

```
##
## z test of coefficients:
##
##   Estimate Std. Error z value Pr(>|z|)
## A   -1.052      0.263   -4.00  6.2e-05 ***
## B   -0.220      0.438   -0.50     0.62
## C    0.125      0.144    0.87     0.39
## D   -0.082      0.150   -0.55     0.59
## E    0.200      0.200    1.00     0.32
## F   -0.189      0.305   -0.62     0.54
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Odds ratio only significant, $\log(\theta) \neq 0$ for department A
- For department A, men are only $\exp(-1.05) = .35$ times as likely to be admitted as women
- The overall analysis ignoring department is misleading: falsely assumes no associations of admission with department and gender with department.

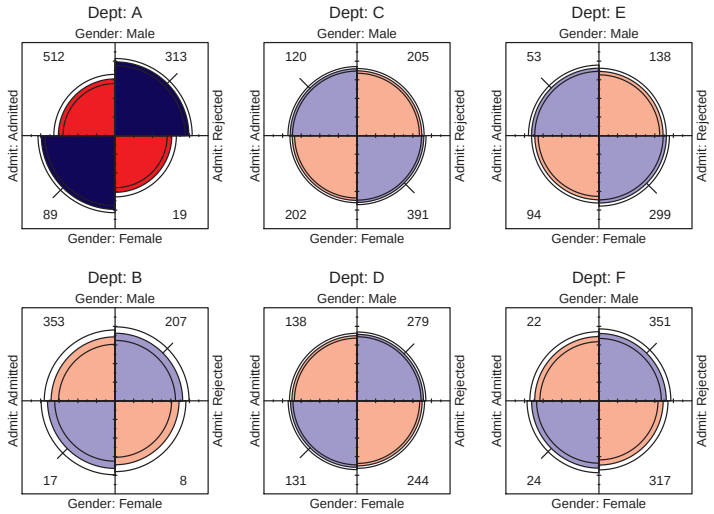




# Stratified $2 \times 2 \times k$ tables

Fourfold plots by department (intense shading where significant):

```
fourfold(UCBAdmissions)
```



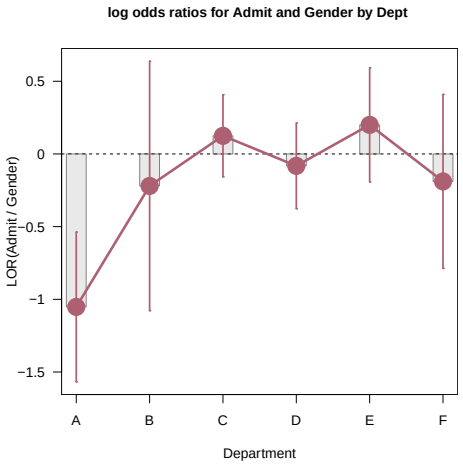





# Stratified $2 \times 2 \times k$ tables

Or plot odds ratios directly:

```
plot(oddsratio(UCBAdmissions), cex=1.5, xlab="Department")
```








# Stratified tables: Homogeneity of odds ratios

**Related questions:**

- Are the $k$ odds ratios all equal, $\theta_1 = \theta_2, \ldots, \theta_k$? (Woolf's test: `woolf_test()`)
- (This is equivalent to the hypothesis of no three-way association)
- *If* homogeneous, is the common odds ratio different from 1? (Mantel-Haenszel test: `mantelhaen.test()`)

