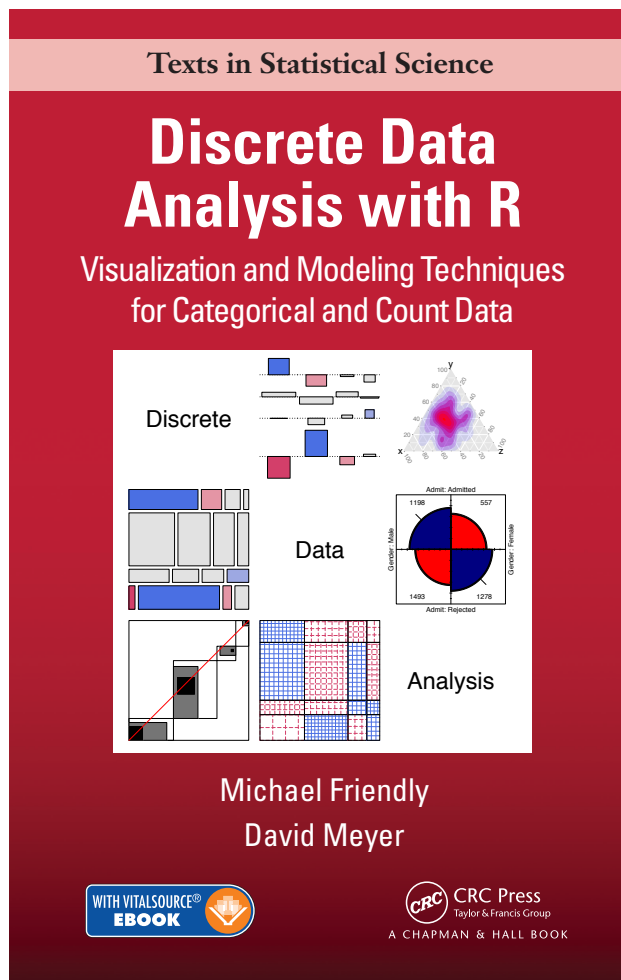# Discrete Data Analysis with R:
Solutions and Hints to Exercises

January 27, 2016

This document is intended as an aid to instructors who wish to use *Discrete Data Analysis with R* in a course. It contains the text of the **Exercises** sections from all chapters, together with some solutions or hints for the various problems. Answers are indicated with the ★ symbol, and with text in this font.

All R code for the book, and other materials are available on the web site, http://ddar.datavis.ca.

Chapter 1

Introduction

These questions are all conceptual, or based on judgment. No solutions are provided. In general, students should come up with some interesting examples related to the questions and explain why they consider them to be good or bad graphic or tabular displays.

Exercise 1.1 A web page, "The top ten worst graphs, " http://www.biostat.wisc.edu/~kbroman/topten_worstgraphs/ by Karl Broman lists his picks for the worst graphs (and a table) that have appeared in the statistical and scientific literature. Each entry links to graph(s) and a brief discussion of what is wrong and how it could be improved.

(a) Examine a number of recent issues of a scientific or statistical journal in which you have some interest. Find one or more examples of a graph or table that is a particularly bad use of display material to summarize and communicate research findings. Write a few sentences indicating how or why the display fails and how it could be improved.

(b) Do the same task for some popular magazine or newspaper that uses data displays to supplement the text for some story. Again, write a few sentences describing why the display is bad and how it could be improved.

Exercise 1.2 As in the previous exercise, examine the literature in recent issues of some journal of interest to you. Find one or more examples of a graph or table that you feel does a *good* job of summarizing and communicating research findings.

(a) Write a few sentences describing why you chose these displays.

(b) Now take the role of a tough journal reviewer. Are there any features of the display that could be modified to make them more effective?

Exercise 1.3 Infographics are another form of visual displays, quite different from the data graphics featured in this book, but often based on some data or analysis. Do a Google image search for the topic "Global warming" to see a rich collection.

(a) Find and study one or two images that attempt some visual explanation of causes and/or effects of global warming. Describe the main message in a sentence or two.

(b) What visual and graphic features are used in these to convey the message?

Exercise 1.4 The Wikipedia web page en.wikipedia.org/wiki/Portal:Global_warming gives a few data-based graphics on the topic of global warming. Read the text and study the graphs.

