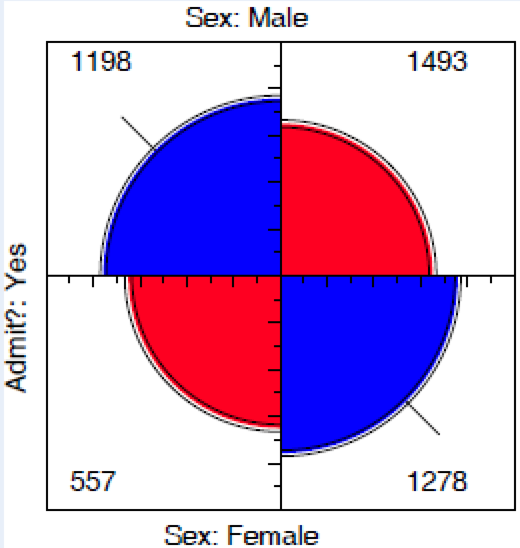

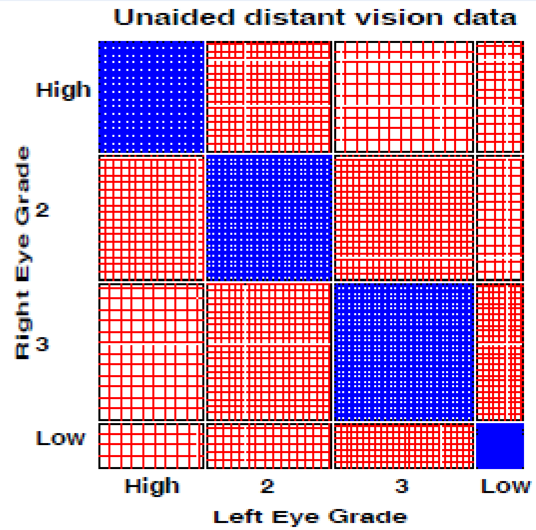

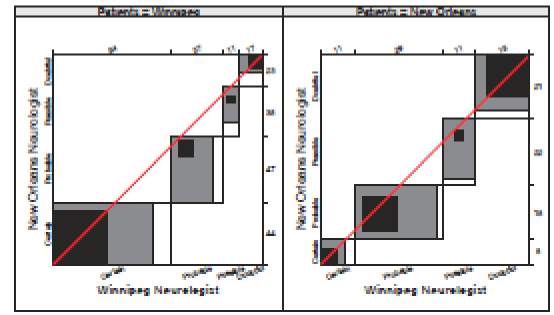

Two-way tables
Independence & association

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Psych 6136

http://friendly.github.io/psy6136

Two-way tables: Overview

Two-way frequency tables are a convenient way to represent a dataset cross-classified by two discrete variables, A & B

Special cases:

- 2×2 tables: two binary factors (e.g., gender, admitted?, died?, ...)
- $2 \times 2 \times k$ tables: a collection of 2×2s, 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: 2×2— odds ratio; $r \times c$— Pearson χ^2, LR G^2
- How to understand the pattern or nature of association?

Methods

- The methods discussed this week are generally simple non-parametric or randomization methods
- There is no underlying formal model with parameters
- Hypothesis tests based on some test statistic:
  - Pearson X^2
  - Odds ratio
  - Cohen's κ
- p-values, confidence intervals based on
  - Large sample theory: $X^2 \sim \chi^2$ as $N \rightarrow \infty$
  - Permutation or simulation distributions

2 × 2 Example: Berkeley admissions

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

odds ratio (θ) = 1.84

Males were nearly twice as likely to be admitted

- Is there an association between gender & admission?
- If so, is this evidence for gender bias?
- How to measure strength of association?
- How to test for significance?
- How to visualize?

UCBAdmissions data

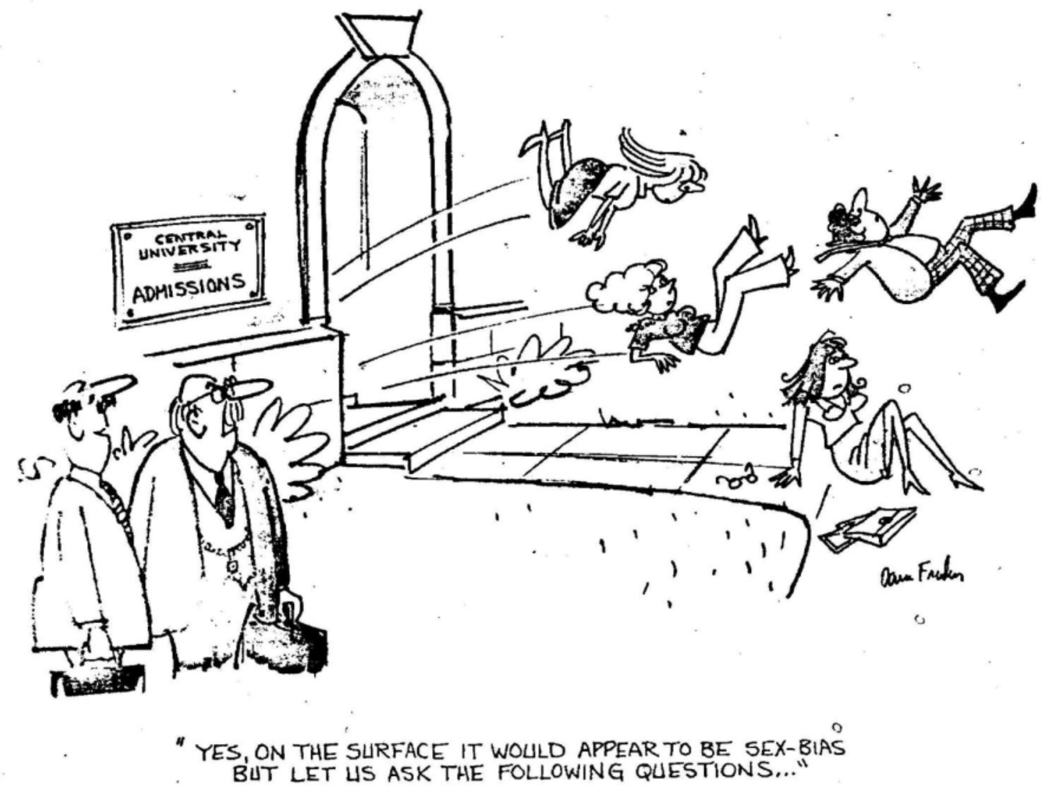
In R, the data is contained in UCBAdmissions, a 2 x 2 x 6 table for 6 deparatments. We collapse over department

```
> data(UCBAdmissions)
> UCB <- margin.table(UCBAdmissions, 2:1)
> UCB
        Admit
Gender   Admitted Rejected
  Male       1198     1493
  Female      557     1278
```

$odds_M = 1198 / 1493 = 0.802$
$odds_F = 557 / 1278 = 0.437$

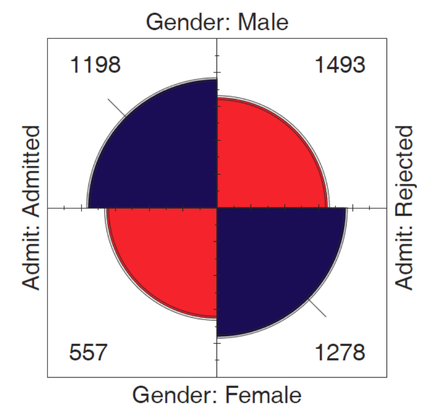
Association in 2 x 2 table can be measured by the odds ratio (θ): odds of admission for males vs. females

```
> oddsratio(UCB, log=FALSE)
 odds ratios for Gender and Admit

[1] 1.84
> confint(oddsratio(UCB, log=FALSE))
                              2.5 % 97.5 %
Male:Female/Admitted:Rejected  1.62   2.09
```



Questions:

- How to analyze these results? What tests for odds ratio?
- How to visualize & interpret?
- Does it matter that we collapsed over Department?



r × c Example: Hair color, eye color

Data from 592 students in a 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

- Is there an association between hair color and eye color?
- How to measure strength of association?
- How to test for significance?
- How to visualize?
- How to understand the pattern (nature) of association?

HairEyeColor data

In R, the dataset is HairEyeColor, a 4 x 4 x 2 table: Hair x Eye x Sex.
For now, collapse over sex.

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

```
> chisq.test(HEC)

        Pearson's Chi-squared test

data:  HEC
X-squared = 138, df = 9, p-value <2e-16
```

Association can be tested by the standard Pearson χ^2 test. Details later

```
> MASS::loglm(~Hair + Eye, data=HEC)

Statistics:
                 X^2 df P(> X^2)
Likelihood Ratio 146  9        0
Pearson          138  9        0
```

Or, as a loglinear model for independence
Formula: $\sim A + B \;=\; A \perp B$

HairEyeColor data

vcd::assocstats() collects tests and measures in a convenient summary

```
> 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
```

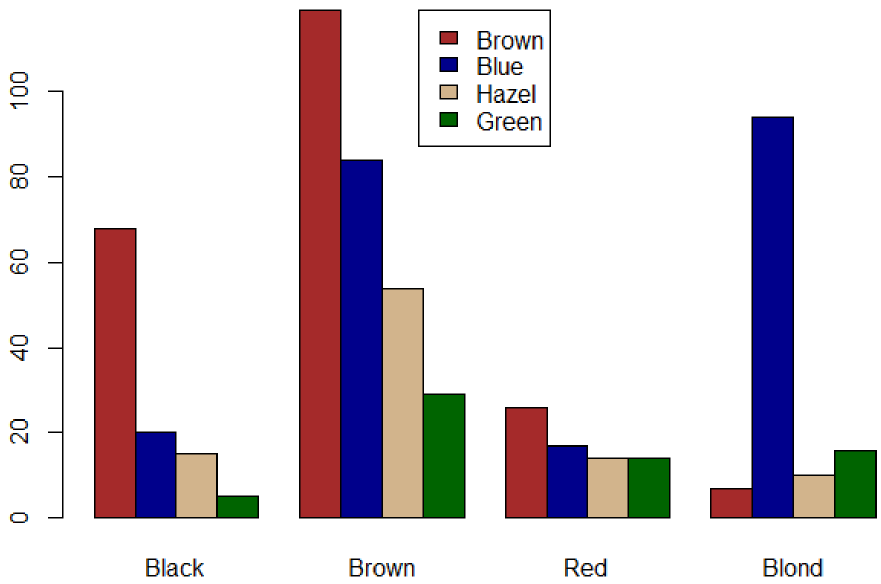
For 3+ way tables, it gives the results for the strata defined by all last dimensions

```
> assocstats(HairEyeColor)
$`Sex:Male`
                    X^2 df  P(> X^2)
Likelihood Ratio 44.445  9 1.168e-06
Pearson          41.280  9 4.447e-06

Phi-Coefficient   : NA
Contingency Coeff.: 0.359
Cramer's V        : 0.222
```