```
woolf_test(UCBAdmissions)
```

```
##
##  Woolf-test on Homogeneity of Odds Ratios (no 3-Way assoc.)
##
## data:  UCBAdmissions
## X-squared = 17.9, df = 5, p-value = 0.0031
```

Odds ratios differ across departments, so no sense in testing their common value.

# Exegesis: What happened at UC Berkeley?

Why do the results *collapsed over* department disagree with the results *by* department?

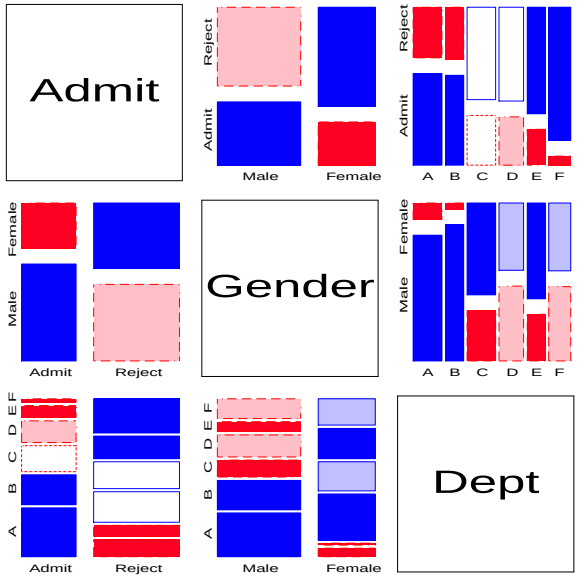
## Simpson's paradox

- Aggregate data are misleading because they falsely assume men and women apply *equally* in each field.
- But:
  - Large differences in admission rates across departments.
  - Men and women apply to these departments differentially.
  - Women applied in large numbers to departments with low admission rates.
- Other graphical methods can show these effects.
- (This ignores possibility of *structural bias* against women: differential funding of fields to which women are more likely to apply.)





Mosaic matrix shows all pairwise associations:








# $r \times c$ tables: Overall analysis

- **Overall tests** of association: `assocstats()`: Pearson chi-square and LR $G^2$
- **Strength** of association: $\phi$ coefficient, contingency coefficient (C), Cramer's V ($0 \leq V \leq 1$)

$$\phi^2 = \frac{\chi^2}{n}, \qquad C = \sqrt{\frac{\chi^2}{n+\chi^2}}, \qquad V = \sqrt{\frac{\chi^2/n}{\min(r-1, c-1)}}$$

- For a $2 \times 2$ table, $V = \phi$.
- (If the data table was collapsed from a 3+ way table, the two-way analysis may be misleading)

```
assocstats(HEC)

##                     X^2 df P(> X^2)
## Likelihood Ratio 146.44  9        0
## Pearson          138.29  9        0
##
## Phi-Coefficient   : NA
## Contingency Coeff.: 0.435
## Cramer's V        : 0.279
```





# $r \times c$ tables: Overall analysis and residuals

- The Pearson $X^2$ and LR $G^2$ statistics have the following forms:

$$X^2 = \sum_{ij} \frac{(n_{ij} - \widehat{m}_{ij})^2}{\widehat{m}_{ij}} \qquad G^2 = \sum_{ij} n_{ij} \log\left(\frac{n_{ij}}{\widehat{m}_{ij}}\right)$$

- Expected (fitted) frequencies under independence: $\widehat{m}_{ij} = n_{i+} n_{+j} / n_{++}$
- Each of these is a sum-of-squares of corresponding residuals
- Degrees of freedom: $df = (r-1)(c-1)$ — # independent residuals

Can get residuals from `loglm()` in MASS:

```
library(MASS)
mod <- loglm(~Hair + Eye, data=HEC, fitted=TRUE)
mod

## Call:
## loglm(formula = ~Hair + Eye, data = HEC, fitted = TRUE)
##
## Statistics:
##                     X^2 df P(> X^2)
## Likelihood Ratio 146.44  9        0
## Pearson          138.29  9        0
```

Extract residuals:

```
res.P  <- residuals(mod, type="pearson")
res.LR <- residuals(mod, type="deviance")  # default
res.P
```

```
##        Hair
## Eye      Black  Brown    Red  Blond
##   Brown  4.398  1.233 -0.075 -5.851
##   Blue  -3.069 -1.949 -1.730  7.050
##   Hazel -0.477  1.353  0.852 -2.228
##   Green -1.954 -0.345  2.283  0.613
```

Demonstrate SSQ property:

```
unlist(mod[c("pearson", "deviance", "df")])
```

```
##  pearson deviance       df
##   138.29   146.44     9.00
```

```
sum(res.P^2)       # Pearson chisq
```

```
## [1] 138.29
```

```
sum(res.LR^2)      # LR chisq
```

```
## [1] 146.44
```

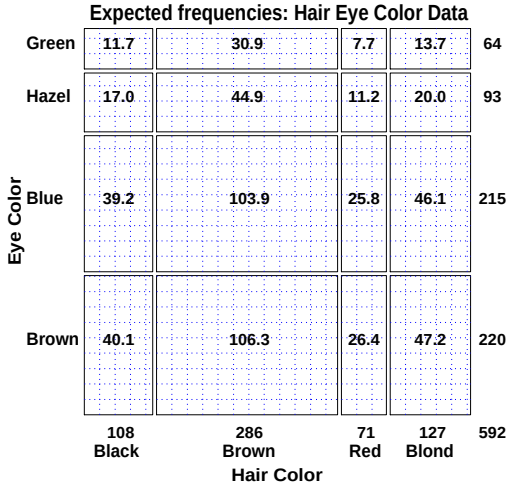




# Visualizing association: Sieve diagrams

Visual metaphor: **count** $\sim$ **area**

- When row/col variables are independent, $n_{ij} \approx \hat{m}_{ij} \sim n_{i+} n_{+j}$
- $\Rightarrow$ each cell can be represented as a rectangle, with area = height $\times$ width $\sim$ frequency, $n_{ij}$ (under independence)



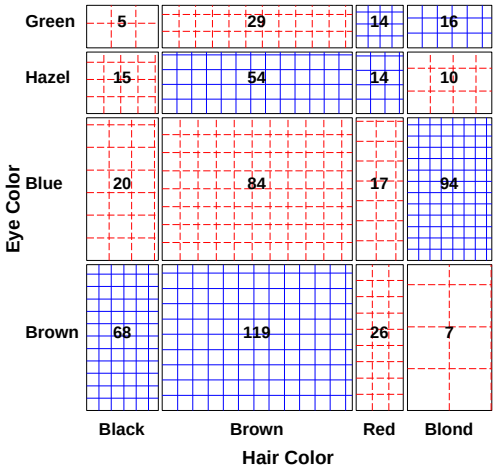

- This display shows expected frequencies, assuming independence, as # boxes within each cell
- The boxes are all of the same size (equal density)
- Real sieve diagrams use # boxes = observed frequencies, $n_{ij}$





# Sieve diagrams

- Height, width $\sim$ marginal frequencies, $n_{i+}$, $n_{+j}$
- $\Longrightarrow$ Area $\sim$ expected frequency, $\hat{m}_{ij} \sim n_{i+} n_{+j}$
- Shading $\sim$ observed frequency, $n_{ij}$, color: sign$(n_{ij} - \hat{m}_{ij})$.
- $\Longrightarrow$ Independence: Shown when density of shading is uniform.

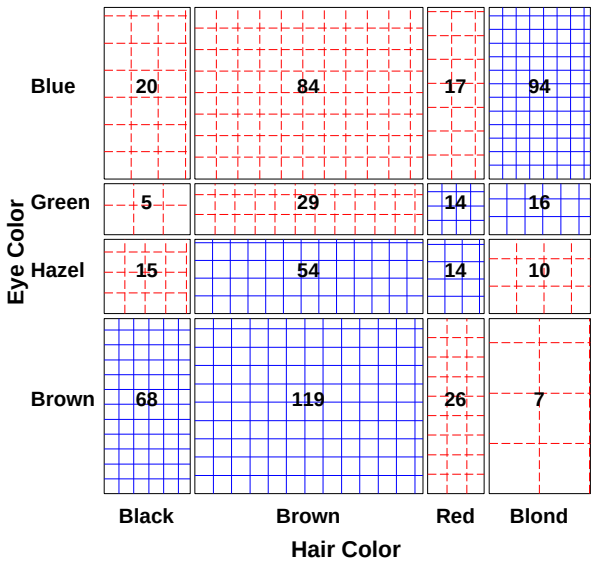






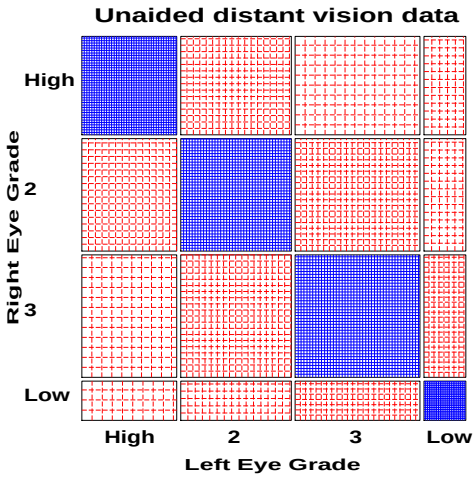

# Sieve diagrams

Effect ordering: Reorder rows/cols to make the pattern coherent



# Sieve diagrams

Vision classification data for 7477 women: visual acuity in left, right eyes




- The obvious association is apparent on the diagonal cells
- A more subtle pattern appears on the off-diagonal cells
- Analysis methods for square tables (later) allow testing hypotheses of symmetry, quasi-symmetry, etc.





# Ordinal factors

The Pearson $\chi^2$ and LR $G^2$ give tests of general association, with $(r-1)(c-1)$ df.

## More powerful CMH tests

- When either the row or column levels are ordered, more specific CMH (Cochran–Mantel–Haentzel) tests which take order into account have greater power to detect ordered relations.
- This is similar to testing for linear trends in ANOVA
- Essentially, these assign scores to the categories, and test for differences in row / column means, or non-zero correlation.