(a) Write a short figure title for each that would announce the conclusion to be drawn in a presentation graphic.

(b) Write a figure caption for each that would explain what is shown and the important graphical details for a reader to understand.

Exercise 1.5 The R Graph Gallery, http://rgraphgallery.blogspot.com/, contains a large collection of examples of graphs in R, tagged by type or content, together with the R code to produce them. Explore this collection for the terms (a) association plot (b) bar chart (c) categorical data (d) fluctuation diagram (e) mosaic plot Find one or two you particularly like and write a few sentences saying why you do.

Chapter 2

Working with Categorical Data

Exercise 2.1 The packages vcd (Meyer et al., 2015) and vcdExtra (Friendly, 2015) contain many data sets with some examples of analysis and graphical display. The goal of this exercise is to familiarize yourself with these resources.

You can get a brief summary of these using the function `datasets()` from vcdExtra. Use the following to get a list of these with some characteristics and titles.

```
> ds <- datasets(package = c("vcd", "vcdExtra"))
> str(ds, vec.len = 2)

'data.frame': 75 obs. of  5 variables:
 $ Package: chr  "vcd" "vcd" ...
 $ Item   : chr  "Arthritis" "Baseball" ...
 $ class  : chr  "data.frame" "data.frame" ...
 $ dim    : chr  "84x5" "322x25" ...
 $ Title  : chr  "Arthritis Treatment Data" "Baseball Data" ...
```

(a) How many data sets are there altogether? How many are there in each package?
★ `nrow()` gives the number of rows in a data frame. `table()` for a single variable gives the frequencies for each level.

```
> ds <- datasets(package=c("vcd", "vcdExtra"))
> nrow(ds)

[1] 75

> table(ds$Package)

    vcd vcdExtra
     33       42
```

(b) Make a tabular display of the frequencies by `Package` and `class`.
★ Use `table()`, but now for `Package` and `class`.

```
> table(ds$Package, ds$class)

           array data.frame matrix table
  vcd          1         17      0    15
  vcdExtra     3         23      1    15
```

(c) Choose one or two data sets from this list, and examine their help files (e.g., `help(Arthritis)` or `?Arthritis`). You can use, e.g., `example(Arthritis)` to run the R code for a given example.
★ Run the following types of commands:

```
> ?Arthritis           # Help Files
> ?Baseball            # Help Files
> example(Arthritis)   # Example Syntax/Analysis
> example(Baseball)    # Example Syntax/Analysis
```

Exercise 2.2 For each of the following data sets in the vcdExtra package, identify which are response variable(s) and which are explanatory. For factor variables, which are unordered (nominal) and which should be treated as ordered? Write a sentence or two describing substantitive questions of interest for analysis of the data. (*Hint*: use `data(foo, package="vcdExtra")` to load, and `str(foo)`, `help(foo)` to examine data set `foo`.)

(a) Abortion opinion data: *Abortion*
★ `Support_Abortion` is the response, `Sex` and `Status` are binary, nominal explanatory variables. From `help(Abortion)`, How does support for abortion depend on sex and status?

```
> data(Abortion, package="vcdExtra")
> str(Abortion)

 table [1:2, 1:2, 1:2] 171 152 138 167 79 148 112 133
 - attr(*, "dimnames")=List of 3
  ..$ Sex            : chr [1:2] "Female" "Male"
  ..$ Status         : chr [1:2] "Lo" "Hi"
  ..$ Support_Abortion: chr [1:2] "Yes" "No"
```

(b) Caesarian Births: *Caesar*
★ `Infection` is the response, `Risk`, `Antibiotics` and `Planned` are binary, nominal explanatory variables.

```
> data(Caesar, package="vcdExtra")
> str(Caesar)

 table [1:3, 1:2, 1:2, 1:2] 0 1 17 0 1 1 11 17 30 4 ...
 - attr(*, "dimnames")=List of 4
  ..$ Infection  : chr [1:3] "Type 1" "Type 2" "None"
  ..$ Risk       : chr [1:2] "Yes" "No"
  ..$ Antibiotics: chr [1:2] "Yes" "No"
  ..$ Planned    : chr [1:2] "Yes" "No"
```