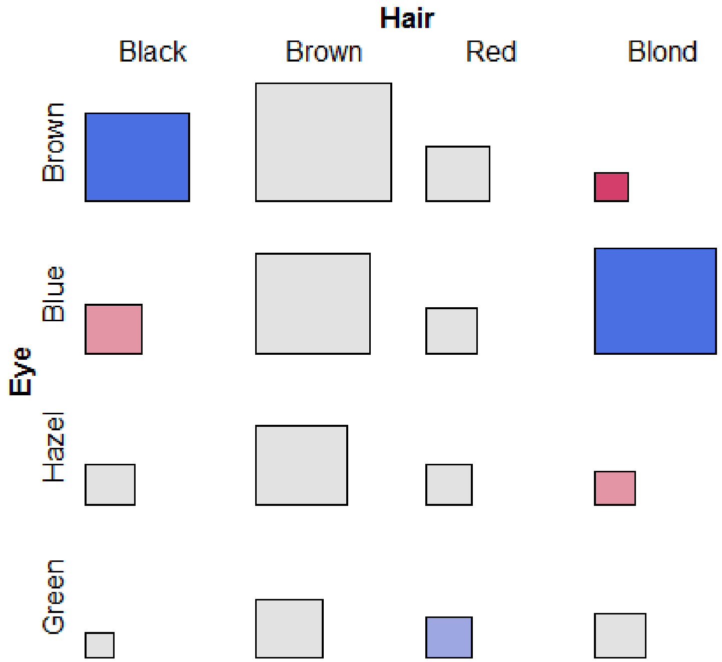
```
$`Sex:Female`
                    X^2 df P(> X^2)
Likelihood Ratio 112.23  9        0
Pearson          106.66  9        0

Phi-Coefficient   : NA
Contingency Coeff.: 0.504
Cramer's V        : 0.337
```

Simple plots for r × c tables

```
barplot(HEC, beside=TRUE, … )
```




```
tile(HEC, shade=TRUE)
```



Ordered tables

r x c table with ordered categories: Mental health and Parents’ SES categories

Table: Mental impairment and parents’ SES

	Mental impairment			
SES	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 a predictor
- How to measure strength of association?
- How to understand the pattern of association?
- How to take ordinal nature of variables into account?

Mental data: Association

The data is contained in `vcdExtra::Mental`, 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 2 2 2 3 ...
 $ mental: Ord.factor w/ 4 levels "Well"<"Mild"<..: 1 2 3 4 1 2 3 4 1 2 ...
 $ Freq  : int  64 94 58 46 57 94 54 40 57 105 ...
```

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 = 5e-05
```

Mental data: Ordinal tests

For ordinal factors, more powerful (focused) tests are available with Cochran-Mantel-Haenszel tests in **`vcdExtra::CMHtest()`**

```
> 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
```

both ordinal
cols ordinal
rows ordinal
neither

$\chi 2$ / df shows why ordered tests are more powerful

```
> xx <- CMHtest(mental.tab)
> xx$table[,"Chisq"] / xx$table[,"Df"]
    cor  rmeans  cmeans general
  37.16    8.06   13.56    3.06
```

Table notation

Row	Column 1	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: π_{ij}; also use $\pi_1 = \pi_{1+}$ and $\pi_2 = \pi_{2+}$
  - Population marginal probabilities: π_{i+} (rows), π_{+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

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

- Joint cell probabilities are the product of the marginal probabilities

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

For 2 x 2 tables, this gives rise to tests and measures based on:

- Difference in row/col marginal probabilities: Test $H_0 : \pi_1 = \pi 2$
- Odds ratio, $\hat{\theta} = (n_{11} / n_{12}) / (n_{21} / n_{22})$. Test $H_0 : \theta = 1$
- Standard χ2 test is for largish n
- Small samples: Fisher's exact test, or simulation / permutation tests

Independence: Example

A contrived example, where I generate cell frequencies as the product of row and column marginal totals: $n_{ij} = n_{i+} \times n_{+j}$

```
> 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
```

Outer product: `outer(r,c)` = `r` × `c`

Independence: Example

- The row proportions of party are the same for each educ group
- The col proportions of educ are the same for each party

```
> prop.table(table, 1)
     NDP Liberal Cons
Low  0.2     0.5  0.3
Med  0.2     0.5  0.3
High 0.2     0.5  0.3
```

```
> prop.table(table, 2)
     NDP  Liberal Cons
Low  0.25    0.25 0.25
Med  0.50    0.50 0.50
High 0.25    0.25 0.25
```

So, the X^2 is exactly zero, and measures of strength are zero

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

Phi-Coefficient   : NA
Contingency Coeff.: 0
Cramer's V        : 0
```

Independence: Arthritis data

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

- $\rightarrow$ row proportions are the same for Treated and Placebo
- $\rightarrow$ cell frequencies $\sim$ row total $\times$ 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
```

But, more people given the Placebo show no improvement; more people Treated show marked improvement

Independence: Arthritis data

If `Treatment` and `Improved` were independent, frequencies ~ row x col margins

```
> row.totals <- margin.table(arth.tab, 1)
> col.totals <- margin.table(arth.tab, 2)
> round(outer(row.totals, col.totals)/ sum(arth.tab), 0)
         Improved
Treatment None Some Marked
  Placebo   22    7     14
  Treated   20    7     14
```

These are the expected frequencies, under independence; but for the data:

```
> chisq.test(arth.tab)

        Pearson's Chi-squared test

data:  arth.tab
X-squared = 13.1, df = 2, p-value = 0.0015
```

Pearson χ^2

$$\chi^2_{(r-1)\times(c-1)} = \sum_{i,j} \frac{(O_{ij} - E_{ij})^2}{E_{ij}} = \sum d_{ij}^2$$

Sampling models: Poisson, Binomial, Multinomial

Subtle distinctions arise concerning whether the row and/or margins are fixed by 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 dist^n, 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
- Makes a difference in how hypothesis tests are justified & explained
- Happily, for most inferential methods, ≈ same results are obtained under the three sampling models

Q: what is an appropriate sampling model for the UCB admissions data? For hair-eye color? For the mental impairment data?

Odds and odds ratios

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

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

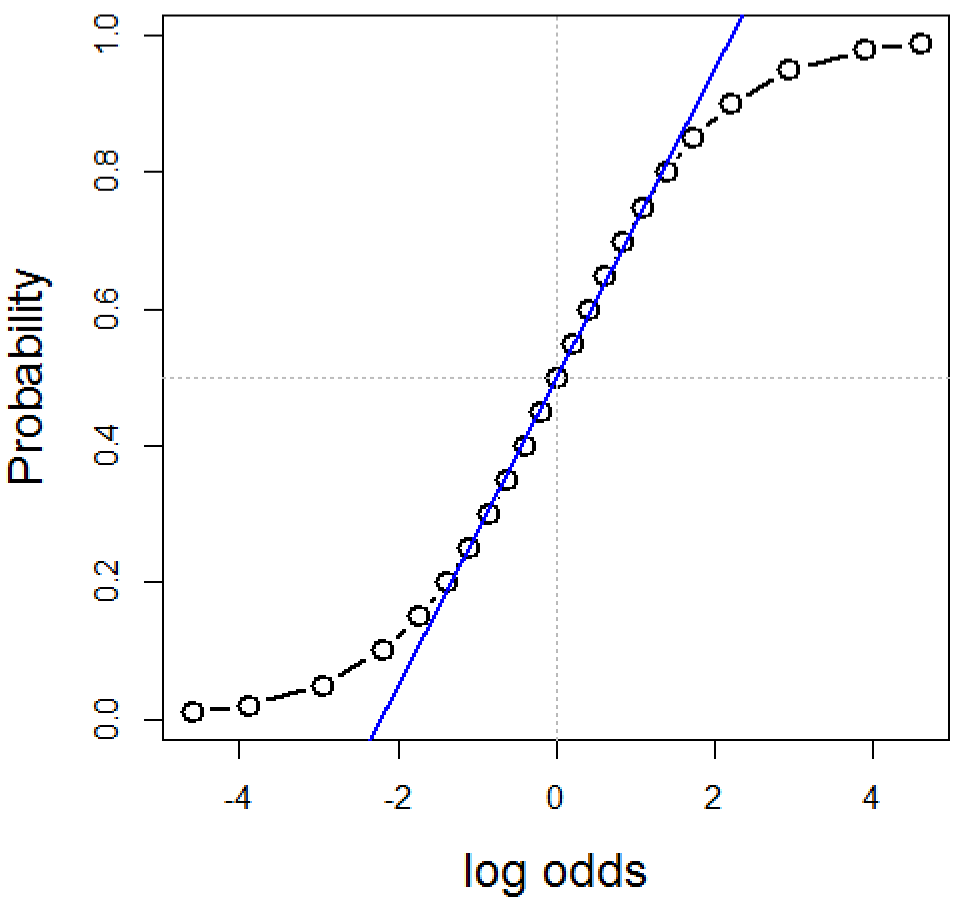
- Odds vary multiplicatively around 1 ("even odds", $\pi = \frac{1}{2}$)
- Taking logs, the log(odds), or ***logit*** varies symmetrically around 0,

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

```
> p <- c( 0.05, .1, .25, .50, .75, .9, .95)
> odds <- p / (1-p)
> logodds <- log(odds)
> (odds.df <- data.frame(p, odds, logodds))
     p    odds logodds
1 0.05  0.0526   -2.94
2 0.10  0.1111   -2.20
3 0.25  0.3333   -1.10
4 0.50  1.0000    0.00
5 0.75  3.0000    1.10
6 0.90  9.0000    2.20
7 0.95 19.0000    2.94
```

Log odds

```
plot(logodds, p, type='b', xlab="log odds", ylab="Probability", …)
abline(lm(p ~ logodds, subset=(p>=.2 & p<=.8)), col="blue")
```



Symmetric around $\pi = ½$:

$\text{logit}(\pi) = -\text{logit}(1-\pi)$

Fairly linear in the middle,

0.2 ⍰ π ⍰ 0.8

The logit transformation of probability is the basis for logistic regression

(An alternative, the cumulative normal, ⍰$^{-1}(\pi)$, gives rise to probit regression)

Odds ratio

For two groups, with probabilities of success π_1, π_2, the ***odds ratio***, θ, 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 & 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 $H_0 : \theta = 1$

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

$$SE(\log(\theta)) = \sqrt{\Sigma_{ij} n_{ij}^{-1}}$$

`vcd::oddsratio()` has option, log=, `TRUE` by default
The `summary()` method calculates z tests

```
> summary(oddsratio(UCB))

z test of coefficients:

                              Estimate Std. Error z value Pr(>|z|)
Male:Female/Admitted:Rejected   0.6104     0.0639    9.55   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Odds ratio: Confidence intervals

Results should be reported with confidence intervals, either for the odds ratio, θ, or for log(θ)

```
> confint(oddsratio(UCB, log = FALSE))
                               2.5 % 97.5 %
Male:Female/Admitted:Rejected 1.624  2.087
> confint(oddsratio(UCB))
                                2.5 % 97.5 %
Male:Female/Admitted:Rejected 0.4851 0.7356
```

Summary in words:

For the Berkeley admissions data:

- The Pearson χ^2 test of association between Gender and Admission was highly significant, $\chi_1^2 = 91.6$, $p < .0001$
- This corresponded to an odds ratio of admission for Males vs. Females of $\theta = 1.84$ (CI: 1.62, 2.09), meaning that overall, males were 84% more likely to be admitted
- On the scale of log odds, $\psi = \log(\theta)$, the estimate was $\psi = 0.610$ (CI: 0.485, 0.736), meaning a significant positive association between Gender(Male) and admission.

Small sample size

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

Example: Cholesterol 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 χ^2 test is not significant
For 2 x 2 tables with small n, a correction $|O - E| - ½$ is standardly applied

```
> chisq.test(fat)

        Pearson's Chi-squared test with Yates' continuity correction

data:  fat
X-squared = 3.19, df = 1, p-value = 0.074
```

Yet, we get a warning

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

Small sample size: Simulation

A Monte-Carlo method uses simulation to calculate a *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 = 0.04
```

This method repeatedly samples cell frequencies from tables with the same margins, and calculates a χ^2 for each. The *p*-value compares the observed X^2 to distribution in the simulations.
The χ^2 test is now significant.