# CMH tests for ordinal variables

Three types of CMH tests:

## Non-zero correlation

- Use when *both* row and column variables are ordinal.
- CMH $\chi^2 = (N-1)r^2$, assigning scores (1, 2, 3, ...)
- most powerful for *linear* association

## Row/Col Mean Scores Differ

- Use when only *one* variable is ordinal
- Analogous to the Kruskal-Wallis non-parametric test (ANOVA on rank scores)

## General Association

- Use when *both* row and column variables are nominal.
- Similar to overall Pearson $\chi^2$ and Likelihood Ratio $G^2$.





# Sample CMH Profiles

***Only general association:***

| | b1 | b2 | b3 | b4 | b5 | Total | Mean |
|---|---|---|---|---|---|---|---|
| a1 | 0 | 15 | 25 | 15 | 0 | 55 | 3.0 |
| a2 | 5 | 20 | 5 | 20 | 5 | 55 | 3.0 |
| a3 | 20 | 5 | 5 | 5 | 20 | 55 | 3.0 |
| Total | 25 | 40 | 35 | 40 | 25 | 165 | |

Output:

Cochran-Mantel-Haenszel Statistics (Based on Table Scores)

| Statistic | Alternative Hypothesis | DF | Value | Prob |
|---|---|---|---|---|
| 1 | Nonzero Correlation | 1 | 0.000 | 1.000 |
| 2 | Row Mean Scores Differ | 2 | 0.000 | 1.000 |
| 3 | General Association | 8 | 91.797 | **0.000** |

# Sample CMH Profiles

***Linear Association:***

| | b1 | b2 | b3 | b4 | b5 | Total | Mean |
|---|---|---|---|---|---|---|---|
| a1 | 2 | 5 | 8 | 8 | 8 | 31 | 3.48 |
| a2 | 2 | 8 | 8 | 8 | 5 | 31 | 3.19 |
| a3 | 5 | 8 | 8 | 8 | 2 | 31 | 2.81 |
| a4 | 8 | 8 | 8 | 5 | 2 | 31 | 2.52 |
| Total | 17 | 29 | 32 | 29 | 17 | 124 | |

Output:

Cochran-Mantel-Haenszel Statistics (Based on Table Scores)

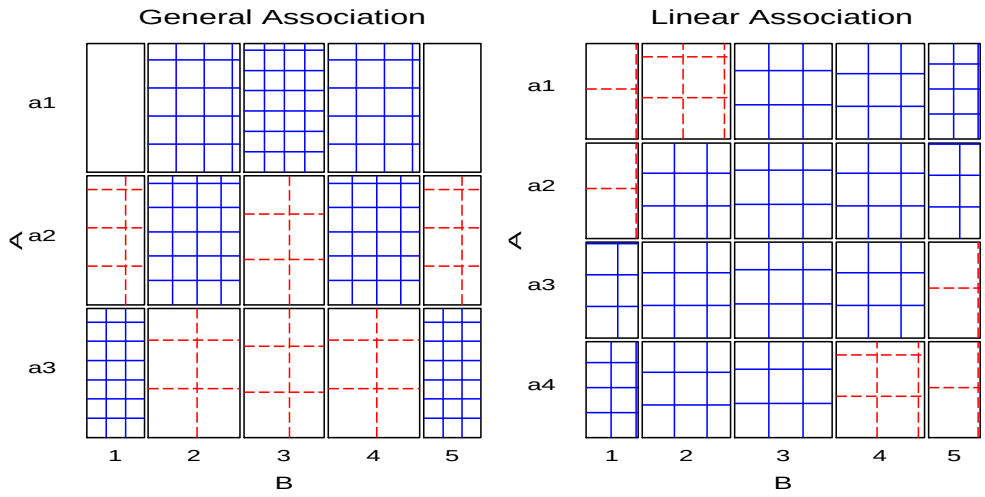
| Statistic | Alternative Hypothesis | DF | Value | Prob |
|---|---|---|---|---|
| 1 | Nonzero Correlation | 1 | 10.639 | **0.001** |
| 2 | Row Mean Scores Differ | 3 | 10.676 | **0.014** |
| 3 | General Association | 12 | 13.400 | 0.341 |





# Sample CMH Profiles

***Visualizing Association:*** Sieve diagrams








# Example: Mental health data

- In R, these tests are provided by `CMHtest()` in the vcdExtra package
- For the mental health data, both factors are ordinal
- All tests are significant
- The nonzero correlation test, with 1 df, has the smallest *p*-value, largest $\chi^2/df$