(c) Dayton Survey: *DaytonSurvey*
★ In `DaytonSurvey`, the variables `cigarette`, `alcohol`, and `marijuana` can all be treated as response variables. `sex` and `race` are potential explanatory variables. Potentially interesting questions are how each of the responses depend on `sex` and `race`, and how they vary jointly.

```
> data(DaytonSurvey, package="vcdExtra")
> str(DaytonSurvey)
```

(d) Minnesota High School Graduates: *Hoyt*
★ `Status` is the response, `Rank`, `Occupation`, and `Sex` are explanatory variables. Both `Rank` and `Occupation` are ordinal. How does `Status` vary with `Rank`, `Occupation`, and `Sex`?

```
> data(Hoyt, package="vcdExtra")
> str(Hoyt)
```

Exercise 2.3 The data set *UCBAdmissions* is a 3-way table of frequencies classified by `Admit`, `Gender`, and `Dept`.

(a) Find the total number of cases contained in this table.
★ For a `table` object, just use `sum()`

```
> data(UCBAdmissions)
> sum(UCBAdmissions)

[1] 4526
```

(b) For each department, find the total number of applicants.
★ Use `margin.table(UCBAdmissions, 3)` to find the marginal total for the third dimension (dept).

```
> margin.table(UCBAdmissions, 3)

Dept
  A   B   C   D   E   F
933 585 918 792 584 714
```

(c) For each department, find the overall proportion of applicants who were admitted.
★

```
> ucb.df <- as.data.frame(UCBAdmissions)
> abd <- xtabs(Freq ~ Dept + Admit, data=ucb.df)
> prop.table(abd, 1)

     Admit
Dept Admitted Rejected
   A 0.644159 0.355841
   B 0.632479 0.367521
   C 0.350763 0.649237
   D 0.339646 0.660354
   E 0.251712 0.748288
   F 0.064426 0.935574
```

(d) Construct a tabular display of department (rows) and gender (columns), showing the proportion of applicants in each cell who were admitted relative to the total applicants in that cell.
★

Exercise 2.4 The data set *DanishWelfare* in vcd gives a 4-way, $3 \times 4 \times 3 \times 5$ table as a data frame in frequency form, containing the variable `Freq` and four factors, `Alcohol`, `Income`, `Status`, and `Urban`. The variable `Alcohol` can be considered as the response variable, and the others as possible predictors.

3

(a) Find the total number of cases represented in this table.

★ This is a data set in the form of a frequency data.frame, so sum the `Freq` variable

```
> data("DanishWelfare", package="vcd")
> sum(DanishWelfare$Freq)

[1] 5144
```

(b) In this form, the variables `Alcohol` and `Income` should arguably be considered *ordered* factors. Change them to make them ordered.

★ Use `ordered()` or `as.ordered()` on the factor variable. `str()` will then show them as `Ord.factor`.

```
> levels(DanishWelfare$Alcohol)

[1] "<1"  "1-2" ">2"

> DanishWelfare$Alcohol <- as.ordered(DanishWelfare$Alcohol)
> DanishWelfare$Income <- as.ordered(DanishWelfare$Income)
> str(DanishWelfare)

'data.frame': 180 obs. of  5 variables:
 $ Freq   : num  1 4 1 8 6 14 8 41 100 175 ...
 $ Alcohol: Ord.factor w/ 3 levels "<1"<"1-2"<">2": 1 1 1 1 1 1 1 1 1 1 ...
 $ Income : Ord.factor w/ 4 levels "0-50"<"50-100"<..: 1 1 1 1 1 1 1 1 1 1 ...
 $ Status : Factor w/ 3 levels "Widow","Married",..: 1 1 1 1 1 2 2 2 2 2 ...
 $ Urban  : Factor w/ 5 levels "Copenhagen","SubCopenhagen",..: 1 2 3 4 5 1 2 3 4 5 ...
```

(c) Convert this data frame to table form, `DanishWelfare.tab`, a 4-way array containing the frequencies with appropriate variable names and level names.