Small sample size: Fisher exact test

Fisher's exact test: calculates probability for all 2 × 2 tables with odds ratio as or more extreme than that in the data, keeping the margins fixed.

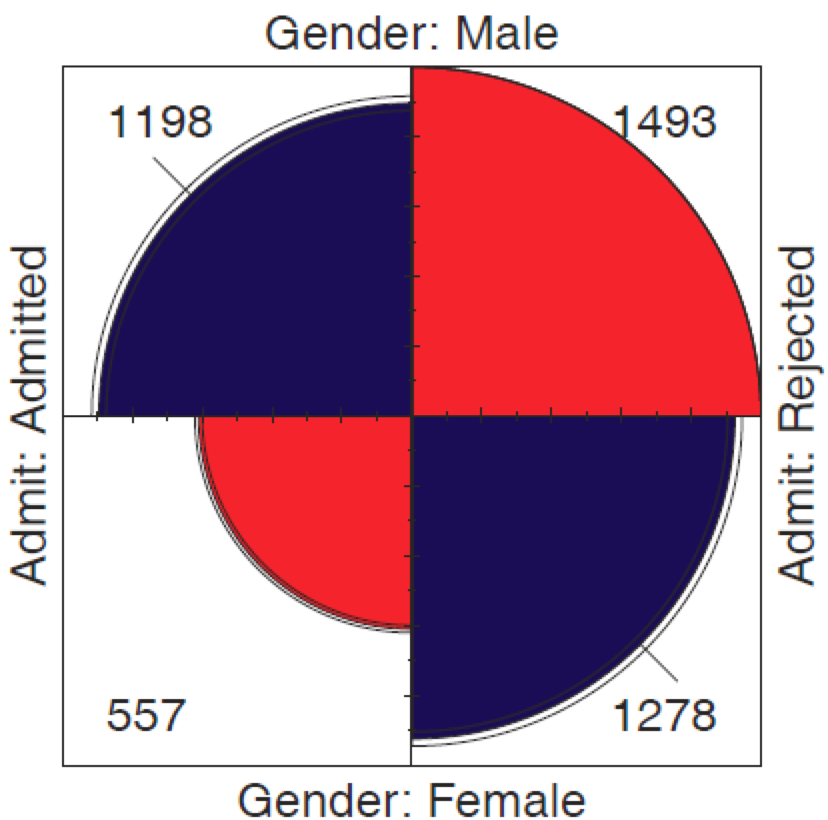
```
> fisher.test(fat)

        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 that obtained using simulation.

Fisher's test is available for larger r × c tables, but the method gets computationally intensive as r * c increases

Visualizing: fourfold plots

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

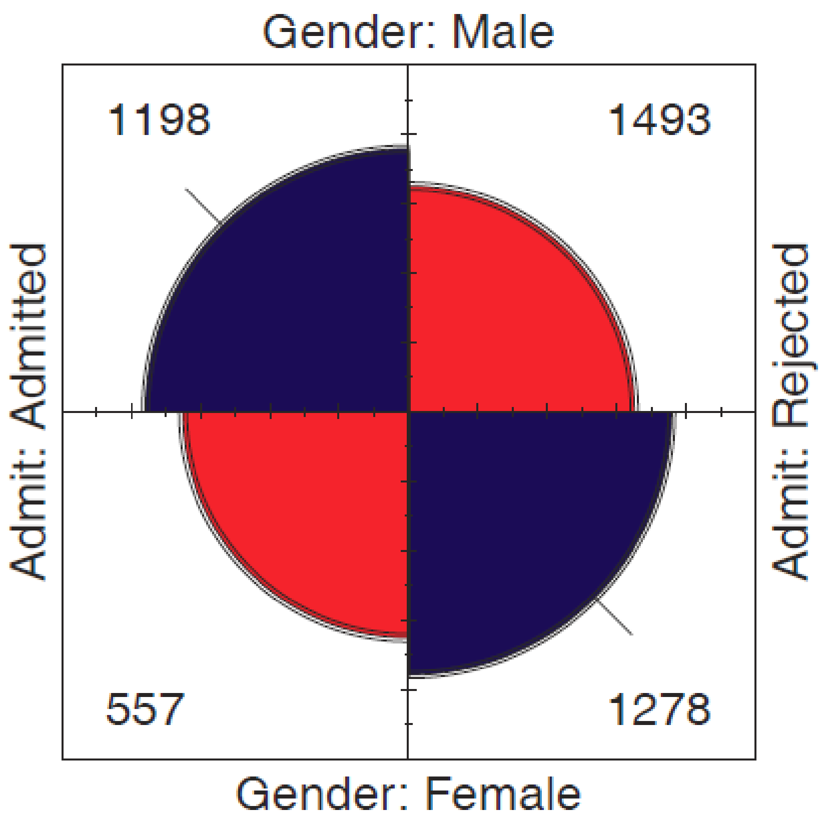


Friendly (1994a):

- Fourfold display: area ~ 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
```

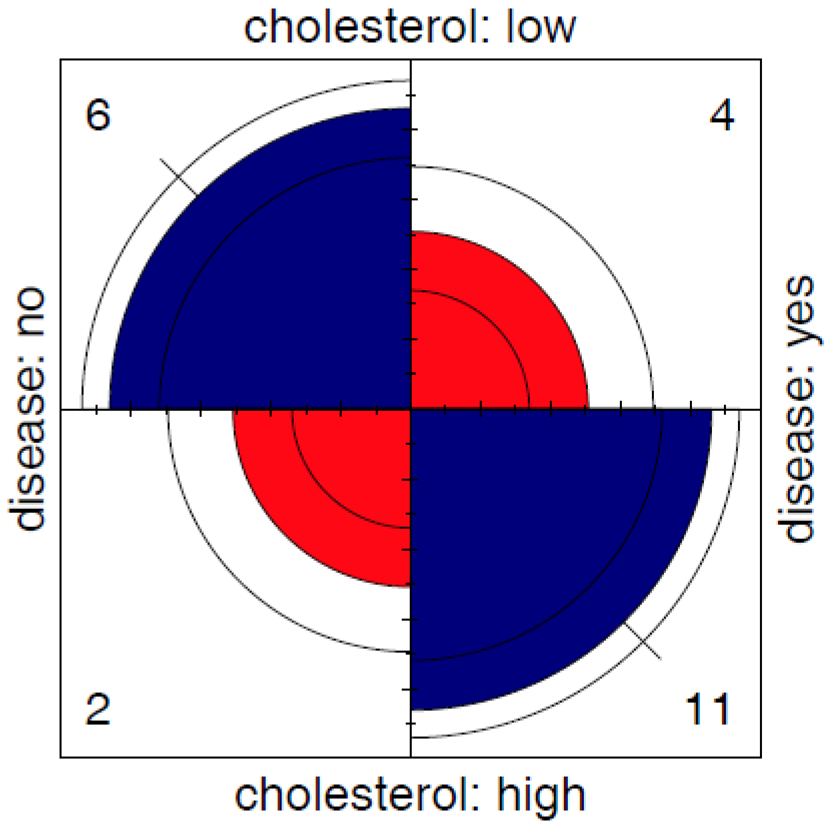


Better version:

- 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 tables: 2 × 2 × k

The UC Berkeley data was obtained from 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)