```
mental.tab <- xtabs(Freq ~ ses + mental, data=Mental)
CMHtest(mental.tab)

## Cochran-Mantel-Haenszel Statistics for ses by mental
##
##                   AltHypothesis Chisq Df     Prob
## cor         Nonzero correlation  37.2  1 1.09e-09
## rmeans   Row mean scores differ  40.3  5 1.30e-07
## cmeans   Col mean scores differ  40.7  3 7.70e-09
## general     General association  46.0 15 5.40e-05
```





# Observer Agreement

- **Inter-observer agreement** often used as to assess reliability of a subjective classification or assessment procedure
  - → square table, Rater 1 x Rater 2
  - Levels: diagnostic categories (normal, mildly impaired, severely impaired)
- **Agreement vs. Association:** Ratings can be strongly associated without strong agreement
- **Marginal homogeneity:** Different frequencies of category use by raters affects measures of agreement
- **Measures of Agreement:**
  - Intraclass correlation: ANOVA framework— multiple raters!
  - Cohen's $\kappa$: compares the observed agreement, $P_o = \sum p_{ii}$, to agreement expected by chance if the two observer's ratings were independent, $P_c = \sum p_{i+}\, p_{+i}$.

$$\kappa = \frac{P_o - P_c}{1 - P_c}$$

# Cohen's $\kappa$

**Properties of Cohen's $\kappa$:**

- perfect agreement: $\kappa = 1$
- minimum $\kappa$ may be $< 0$; lower bound depends on marginal totals
- Unweighted $\kappa$: counts only diagonal cells (same category assigned by both observers).
- Weighted $\kappa$: allows partial credit for near agreement. (Makes sense only when the categories are *ordered*.)

Weights:

- Cicchetti-Alison (inverse integer spacing)
- Fleiss-Cohen (inverse square spacing)