★ Use `xtabs()` with `Freq` as the response.

```
> DanishWelfare.tab <-xtabs(Freq ~ ., data = DanishWelfare)
> str(DanishWelfare.tab)

 xtabs [1:3, 1:4, 1:3, 1:5] 1 3 2 8 1 3 2 5 2 42 ...
 - attr(*, "dimnames")=List of 4
  ..$ Alcohol: chr [1:3] "<1" "1-2" ">2"
  ..$ Income : chr [1:4] "0-50" "50-100" "100-150" ">150"
  ..$ Status : chr [1:3] "Widow" "Married" "Unmarried"
  ..$ Urban  : chr [1:5] "Copenhagen" "SubCopenhagen" "LargeCity" "City" ...
 - attr(*, "class")= chr [1:2] "xtabs" "table"
 - attr(*, "call")= language xtabs(formula = Freq ~ ., data = DanishWelfare)
```

(d) The variable `Urban` has 5 categories. Find the total frequencies in each of these. How would you collapse the table to have only two categories, `City, Non-city`?

★ `margin.table()` handles the first part; `collapse.table()` is designed for the second part. It is arguable whether `SubCopenhagen` should be considered City or NonCity.

```
> margin.table(DanishWelfare.tab, 4)

Urban
   Copenhagen SubCopenhagen     LargeCity          City       Country
          552           614           594          1765          1619

> DW2 <- vcdExtra::collapse.table(DanishWelfare.tab,
+                        Urban=c("City","NonCity","City","City","NonCity"))
> head(ftable(DW2))

                              "Urban" "City" "NonCity"
 "Alcohol" "Income"  "Status"
 "<1"      "0-50"    "Widow"             10        10
                     "Married"          155       183
                     "Unmarried"         14        10
           "50-100"  "Widow"             29         7
                     "Married"          338       306
                     "Unmarried"         36        32
```

(e) Use `structable()` or `ftable()` to produce a pleasing flattened display of the frequencies in the 4-way table. Choose the variables used as row and column variables to make it easier to compare levels of `Alcohol` across the other factors.

★

Exercise 2.5 The data set *UKSoccer* in vcd gives the distributions of number of goals scored by the 20 teams in the 1995/96 season of the Premier League of the UK Football Association.

```
> data("UKSoccer", package = "vcd")
> ftable(UKSoccer)

    Away  0  1  2  3  4
Home
0          27 29 10  8  2
1          59 53 14 12  4
2          28 32 14 12  4
3          19 14  7  4  1
4           7  8 10  2  0
```

This two-way table classifies all $20 \times 19 = 380$ games by the joint outcome (Home, Away), the number of goals scored by the Home and Away teams. The value 4 in this table actually represents 4 or more goals.

(a) Verify that the total number of games represented in this table is 380.
★
```
> data("UKSoccer", package="vcd")
> sum(UKSoccer)

[1] 380

> margin.table(UKSoccer)

[1] 380
```

(b) Find the marginal total of the number of goals scored by each of the home and away teams.
★ Use margin.table() for each dimension:
```
> margin.table(UKSoccer, 1)

Home
  0   1   2   3   4
 76 142  90  45  27

> margin.table(UKSoccer, 2)

Away
  0   1   2   3   4
140 136  55  38  11
```

(c) Express each of the marginal totals as proportions.
★ Use prop.table() on the result of margin.table() for each dimension:
```
> prop.table(margin.table(UKSoccer, 1))

Home
       0        1        2        3        4
0.200000 0.373684 0.236842 0.118421 0.071053

> prop.table(margin.table(UKSoccer, 2))

Away
       0        1        2        3        4
0.368421 0.357895 0.144737 0.100000 0.028947
```

(d) Comment on the distribution of the numbers of home-team and away-team goals. Is there any evidence that home teams score more goals on average?
★ You could find the mean number of goals, weighted by their marginal frequencies. On average, home teams score about 0.4 more goals.
```
> weighted.mean(0:4, w=margin.table(UKSoccer,1))

[1] 1.4868

> weighted.mean(0:4, w=margin.table(UKSoccer,2))

[1] 1.0632
```
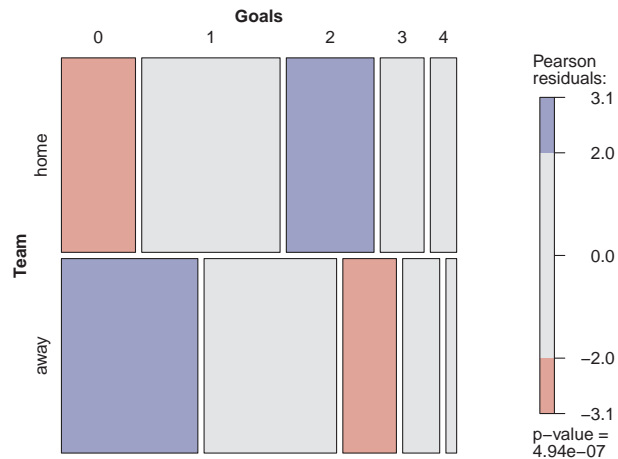
Graphically, you could also compare the marginal frequencies in a mosaic plot, or use agreementplot().

```
> margins <- rbind(home=margin.table(UKSoccer,1),
+                   away=margin.table(UKSoccer,2))
> names(dimnames(margins)) <- c("Team", "Goals")
> margins
```

```
        Goals
Team      0   1   2   3   4
   home  76 142  90  45  27
   away 140 136  55  38  11

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


Exercise 2.6 The one-way frequency table *Saxony* in vcd records the frequencies of families with 0, 1, 2, ... 12 male children, among 6115 families with 12 children. This data set is used extensively in Chapter 3.