Odds ratios by department

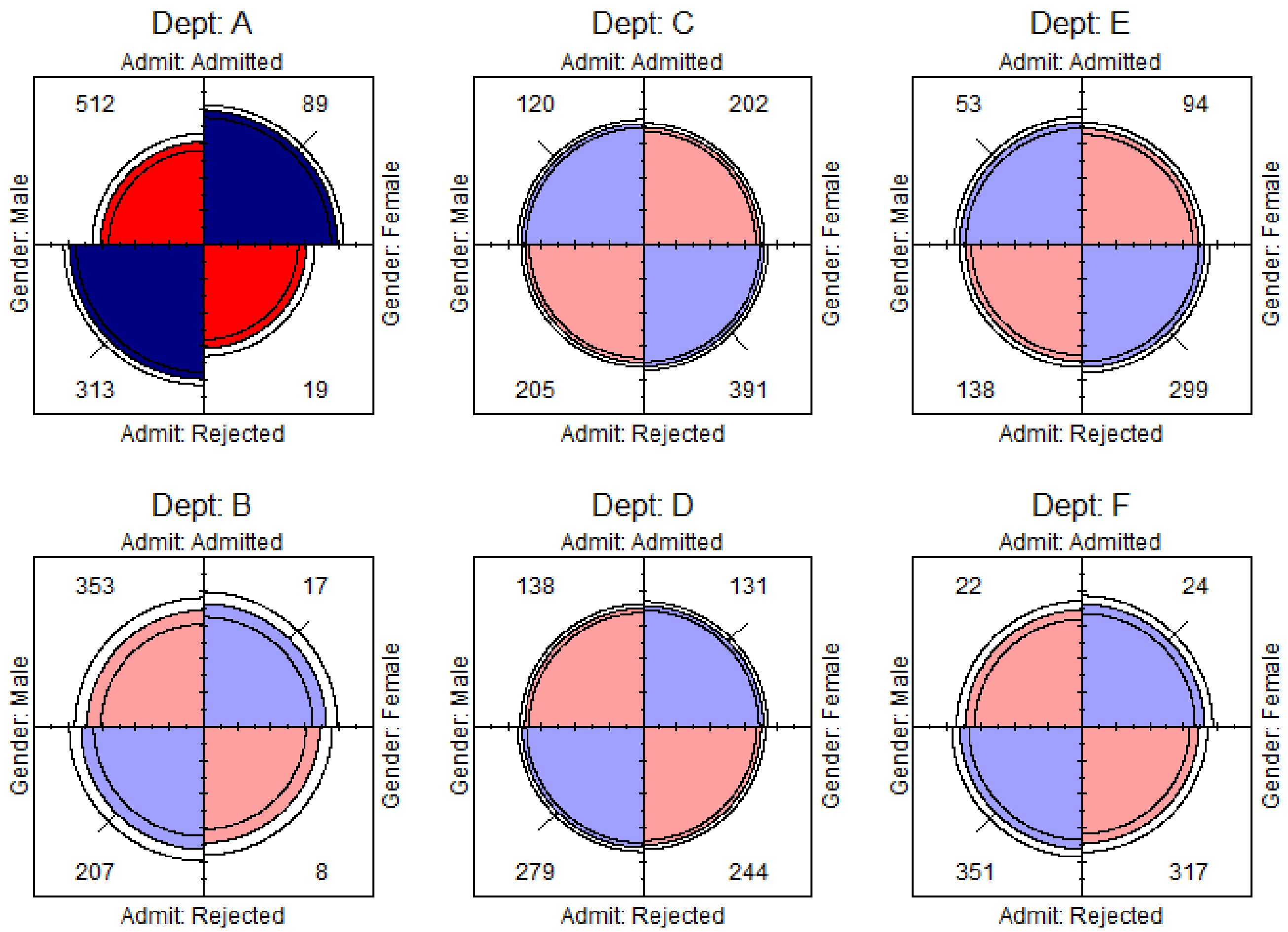
```
> summary(oddsratio(UCBAdmissions))

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 dept. 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 association of {admission, department} and {gender, department}

Stratified fourfold plots

Fourfold plots by department (intense shading where significant)

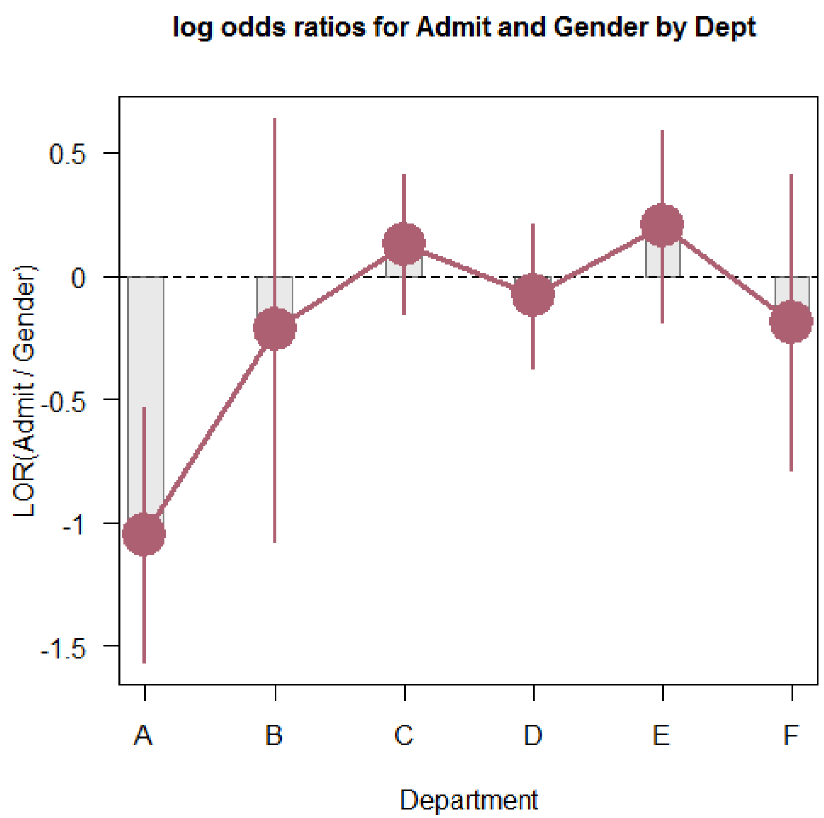
```
> fourfold(UCBAdmissions)
```



Log odds ratio plot

Plot the log odds ratios with confidence limits

```
> plot(oddsratio(UCBAdmissions), cex=2, xlab="Department")
```



Stratified tables: Homogeneity of association

Questions:

- Are the k odds ratios all equal, $\theta_1 = \theta_2 = \ldots = \theta_k$?
  - Woolf's test: `vcd::woolftest()`
- This is the same as the hypothesis of no three-way association
- If homogeneous, is the common odds ratio different from 1?
  - Mantel-Haenszel test: `stats::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
```

The odds ratios differ across departments, so no sense testing their common value

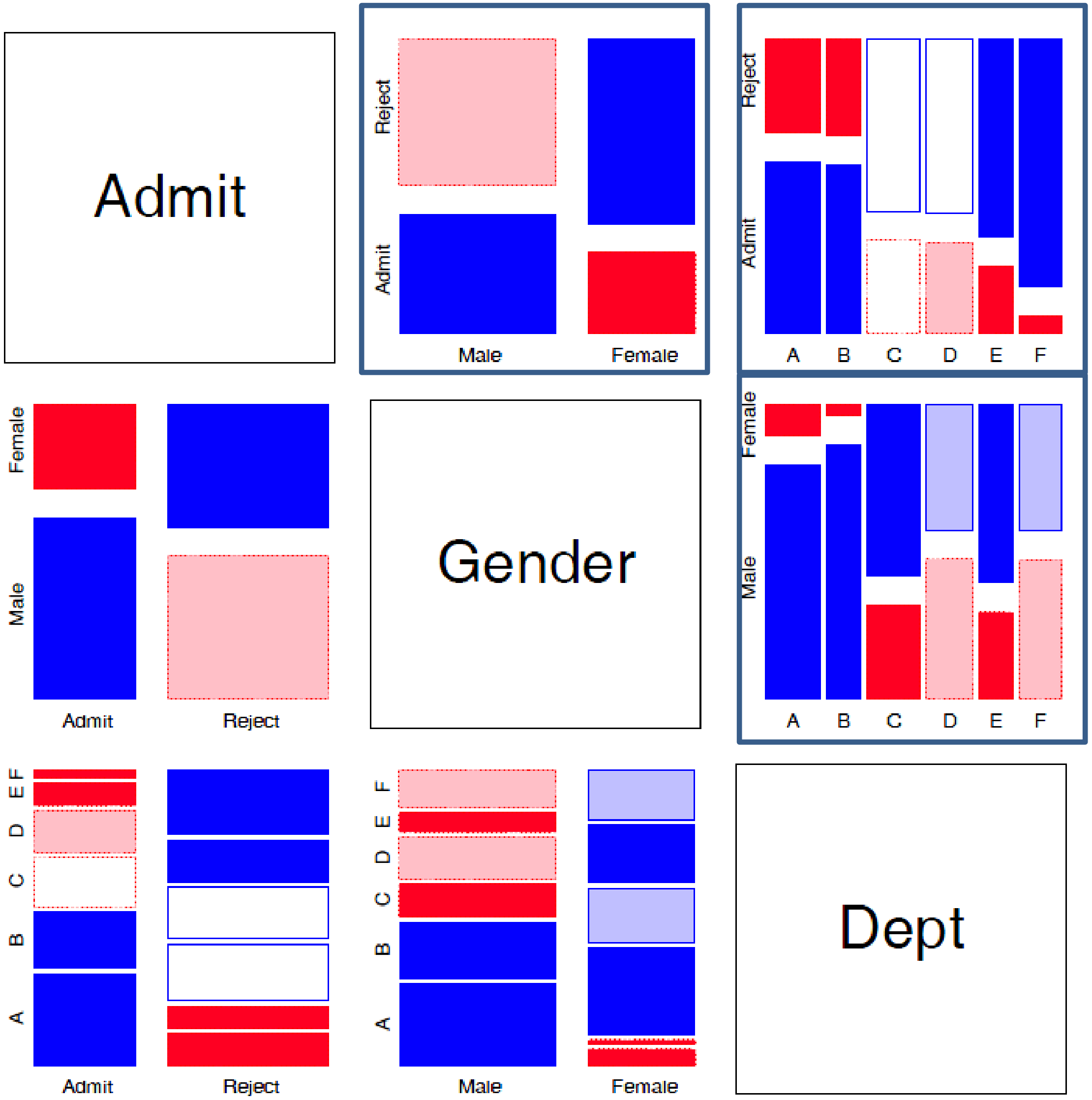
What happened at UC Berkeley?

Why do 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 matrices



Scatterplot matrix analog for categorical data

All pairwise views

Small multiples → comparison

The answer: Simpson's Paradox

- Depts A, B were easiest
- Applicants to A, B mostly male
- ∴ Males more likely to be admitted overall

$r \times c$ tables: Overall analysis

- **Overall tests** of association: `assocstats()`: Pearson chi-square and LR G^2
- **Strength** of association: ϕ 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 2×2 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 × c tables: Overall analysis

- 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

Residuals, fitted values, test statistics returned by `MASS::loglm()`

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

Residuals and fitted values are obtained with “extractor” methods

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

```
> fitted(mod)
       Hair
Eye       Black Brown   Red Blond
  Brown   40.1 106.3 26.39  47.2
  Blue    39.2 103.9 25.79  46.1
  Hazel   17.0  44.9 11.15  20.0
  Green   11.7  30.9  7.68  13.7
```

Direct calculation of Pearson & LR χ^2

```
> sum(res.P^2)   # Pearson chisq
[1] 138.29
> sum(res.LR^2)  # LR chisq
[1] 146.44
```

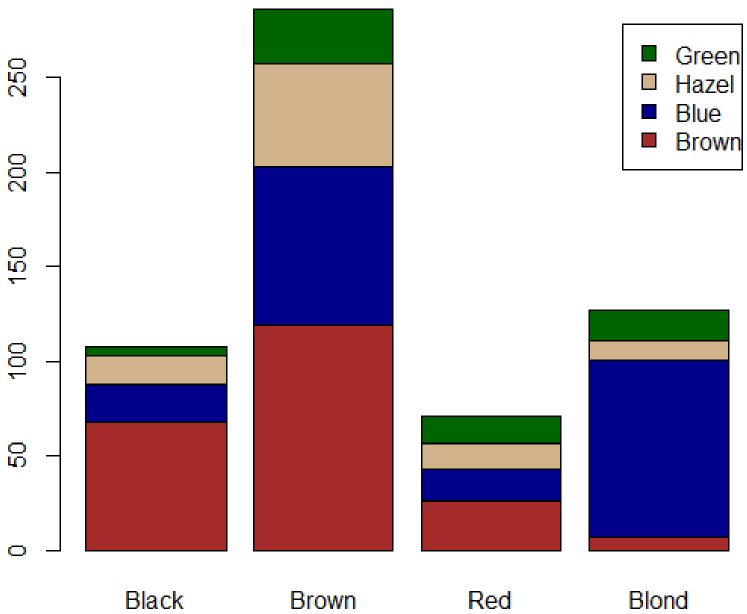
loglm() returns an object (mod) of class “loglm”
Method functions, *.loglm() include:
residuals(), fitted(), anova(), summary()
& various plot methods