```
      Integer Weights                 Fleiss-Cohen Weights
  1     2/3     1/3       0         1     8/9     5/9       0
2/3       1     2/3     1/3       8/9       1     8/9     5/9
1/3     2/3       1     2/3       5/9     8/9       1     8/9
  0     1/3     2/3       1         0     5/9     8/9       1
```





# Cohen's $\kappa$: Example

The table below summarizes responses of 91 married couples to a questionnaire item,

> *Sex is fun for me and my partner (a) Never or occasionally, (b) fairly often, (c) very often, (d) almost always.*

| Husband's Rating | Wife's Rating: Never fun | Fairly often | Very Often | Almost always | SUM |
|---|---|---|---|---|---|
| Never fun | **7** | 7 | 2 | 3 | 19 |
| Fairly often | 2 | **8** | 3 | 7 | 20 |
| Very often | 1 | 5 | **4** | 9 | 19 |
| Almost always | 2 | 8 | 9 | **14** | 33 |
| SUM | 12 | 28 | 18 | 33 | 91 |





# Cohen's $\kappa$: Example

The `Kappa()` function in vcd calculates unweighted and weighted $\kappa$, using equal-spacing weights by default.

```
data(SexualFun, package="vcd")
Kappa(SexualFun)

##              value    ASE    z Pr(>|z|)
## Unweighted 0.129 0.0686 1.89  0.05939
## Weighted   0.237 0.0783 3.03  0.00244

Kappa(SexualFun, weights="Fleiss-Cohen")

##              value    ASE    z Pr(>|z|)
## Unweighted 0.129 0.0686 1.89 0.059387
## Weighted   0.332 0.0973 3.41 0.000643
```

Unweighted $\kappa$ is not significant, but both weighted versions are.
You can obtain confidence intervals with the `confint()` method





# Observer agreement: Multiple strata

When the individuals rated fall into multiple groups, one can test for:

- Agreement within each group
- Overall agreement (controlling for group)
- Homogeneity: Equal agreement across groups

**Example: Diagnostic Classification of MS patients**

Patients in Winnipeg and New Orleans were each classified by a neurologist in each city

| NO rater: | Winnipeg patients: Cert | Prob | Pos | Doubt | New Orleans patients: Cert | Prob | Pos | Doubt |
|---|---|---|---|---|---|---|---|---|
| Winnipeg rater: | | | | | | | | |
| Certain MS | 38 | 5 | 0 | 1 | 5 | 3 | 0 | 0 |
| Probable | 33 | 11 | 3 | 0 | 3 | 11 | 4 | 0 |
| Possible | 10 | 14 | 5 | 6 | 2 | 13 | 3 | 4 |
| Doubtful MS | 3 | 7 | 3 | 10 | 1 | 2 | 4 | 14 |

# Observer agreement: Multiple strata

Here, simply assess agreement between the two raters in each stratum separately

```
data(MSPatients, package="vcd")
Kappa(MSPatients[,,1])

##              value    ASE    z Pr(>|z|)
## Unweighted 0.208 0.0505 4.12 3.77e-05
## Weighted   0.380 0.0517 7.35 1.99e-13

Kappa(MSPatients[,,2])