```
> data("Saxony", package = "vcd")
> Saxony

nMales
   0    1    2    3    4    5    6    7    8    9   10   11   12
   3   24  104  286  670 1033 1343 1112  829  478  181   45    7
```

Another data set, *Geissler*, in the vcdExtra package, gives the complete tabulation of all combinations of boys and girls in families with a given total number of children (size). The task here is to create an equivalent table, Saxony12 from the *Geissler* data.

```
> data("Geissler", package = "vcdExtra")
> str(Geissler)

'data.frame': 90 obs. of  4 variables:
 $ boys : int  0 0 0 0 0 0 0 0 0 0 ...
 $ girls: num  1 2 3 4 5 6 7 8 9 10 ...
 $ size : num  1 2 3 4 5 6 7 8 9 10 ...
 $ Freq : int  108719 42860 17395 7004 2839 1096 436 161 66 30 ...
```

(a) Use subset() to create a data frame, sax12 containing the *Geissler* observations in families with size==12.
★

```
> data("Saxony", package="vcd")
> data("Geissler", package="vcdExtra")
> sax12 <- subset(Geissler, size==12)
> sax12

   boys girls size Freq
12    0    12   12    3
24    1    11   12   24
35    2    10   12  104
45    3     9   12  286
54    4     8   12  670
62    5     7   12 1033
```

6

```
69    6     6    12 1343
75    7     5    12 1112
80    8     4    12  829
84    9     3    12  478
87   10     2    12  181
89   11     1    12   45
90   12     0    12    7
```

(b) Select the columns for `boys` and `Freq`.

★

```
> sax12 <- subset(sax12, select=c("boys","Freq"))
```

(c) Use `xtabs()` with a formula, `Freq ~ boys`, to create the one-way table.

★

```
> Saxony12<-xtabs(Freq~boys, data=sax12)
> Saxony12

boys
   0    1    2    3    4    5    6    7    8    9   10   11   12
   3   24  104  286  670 1033 1343 1112  829  478  181   45    7
```

(d) Do the same steps again to create a one-way table, `Saxony11`, containing similar frequencies for families of `size==11`.

★

```
> sax11 <- subset(Geissler, size==11, select = c("boys","Freq"))
> Saxony11 <- xtabs(Freq~boys, data=sax11)
> Saxony11

boys
   0    1    2    3    4    5    6    7    8    9   10   11
   8   72  275  837 1540 2161 2310 1801 1077  492   93   24
```

Exercise 2.7 * *Interactive coding of table factors*: Some statistical and graphical methods for contingency tables are implemented only for two-way tables, but can be extended to 3+-way tables by recoding the factors to interactive combinations along the rows and/or columns, in a way similar to what `ftable()` and `structable()` do for printed displays.

For the *UCBAdmissions* data, produce a two-way table object, `UCB.tab2`, that has the combinations of `Admit` and `Gender` as the rows, and `Dept` as its columns, to look like the result below:

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

(a) Try this the long way: convert *UCBAdmissions* to a data frame (`as.data.frame()`), manipulate the factors (e.g., `interaction()`), then convert back to a table (`as.data.frame()`).

★

```
> ucb.df$AG <- with(ucb.df, interaction(Admit, Gender, sep=":"))
> ucb <- subset(ucb.df, select = c("Dept", "AG", "Freq"))
> ucb.tab2 <- xtabs(Freq ~ AG + Dept, data=ucb)
> ucb.tab2

