Two-way tables: Independence and association

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Psych 6136

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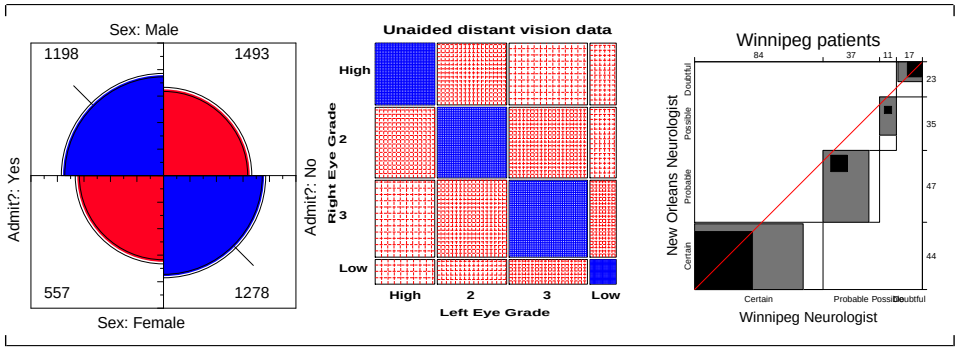


Two-way tables: Overview

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:

- 2×2 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?

Two-way tables: Examples

2×2 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?

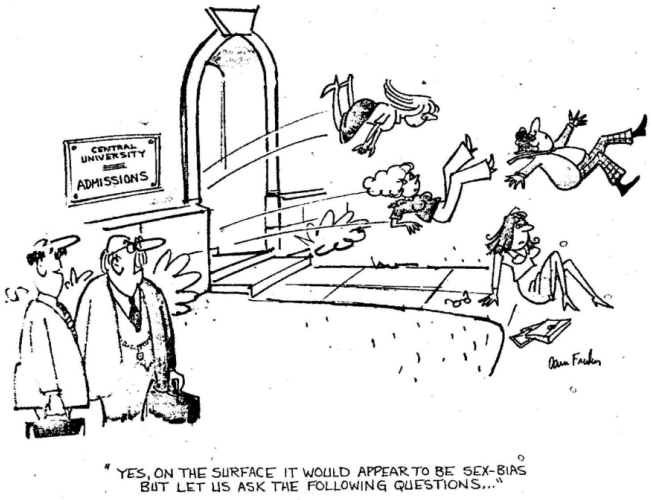
2×2 tables: UCB data

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)

## [1] 1.8411

confint(oddsratio(UCB, log=FALSE))

##          lwr    upr
## [1,] 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
Green	5	29	14	16	64
Hazel	15	54	14	10	93
Blue	20	84	17	94	215
Brown	68	119	26	7	220
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 χ^2 test. Details later.

```
chisq.test(HEC)

##
##  Pearson's Chi-squared test
##
## data:  HEC
## X-squared = 138.29, df = 9, p-value < 2.2e-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 = 45.985, df = 15, p-value = 5.346e-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
## cmeans   Col mean scores differ  40.3  5 1.30e-07
## rmeans   Row mean scores differ  40.7  3 7.70e-09
## general     General association  46.0 15 5.40e-05
```

Details later, but χ^2/df gives a useful comparison.

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: 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

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

- Joint cell probabilities are the product of the marginal probabilities

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

For 2×2 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 χ^2 tests also apply for large n
- Fisher's exact test or simulation required in small samples.

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

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

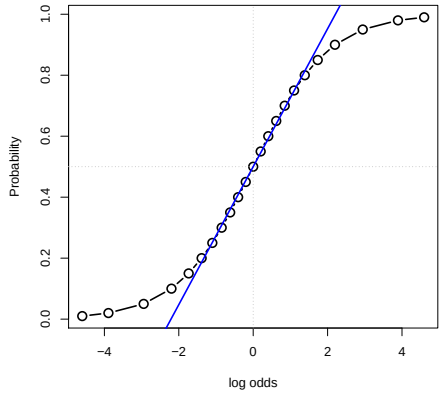
- Odds vary multiplicatively around 1 ("even odds", $\pi = \frac{1}{2}$)
- Taking logs, the log(odds), or ***logit*** varies symmetrically around 0,

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

```
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 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 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)

## [1] 0.61035

summary(oddsratio(UCB))

##      Log Odds Ratio Std. Error z value Pr(>|z|)
## [1,]         0.6104     0.0639    9.55   <2e-16 ***
## ---
## 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)

## [1] 1.8411

confint(oddsratio(UCB, log=FALSE))

##          lwr    upr
## [1,] 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 = 91.61, df = 1, p-value < 2.2e-16
```