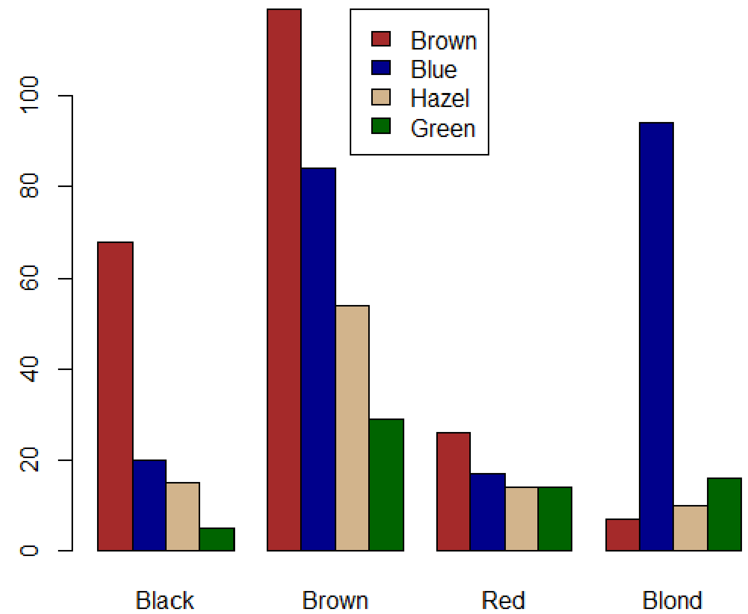
Plots for two-way tables

Barplots are easy, but not often very useful. Why?

```
col <- c("brown", "darkblue", "tan",
         "darkgreen")
barplot(HEC, col = col, legend=TRUE)
```

```
barplot(HEC, col = col,
      beside=TRUE, legend=TRUE, …)
```



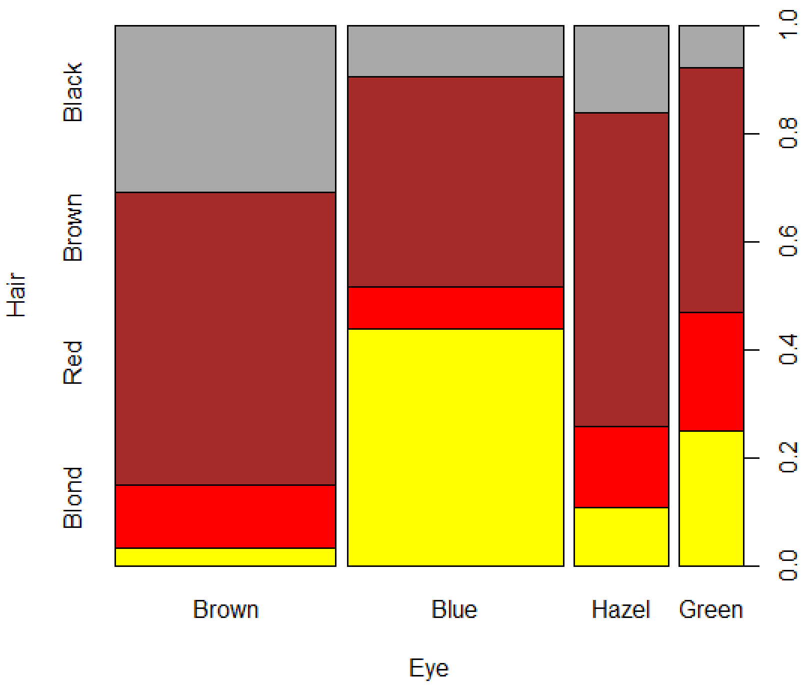


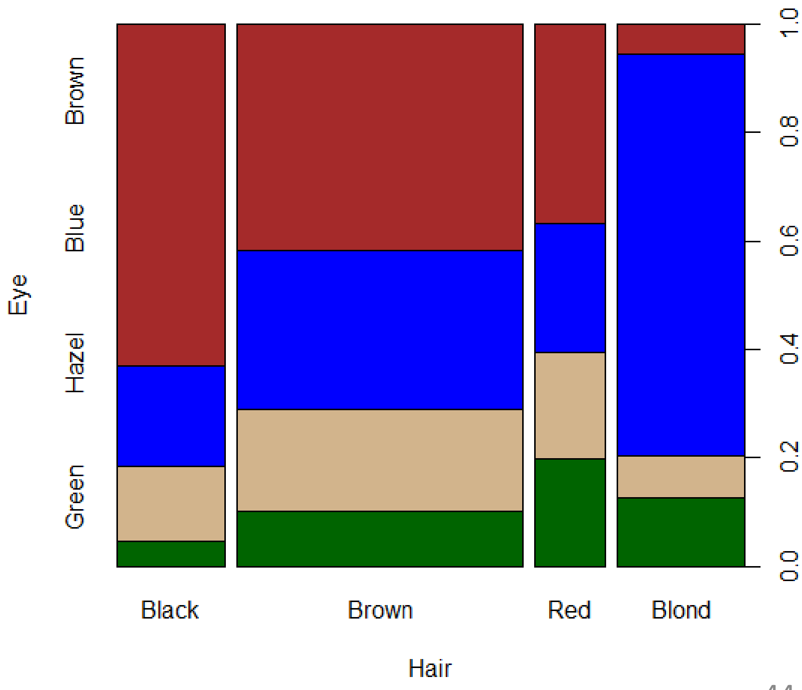
Spine plots

Spine plots show the marginal proportions of one variable, and the conditional proportions of the other. Independence: cells align

```
col <- c("darkgrey", "brown", "red",
         "yellow")
spineplot(HEC, col=rev(col))
```

```
col <- c("brown", "blue", "tan",
         "darkgreen")
spineplot(t(HEC), col=rev(col))
```

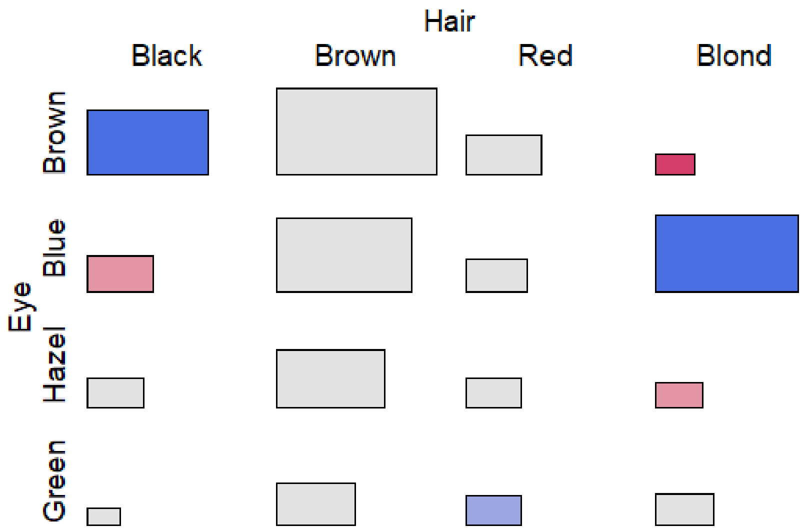




Tile plots

Tile plots show a matrix of rectangular tiles, area ~ frequency.
They can be scaled to facilitate different types of comparisons: cells, rows, cols
They can be shaded to show the sign & magnitude of residuals from independence

tile(HEC, shade=TRUE, legend=FALSE)

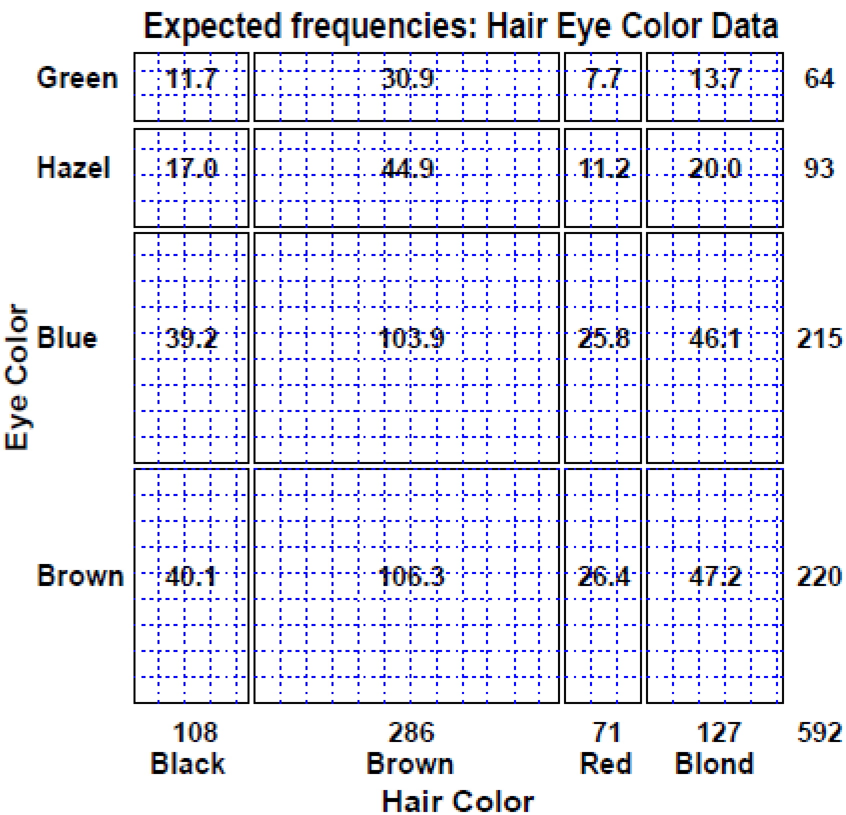


tile(HEC, tile_type="width", ...)