##              value    ASE    z Pr(>|z|)
## Unweighted 0.297 0.0785 3.78 1.59e-04
## Weighted   0.477 0.0730 6.54 6.35e-11
```

The irr package (inter-rater reliability) provides ICC and other measures, and handles the case of $k > 2$ raters.





# Bangdiwala's Observer Agreement Chart

The observer agreement chart Bangdiwala (1987) provides

- a simple graphic representation of the strength of agreement, and
- a measure of strength of agreement with an intuitive interpretation.

**Construction:**

- $n \times n$ square, $n$=total sample size
- Black squares, each of size $n_{ii} \times n_{ii} \rightarrow$ observed agreement
- Positioned within larger rectangles, each of size $n_{i+} \times n_{+i} \rightarrow$ maximum possible agreement
- $\Rightarrow$ visual impression of the strength of agreement is $B$:

$$B = \frac{\text{area of dark squares}}{\text{area of rectangles}} = \frac{\sum_i^k n_{ii}^2}{\sum_i^k n_{i+}\, n_{+i}}$$

- $\Rightarrow$ Perfect agreement: $B = 1$, all rectangles are completely filled.





# Weighted Agreement Chart: Partial agreement

Partial agreement: include weighted contribution from off-diagonal cells, $b$ steps from the main diagonal, using weights $1 > w_1 > w_2 > \cdots$.

$$\begin{array}{ccccc} & & n_{i-b,i} & & \\ & & \vdots & & \\ n_{i,i-b} & \cdots & n_{i,i} & \cdots & n_{i,i+b} \\ & & \vdots & & \\ & & n_{i-b,i} & & \end{array} \qquad \begin{array}{ccccc} & & w_2 & & \\ & & w_1 & & \\ w_2 & w_1 & 1 & w_1 & w_2 \\ & & w_1 & & \\ & & w_2 & & \end{array}$$

- Add shaded rectangles, size $\sim$ sum of frequencies, $A_{bi}$, within $b$ steps of main diagonal
- $\Rightarrow$ weighted measure of agreement,

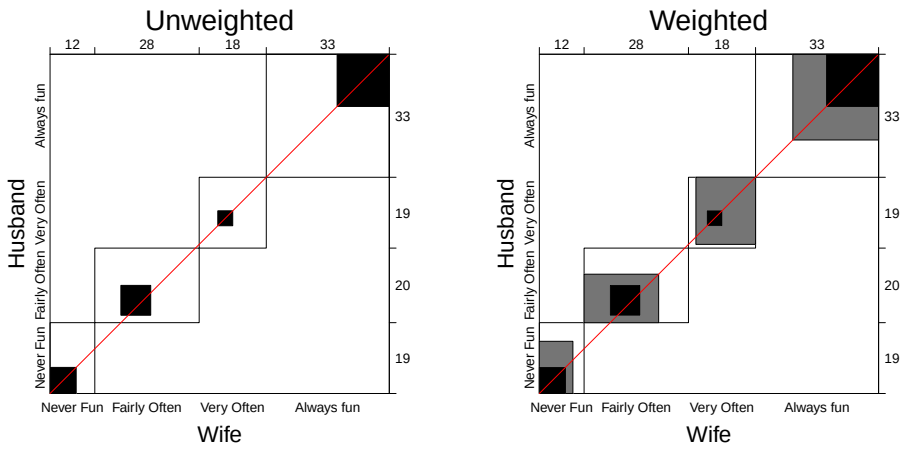
$$B^w = \frac{\text{weighted sum of agreement}}{\text{area of rectangles}} = 1 - \frac{\sum_i^k [n_{i+}n_{+i} - n_{ii}^2 - \sum_{b=1}^q w_b A_{bi}]}{\sum_i^k n_{i+}\, n_{+i}}$$





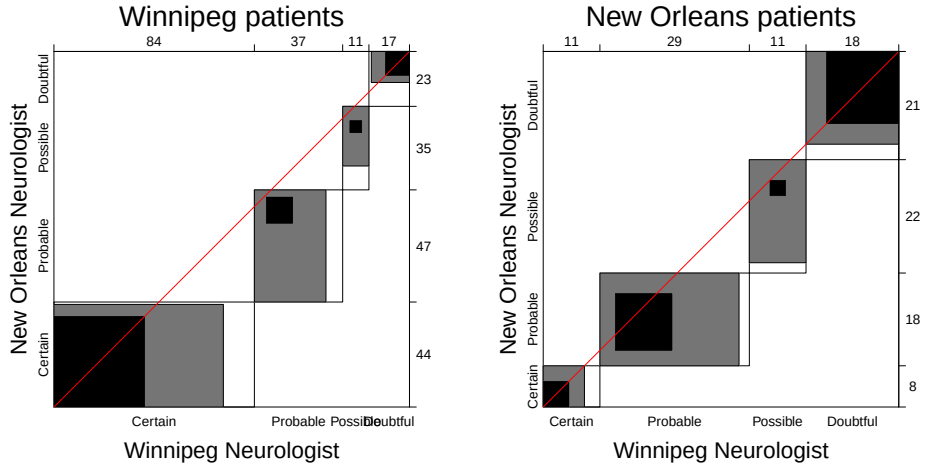
Husbands and wives: $B = 0.146$, $B^w = 0.498$