Small sample size

- Pearson χ^2 and LR G^2 tests are valid only when most expected frequencies ≥ 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 χ^2 is not significant:

```
chisq.test(fat)

##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  fat
## X-squared = 3.1879, df = 1, p-value = 0.07418
```

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 = 4.9597, df = NA, p-value = 0.03798
```

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

Small sample size

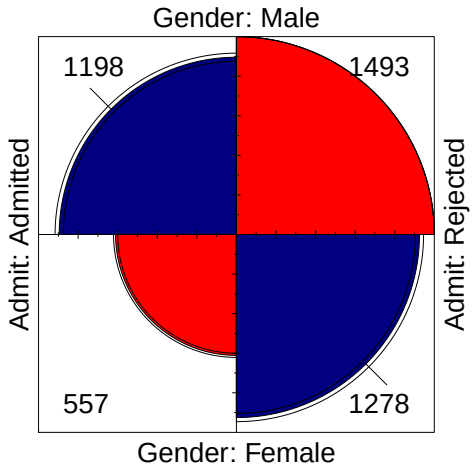
Fisher's exact test: calculates probability for all 2×2 tables as or more extreme than the data.

```
fisher.test(fat)

##
##  Fisher's Exact Test for Count Data
##
## data:  fat
## p-value = 0.03931
## 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
```

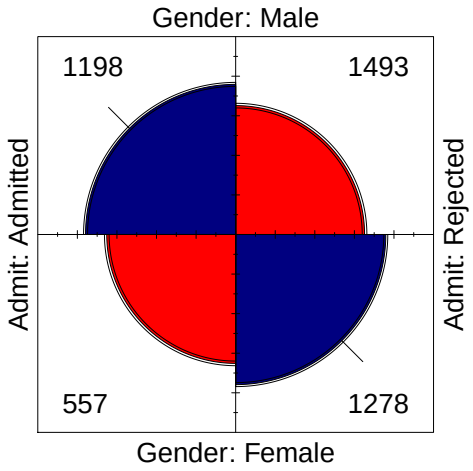


Friendly (1994a):

- 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
```

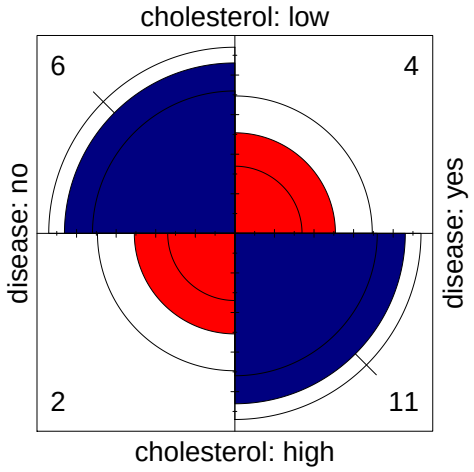


Better version:

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

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:

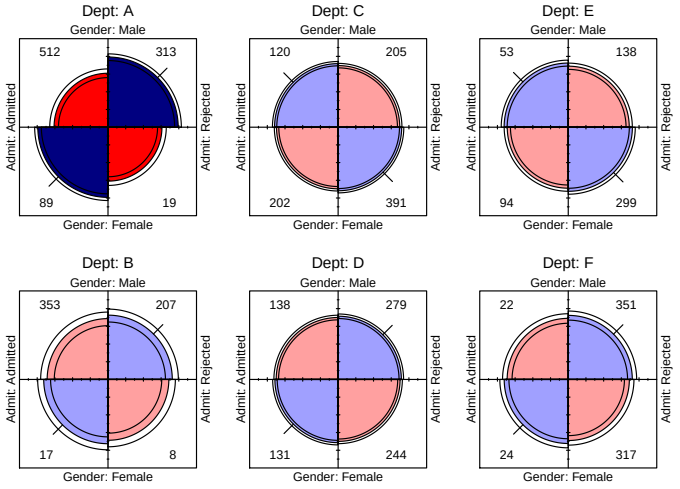
```
summary(oddsratio(UCBAdmissions))

##   Log Odds Ratio 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):

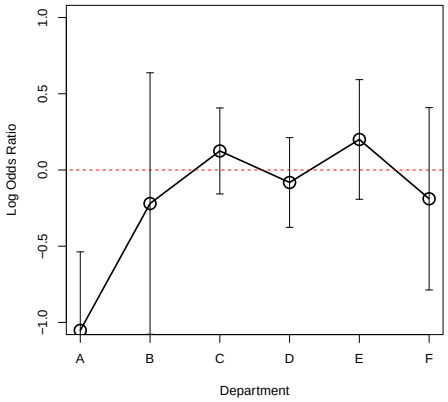
```
fourfold(UCBAdmissions)
```



Stratified $2 \times 2 \times k$ tables

Or plot odds ratios directly:

```
plot(oddsratio(UCBAdmissions), lwd=2, cex=2, 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 = 17.902, df = 5, p-value = 0.003072
```

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

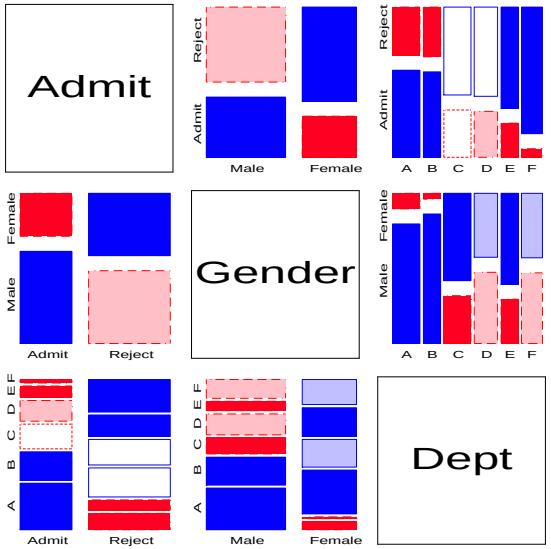
Exegesis: What happened at UC Berkeley?

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: ϕ coefficient, contingency coefficient (C), Cramer's V ($0 \le V \le 1$)

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

- 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   : 0.483
## 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:

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

- Expected (fitted) frequencies under independence: $\hat{m}_{ij} = n_{i+} n_{+j} / n_{++}$
- 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
```