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)



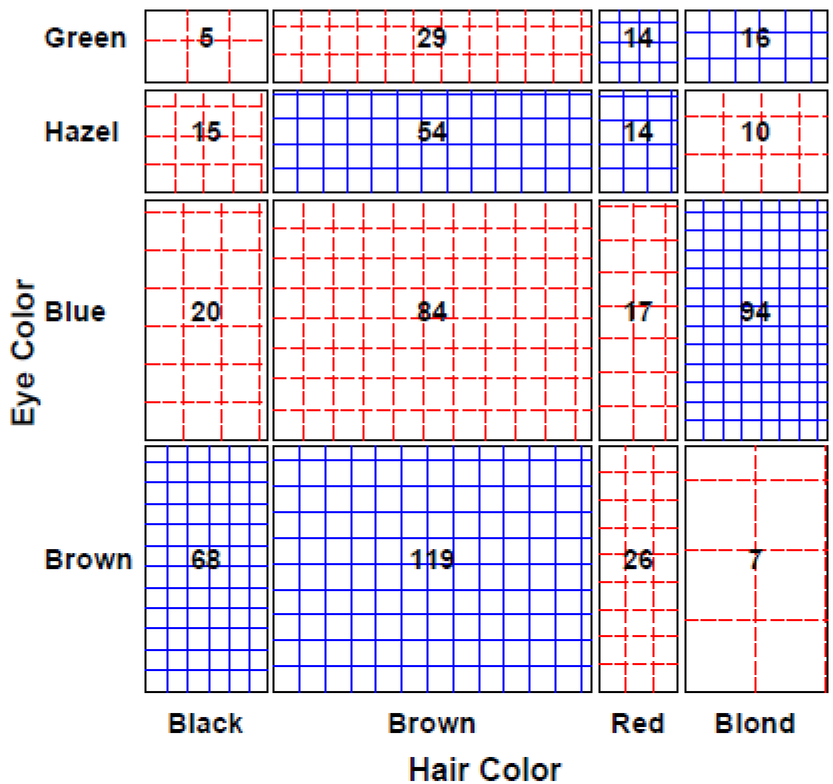
This display shows expected frequencies, m_{ij}, as # boxes within each cell

Under independence, boxes 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: $\text{sign}(n_{ij} - \hat{m}_{ij})$.
- $\Longrightarrow$ Independence: Shown when density of shading is uniform.



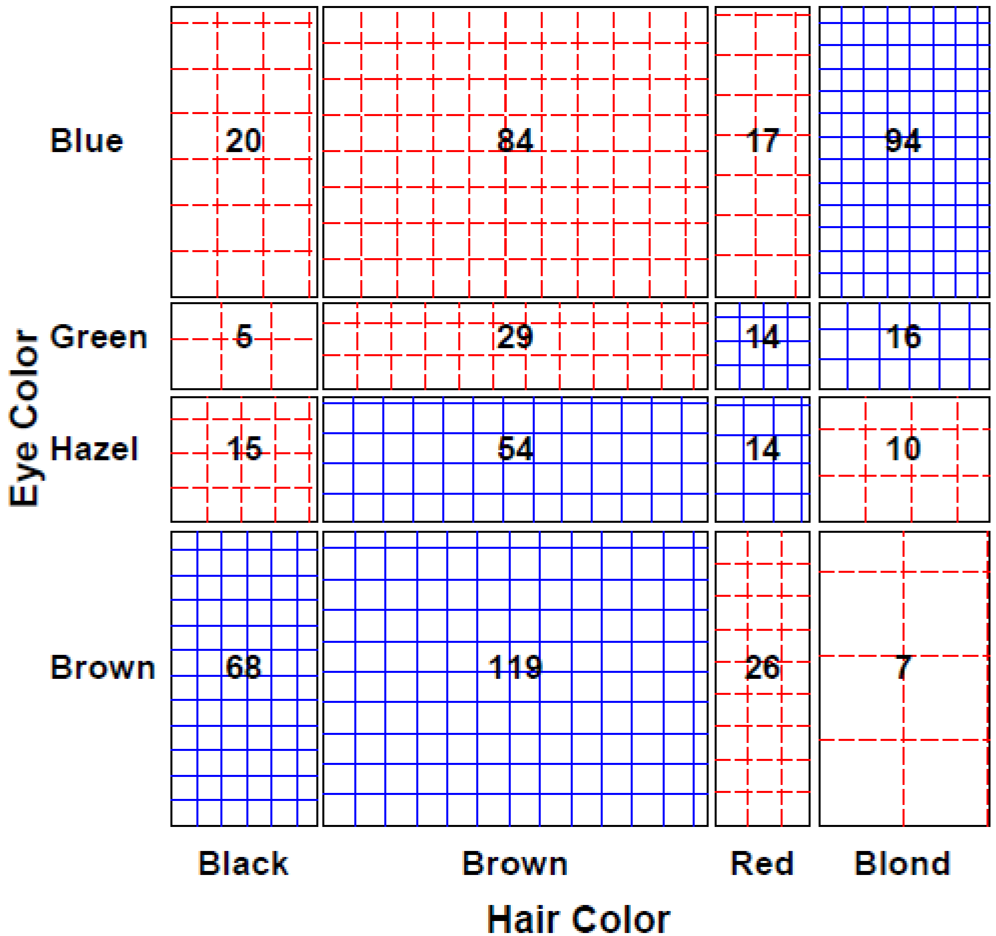
The rectangles have area ~ expected frequency

\# boxes = observed frequency

$n_{ij} > m_{ij} \rightarrow$ greater density
$n_{ij} < m_{ij} \rightarrow$ less density

Sieve diagrams: Effect ordering

Permuting the rows / cols to make the pattern more coherent

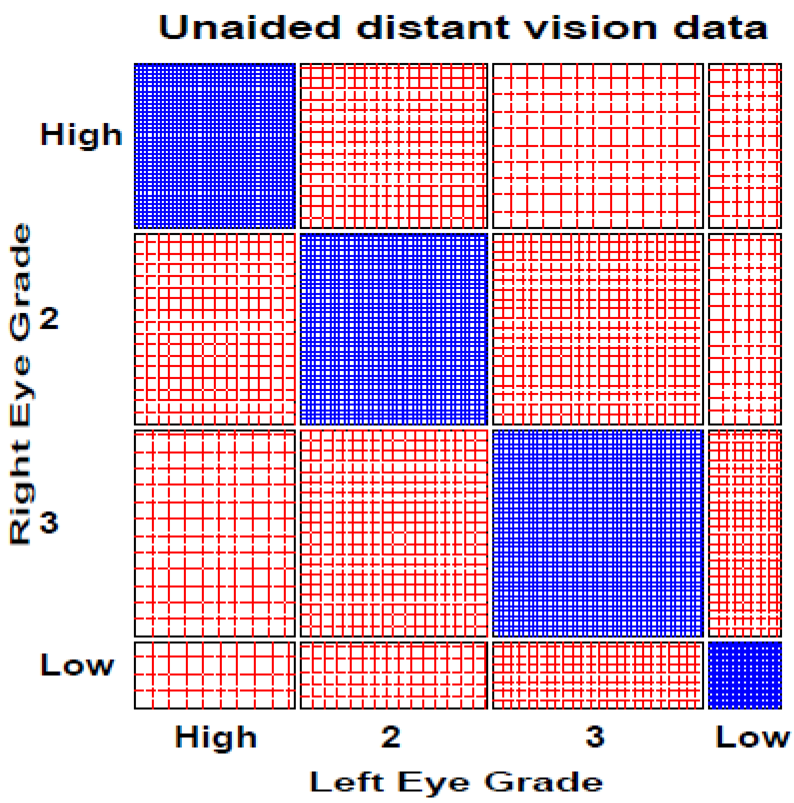


Here, I reordered the eye colors according to lightness

The opposite-corner pattern suggests an explanation for the association

Sieve diagrams: Subtle patterns

Vision classification of 7477 women in Royal Ordnance factories: visual acuity grade in left & right eyes



- The obvious association is apparent in the diagonal cells
- A more subtle pattern appears in the off-diagonal cells

- Analysis methods for square tables allow testing hypotheses beyond independence
  - Symmetry
  - Quasi-symmetry, …

Ordinal factors

The standard Pearson χ^2 and LR G^2 give tests of general association, with (r-1) × (c-1) df

More powerful CMH tests:

- When either row or col levels are ordered, more specific CMH (Cochran–Mantel–Haentzel) tests which take order into account have greater power to detect ordered relations.
  - Use fewer df, so ordinal tests are more focused on detecting a particular "signal"
- This is similar to testing for linear trends in ANOVA
- Essentially, these assign scores to the categories & test for differences in row / col means, or non-zero correlation

CMH tests for ordinal factors

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 χ^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:

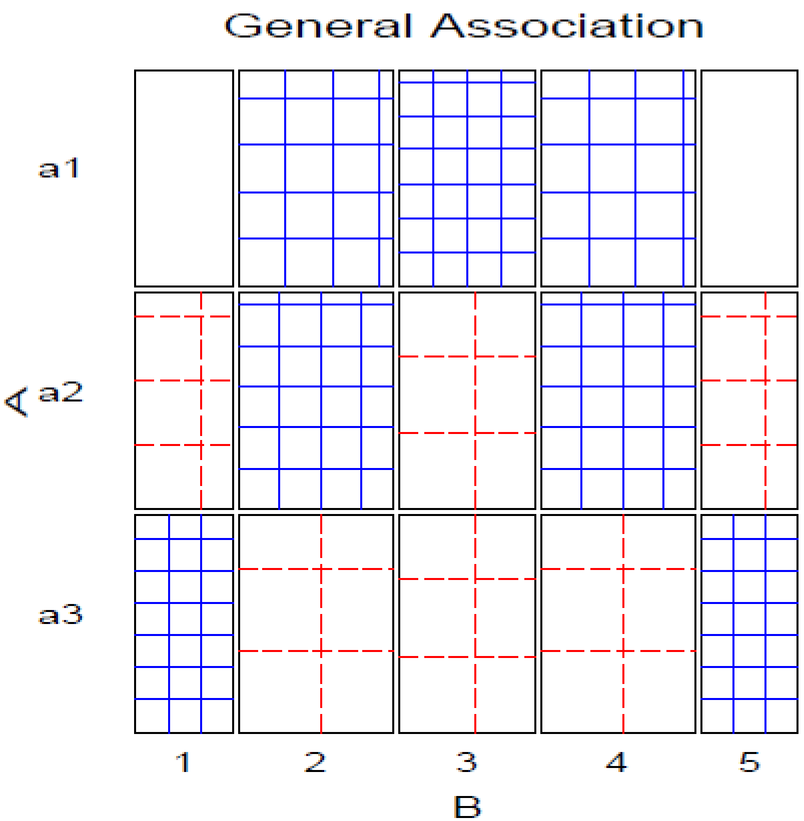
Cochran-Mantel-Haenszel Statistics (Based on Table Scores)