```
agreementplot(SexualFun, main="Unweighted", weights=1)
agreementplot(SexualFun, main="Weighted")
```



# Marginal homogeneity and Observer bias

- Different raters may consistently use higher or lower response categories
- Test– marginal homogeneity: $H_0 : n_{i+} = n_{+i}$
- Shows as departures of the squares from the diagonal line




- Winnipeg neurologist tends to use more severe categories





# Looking ahead

## Loglinear models

Loglinear models generalize the Pearson $\chi^2$ and LR $G^2$ tests of association to 3-way and larger tables.

- Allows a range of models from mutual independence ($[A][B][C]$) to the saturated model ($[ABC]$)
- Intermediate models address questions of conditional independence, controlling for some factors
- Can test associations in 2-way, 3-way terms analogously to tests of interactions in ANOVA

## Example: UC Berkeley data

- Mutual independence: [Admit] [Gender] [Dept]
- Joint independence: [Admit] [Gender*Dept]
- Conditional independence: [Admit*Dept] [Admit*Gender]: A specific test for absence of gender bias, controlling for department



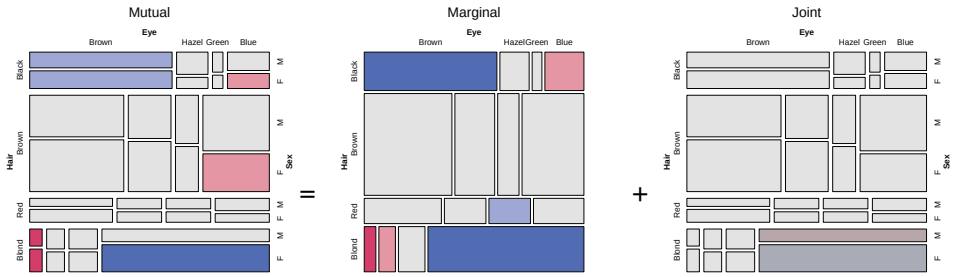


# Looking ahead

## Mosaic displays

Mosaic plots provide visualizations of associations in 2+ way tables.

- Tiles: $\sim$ frequency
- Fit loglinear model
- Shading: $\sim$ residuals




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

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

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

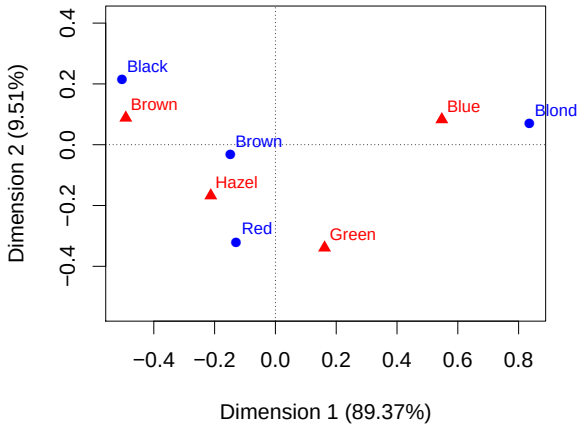




# Looking ahead

## Correspondence analysis

- Account for max. % of $\chi^2$ in few (2-3) dimensions
- Find scores for row and column categories
- Plot of row and column scores shows associations



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