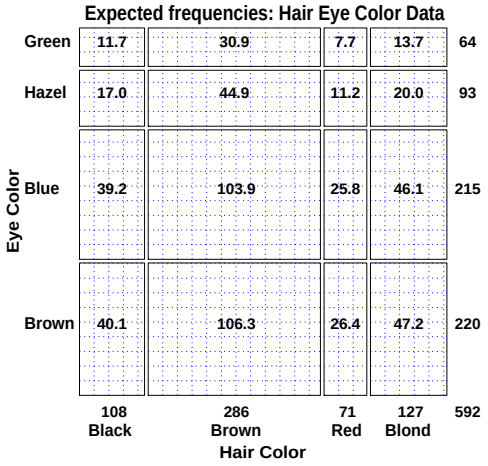
Demonstrate SSQ property:

```
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**

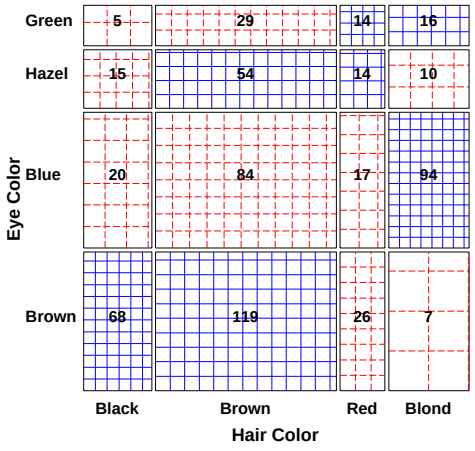
- When row/col variables are independent, $n_{ij} \approx \hat{m}_{ij} \sim n_{i+} n_{+j}$
- $\Rightarrow$ each cell can be represented as a rectangle, with area = height $\times$ width $\sim$ frequency, n_{ij} (under independence)



- 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}

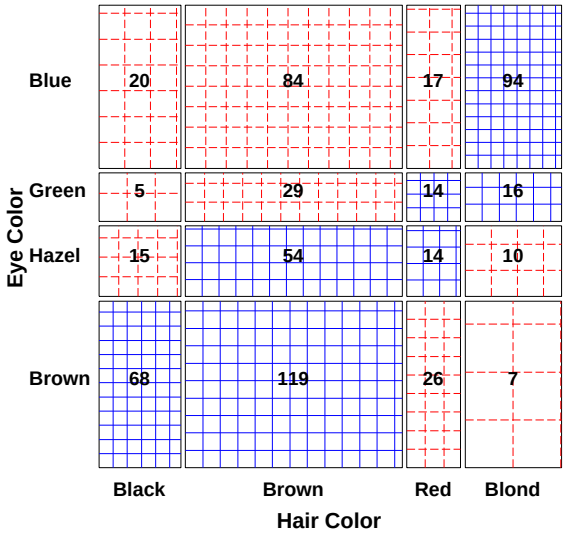
Sieve diagrams

- 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.



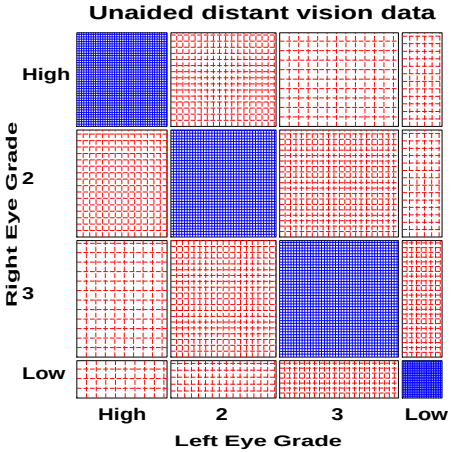
Sieve diagrams

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 χ^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 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	

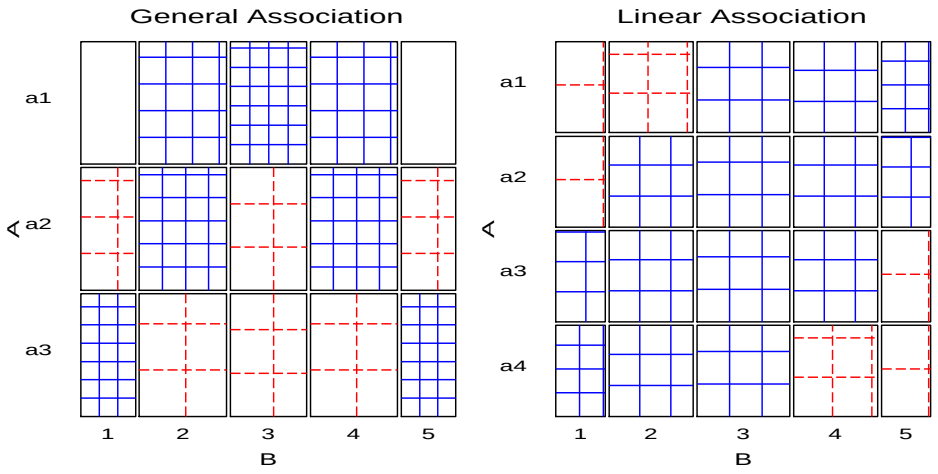
Output:

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

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 χ^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
## cmeans  Col mean scores differ  40.3  5 1.30e-07
## rmeans  Row 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 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

Cohen's κ: 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.*

	Wife's Rating				
Husband'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 κ: Example

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

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

##            value    ASE    z
## Unweighted 0.129 0.0686 1.89
## Weighted   0.237 0.0783 3.03

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

##            value    ASE    z
## Unweighted 0.129 0.0686 1.89
## Weighted   0.332 0.0973 3.41
```

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

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
## Unweighted 0.208 0.0505 4.12
## Weighted   0.380 0.0517 7.35

Kappa(MSPatients[,,2])