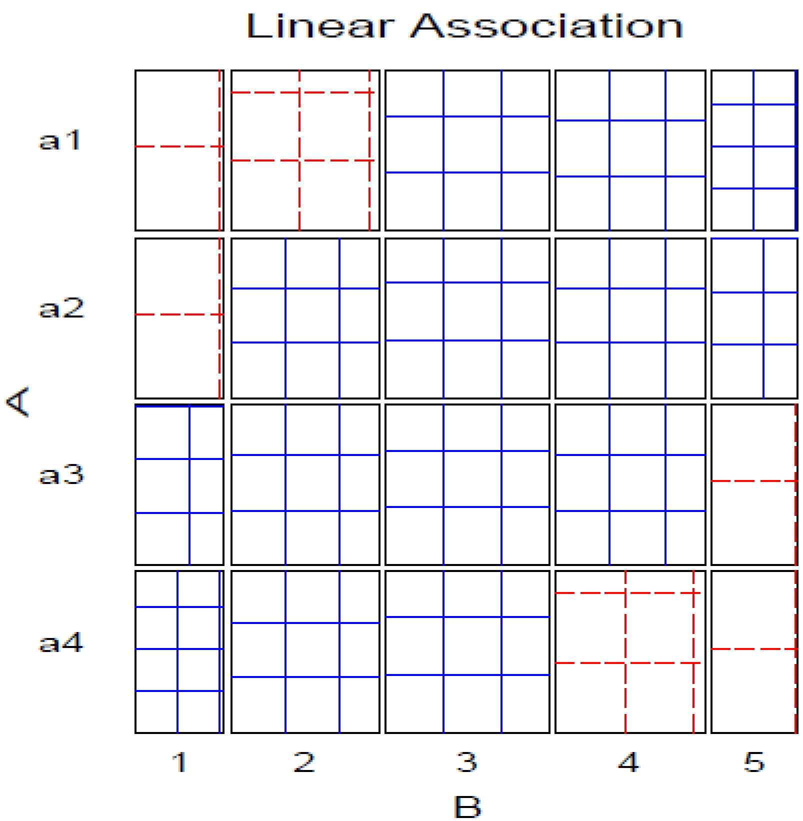
Statistic	Alternative Hypothesis	DF	Value	Prob
1	Nonzero Correlation	1	10.639	**0.001**
2	Row Mean Scores Differ	3	10.676	**0.014**
3	General Association	12	13.400	0.341

Visualizing the association

The association here is U-shaped
Only general association detects this

Higher levels of A are associated
with lower levels of B





Example: Mental health data

For the mental health data, both `ses` and `mental` are ordinal

All tests are significant, but the nonzero correlation test, with 1 df has the smallest p-value & largest χ2 / df

```
> 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
```

both ordinal
cols ordinal
rows ordinal
neither

χ2 / df shows why ordered tests are more powerful

```
> xx <- CMHtest(mental.tab)
> xx$table[,"Chisq"] / xx$table[,"Df"]
    cor  rmeans  cmeans general
  37.16    8.06   13.56    3.06
```

Observer agreement

- **Inter-observer agreement** often used as to assess reliability of a subjective classification or assessment procedure
  - $\rightarrow$ 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 κ: 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 κ

Properties of Cohen's κ:

- perfect agreement: $\kappa = 1$
- minimum κ may be < 0; lower bound depends on marginal totals
- Unweighted κ: counts only diagonal cells (same category assigned by both observers).
- Weighted κ: 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

Example: Cohen's κ

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	Wife's Rating: Fairly often	Wife's Rating: Very Often	Wife's Rating: 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

Example: Cohen's κ

`vcd::Kappa()` calculates unweighted and weighted κ, 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 κ 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				New Orleans patients			
	Cert	Prob	Pos	Doubt	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

To what extent to the neurologists agree?

Do they agree equally for the patients for the two cities

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
```

Winnipeg patients

New Orleans patients

Somewhat larger agreement for the New Orleans patients

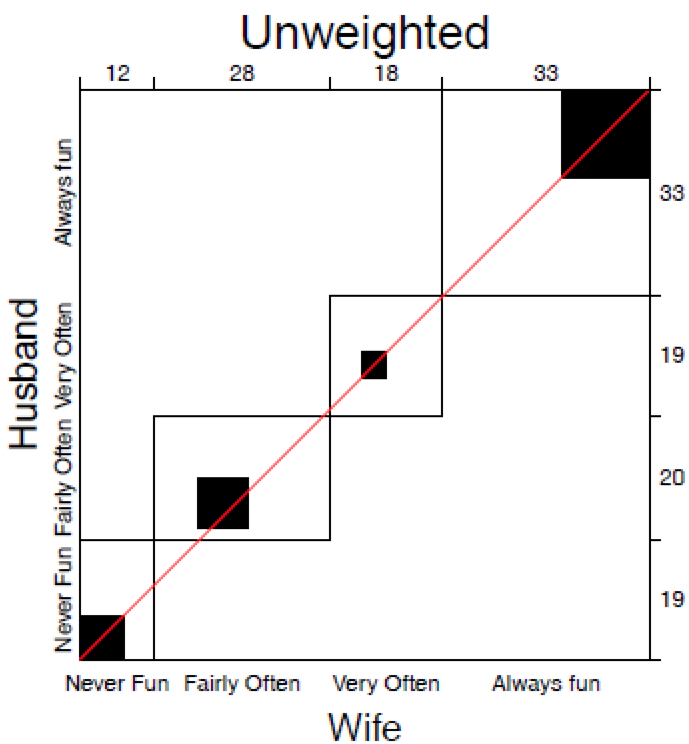
The irr package (inter-rater-reliability) provides ICC and other measures; also handles the case of k > 2 raters

Bangdiwala’s Observer agreement chart

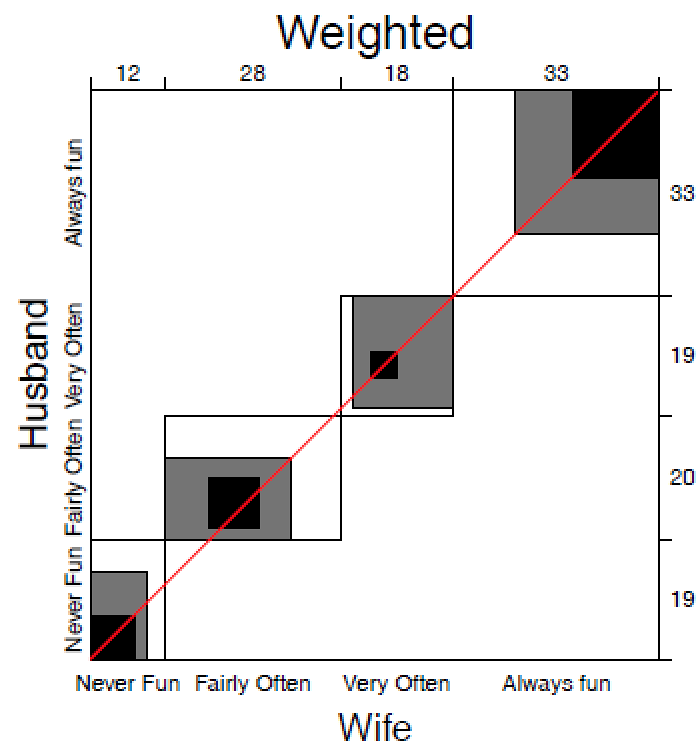
The observer agreement chart (Bangdiawala, 1987) provides:

- A simple graphic representation of the strength of agreement
- A measure of strength of agreement with an intuitive interpretation

B = 0.146



B^{w} = 0.498



Bangdiwala’s Observer agreement chart

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.

observed: n_{ii} x n_{ii}
maximum: n_{i+} x n_{+i}

Weighted agreement chart: Partial agreement

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

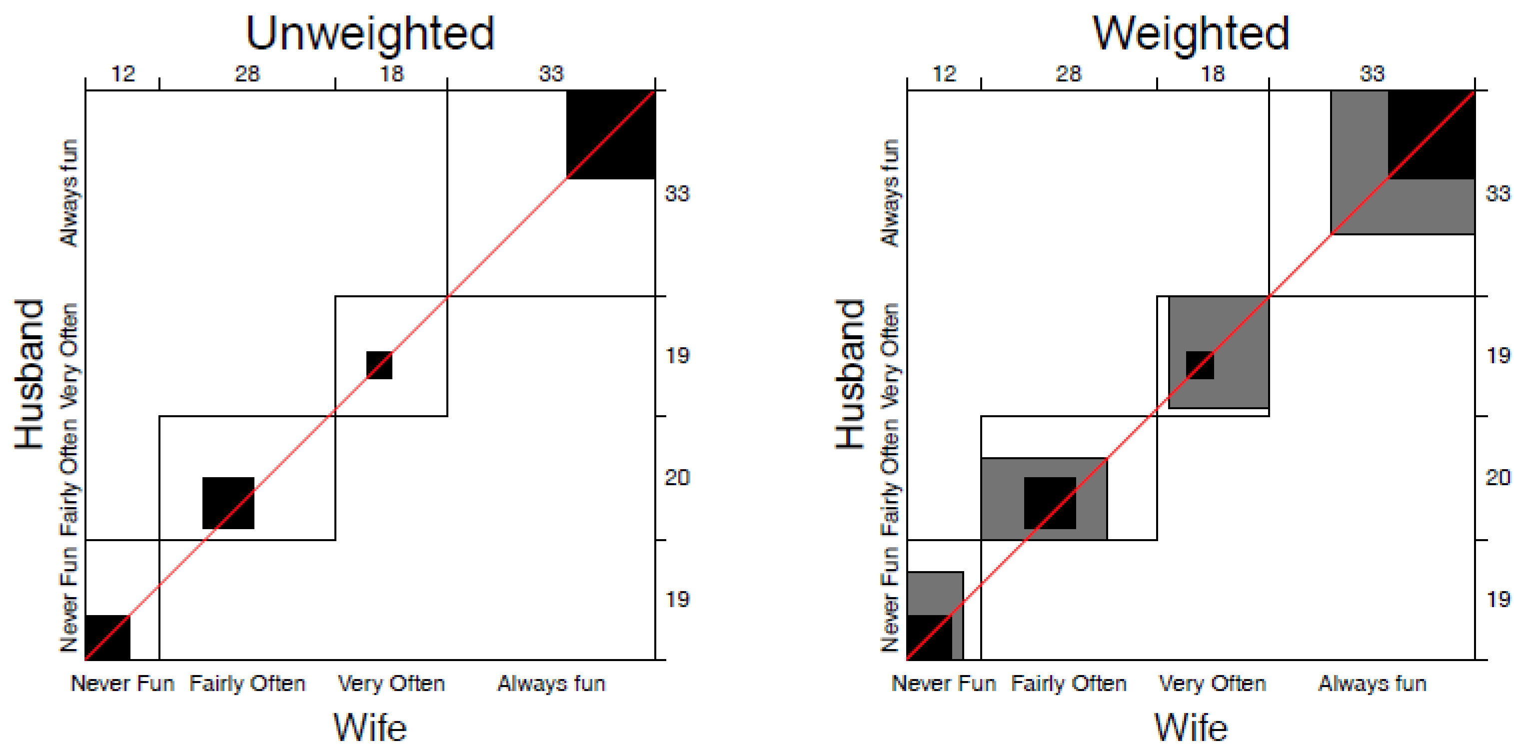
$$
\begin{array}{ccccc}
 & & n_{i-b,i} & & \\
 & & \vdots & & \\
n_{i,i-b} & \cdots & n_{i,i} & \cdots & n_{i,i+b} \\
 & & \vdots & & \\
 & & n_{i-b,i} & &
\end{array}
\qquad\qquad
\begin{array}{ccccc}
 & & w_2 & & \\
 & & w_1 & & \\
w_2 & w_1 & 1 & w_1 & w_2 \\
 & & w_1 & & \\
 & & w_2 & &
\end{array}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

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

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

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

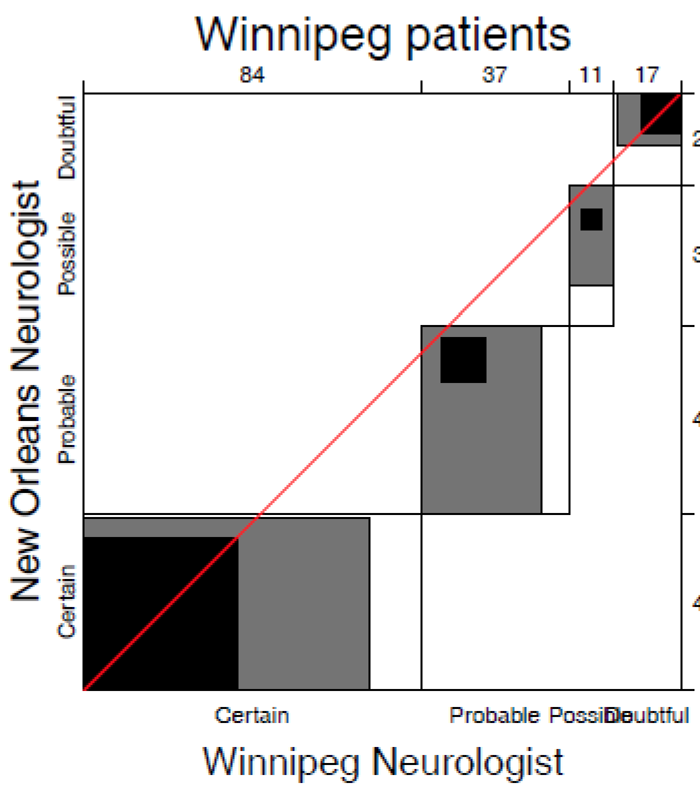
```r
agreementplot(SexualFun, main="Unweighted", weights=1)
agreementplot(SexualFun, main="Weighted")
```

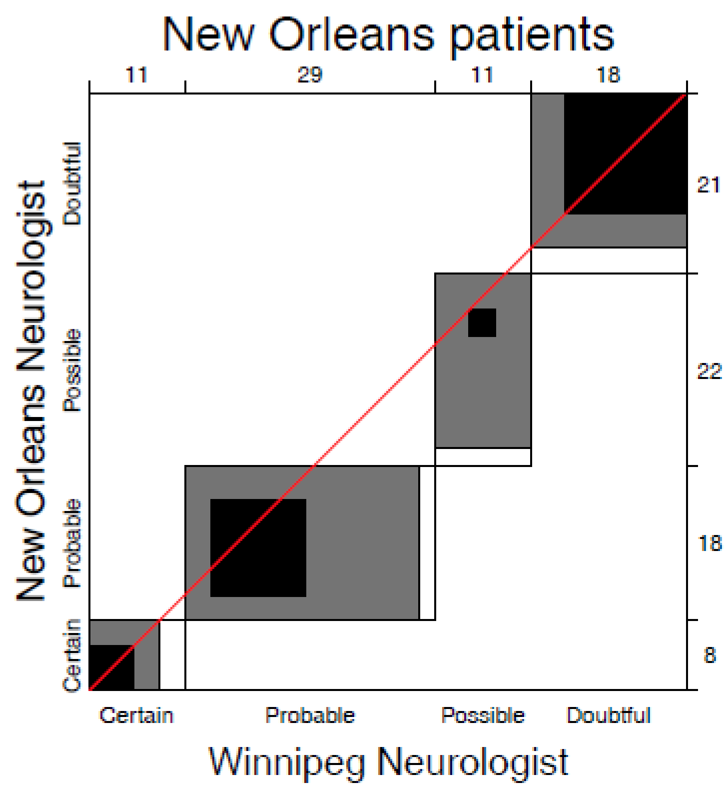


The smallest exact agreement occurs for “very often”, but husbands & wives more on this allowing ± 1 step disagreement

Marginal homogeneity & 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 χ^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

Looking ahead: Models

Loglinear models [loglm()]

- Generalize the Pearson χ^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

Generalized linear models [glm()]

- Similar to ordinary lm(), but w/ Poisson dist^n of counts: family="poisson"
- Formula notation: Freq ~ A + B + C; Freq ~ (A + B + C)^2
- Familiar diagnostic methods & plots (outliers, influence)

Looking ahead: Models

Example: UC Berkeley data

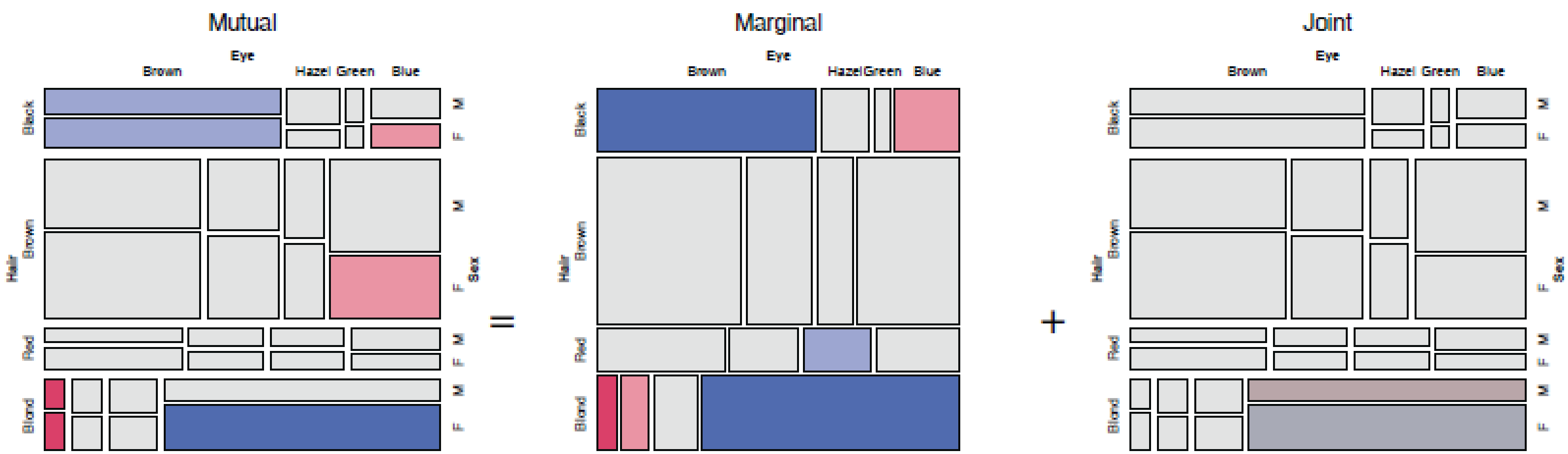
- Mutual independence: [Admit][Gender][Dept] = ~ A + G + D
- Joint independence: [Admit][Gender Dept] = ~ A + G * D
- Conditional independence: [D Admit][D Gender] = ~ D * (A + G)
  - Specific test of absence of gender bias, controlling for department
- No three-way association: [A G][A D][G D] = ~ $(A + D + G)^2$