                 Dept
AG                 A   B   C   D   E   F
  Admitted:Male   512 353 120 138  53  22
  Rejected:Male   313 207 205 279 138 351
  Admitted:Female  89  17 202 131  94  24
  Rejected:Female  19   8 391 244 299 317
```

(b) Try this the short way: both `ftable()` and `structable()` have `as.matrix()` methods that convert their result to a matrix.

★

```
> ucb.tab2 <- as.matrix(structable(Dept ~ Admit + Gender, data = UCBAdmissions))
> ucb.tab2

                 Dept
Admit_Gender       A   B   C   D   E   F
  Admitted_Male   512 353 120 138  53  22
  Admitted_Female  89  17 202 131  94  24
  Rejected_Male   313 207 205 279 138 351
  Rejected_Female  19   8 391 244 299 317
```

Exercise 2.8 The data set $VisualAcuity$ in **vcd** gives a $4 \times 4 \times 2$ table as a frequency data frame.

```
> data("VisualAcuity", package = "vcd")
> str(VisualAcuity)

'data.frame': 32 obs. of  4 variables:
 $ Freq  : num  1520 234 117 36 266 ...
 $ right : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
 $ left  : Factor w/ 4 levels "1","2","3","4": 1 1 1 1 2 2 2 2 3 3 ...
 $ gender: Factor w/ 2 levels "male","female": 2 2 2 2 2 2 2 2 2 2 ...
```

(a) From this, use `xtabs()` to create two 4×4 frequency tables, one for each gender.
★

```
> data("VisualAcuity", package="vcd")
> va.tabm <- xtabs(Freq ~ right+left, data = VisualAcuity, subset=gender=="male")
> va.tabm

     left
right   1   2   3   4
    1 821 112  85  35
    2 116 494 145  27
    3  72 151 583  87
    4  43  34 106 331

> va.tabf <- xtabs(Freq ~ right+left, data = VisualAcuity, subset=gender=="female")
> # or, subset after
> va.tab <- xtabs(Freq ~ ., data = VisualAcuity)
> va.tabm <- va.tab[,,"male"]
> va.tabf <- va.tab[,,"female"]
```

(b) Use `structable()` to create a nicely organized tabular display.
★

```
> structable(right ~ left + gender, data = va.tab)

            right    1    2    3    4
left gender
1    male          821  116   72   43
     female       1520  234  117   36
2    male          112  494  151   34
     female        266 1512  362   82
3    male           85  145  583  106
     female        124  432 1772  179
4    male           35   27   87  331
     female         66   78  205  492
```

(c) Use `xtable()` to create a LATEX or HTML table.
★

```
> library(xtable)
> va.xtab <- xtable(va.tabm)
> print(va.xtab, type="html")
```

Chapter 3

Fitting and Graphing Discrete Distributions

Exercise 3.1 The *Arbuthnot* data in HistData (Friendly, 2014a) (Example 3.1) also contains the variable Ratio, giving the ratio of male to female births.

(a) Make a plot of Ratio over Year, similar to Figure 3.1. What features stand out? Which plot do you prefer to display the tendency for more male births?
★