##            value    ASE    z
## Unweighted 0.297 0.0785 3.78
## Weighted   0.477 0.0730 6.54
```

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 $1 > w_1 > w_2 > \cdots$.

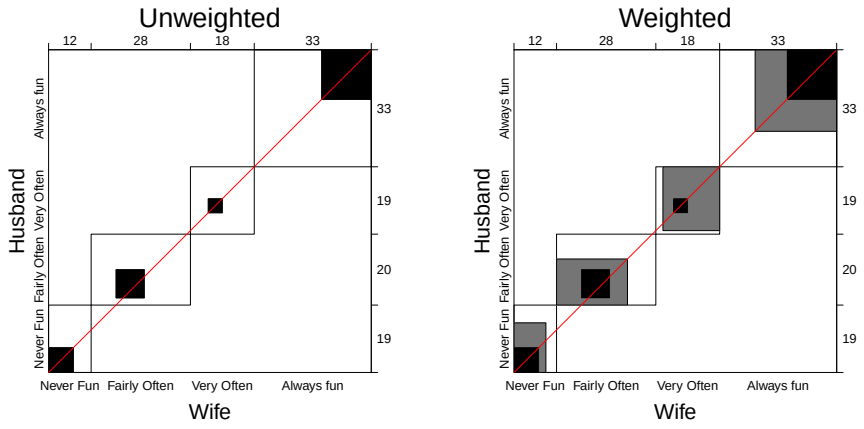
$$\begin{array}{ccccc} & & n_{i-b,i} & & \\ & & \vdots & & \\ n_{i,i-b} & \cdots & n_{i,i} & \cdots & n_{i,i+b} \\ & & \vdots & & \\ & & n_{i-b,i} & & \end{array} \qquad \begin{array}{ccccc} & & w_2 & & \\ & & w_1 & & \\ w_2 & w_1 & 1 & w_1 & w_2 \\ & & w_1 & & \\ & & w_2 & & \end{array}$$

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

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

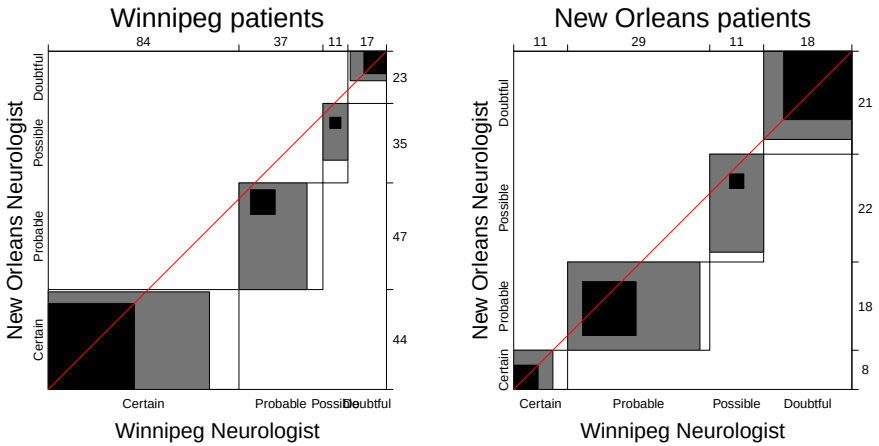
Husbands and wives: $B = 0.146$, $B^w = 0.498$

```
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 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

Example: UC Berkeley data

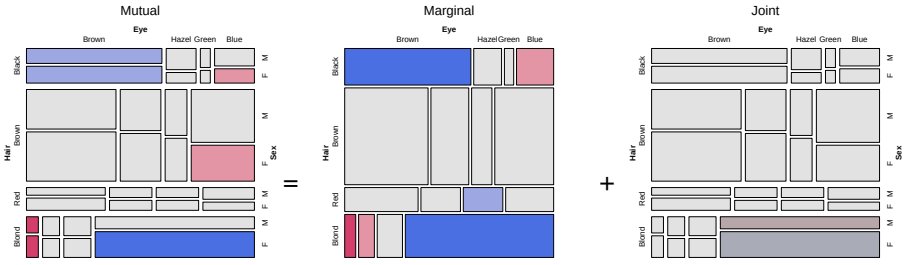
- Mutual independence: [Admit] [Gender] [Dept]
- Joint independence: [Admit] [Gender*Dept]
- Conditional independence: [Admit*Dept] [Admit*Gender]: A specific test for absence of gender bias, controlling for department

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]
$G^2_{(24)} = 166.30$

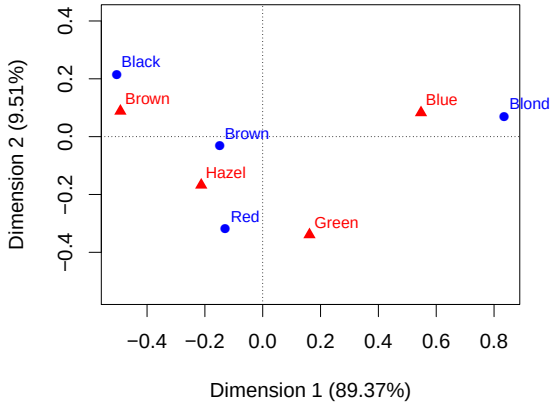
[Hair] [Eye]
$G^2_{(9)} = 146.44$

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

Looking ahead

Correspondence analysis

- Account for max. % of χ^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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