```
library(MASS)
loglm(~ Admit + Dept + Gender, data=UCBAdmissions)      # mutual independence
loglm(~ Admit + Dept * Gender, data=UCBAdmissions)      # joint independence
loglm(~ Dept * (Admit + Gender), data=UCBAdmissions)    # conditional independence
loglm(~ (Admit + Gender + Dept )^2, data=UCBAdmissions) # all two-way, no three-way
```

Looking ahead: Mosaic plots

Mosaic plots provide visualizations of associations in 2+ way tables

- Tiles ~ frequency; conditioned by A, then B, then C, …
- Fit: any loglinear model [A][B][C], [AB][C], [AB][AC], …, [ABC]
- Shading: ~ residuals, contributions to χ^2
- Show: associations not accounted for by model



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

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

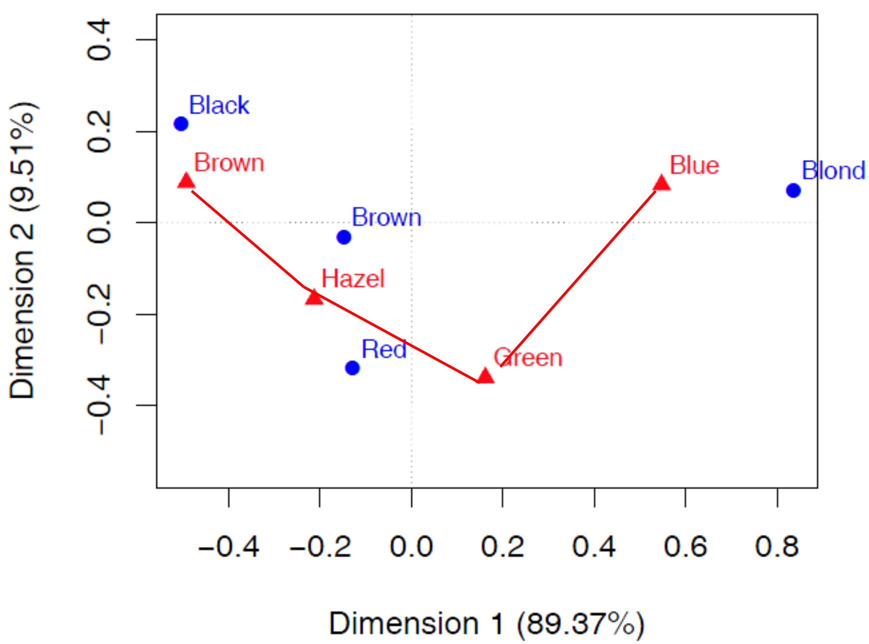
[Hair Eye] [Sex] $G^2_{(15)} = 19.86$

Looking ahead: Correspondence analysis

Like PCA for categorical data

- Account for max % of χ^2 in few (2-3) dimensions
- Find scores for row and col categories
- Plot of row/col scores shows associations

Dim 1: dark to light
Dim 2: something about red hair, green eyes?



Summary

- Two-way tables summarize frequencies of two categorical factors
  - 2 × 2 a special case, with odds ratio as a measure
  - r × c: factors can be unordered or ordered
  - r × c × k – stratified tables
- Tests & measures of association
  - Pearson χ^2, LR G^2: general association
  - More powerful CMH tests for ordered factors
- Visualization
  - 2 × 2: fourfold plots
  - r × c: sieve diagrams, tile plots, …