```
> library(HistData)
> data(Arbuthnot, package ="HistData")
>
>     # plot of Ratio by Year
> par(mar=c(5,4,1,1)+.1)
> with(Arbuthnot, {
+   plot(Year, Ratio, type='b', ylim=c(.95, 1.2),
+        ylab="Birth Ratio (Male/Female)")
+   abline(h=1, col="green", lwd=1)
+   abline(h=mean(Ratio), col="red")
+   text(x=1660, y=1, "Equal M/F ratio", pos=1, col="green3")
+   Arb.smooth <- loess.smooth(Year,Ratio)
+   lines(Arb.smooth$x, Arb.smooth$y, col="blue", lwd=2)
+ })
```
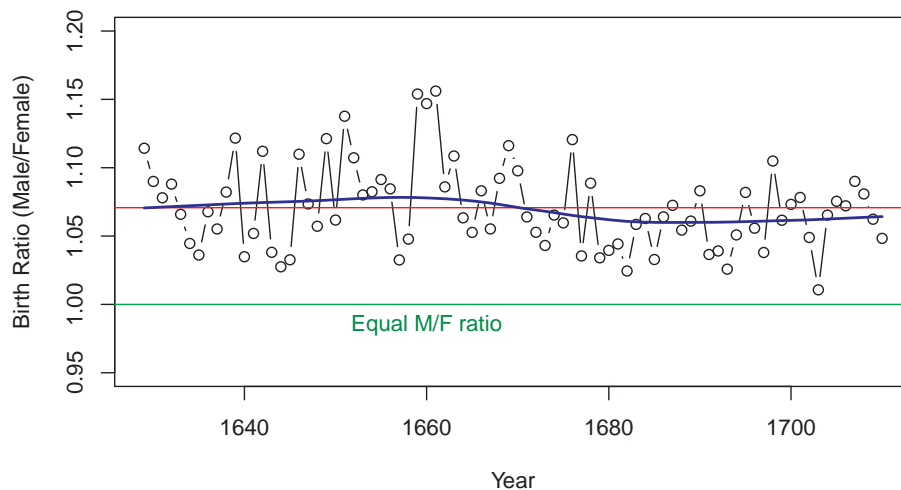

The plot is similar to Figure 3.1 in the text. If it is easier to think in terms of probability of a male birth, plotting that directly may be preferable.

(b) Plot the total number of christenings, Males + Females or Total (in 000s) over time. What unusual features do you see?
★

```
>     # total number of Christenings
> with(Arbuthnot, {
+   Total= Males + Females
+   plot(Year, Total, type='b', ylab="Total Christenings (Male + Female)")
+   Arb.smooth <- loess.smooth(Year,Total)
+   lines(Arb.smooth$x, Arb.smooth$y, col="blue", lwd=2)
+ })
```
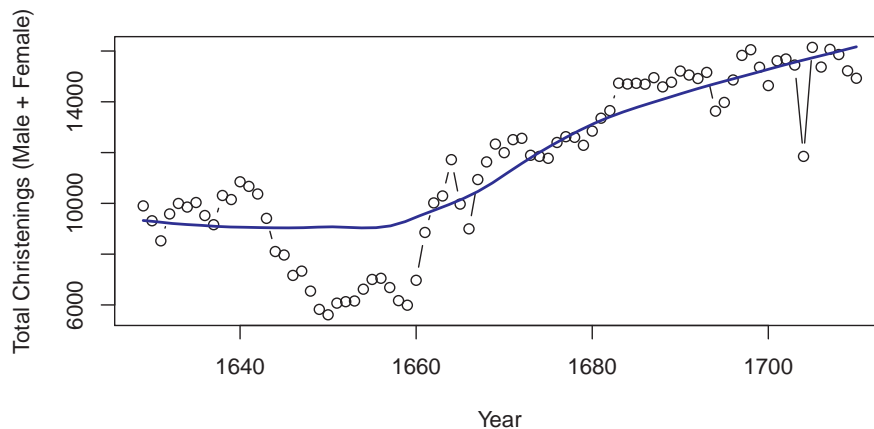
There was a large decline in births between 1640–1660, corresponding to years of plague in England.

Exercise 3.2 Use the graphical methods illustrated in Section 3.2 to plot a collection of geometric distributions for $p = 0.2, 0.4, 0.6, 0.8$, over a range of values of $k = 0, 1, \ldots 10$.

(a) With xyplot(), try the different plot formats using points connected with lines, as in Figure 3.9, or using points and lines down to the origin, as in the panels of Figure 3.10.
★

```
> KL <- expand.grid(k = 0 : 10, p = c(0.2, 0.4, 0.6, 0.8))
> geom_df <- data.frame(KL, prob = dgeom(KL$k, KL$p))
> geom_df$p = factor(geom_df$p)
>
> library(lattice)
> mycol<-palette()[2:5]
> xyplot(prob ~ k | p , data = geom_df, type = c("b"),
+        pch = 16, lwd = 4, cex = 1.25,
+        xlab = list("Number of events (k)", cex = 1.25), layout = c(2,2),
+        ylab = list("Probability", cex = 1.25))
> xyplot(prob ~ k | p , data = geom_df, type = c("h", "p"),
+        pch = 16, lwd = 4, cex = 1.25,
+        xlab = list("Number of events (k)", cex = 1.25), layout = c(2,2),
+        ylab = list("Probability", cex = 1.25))
```


10
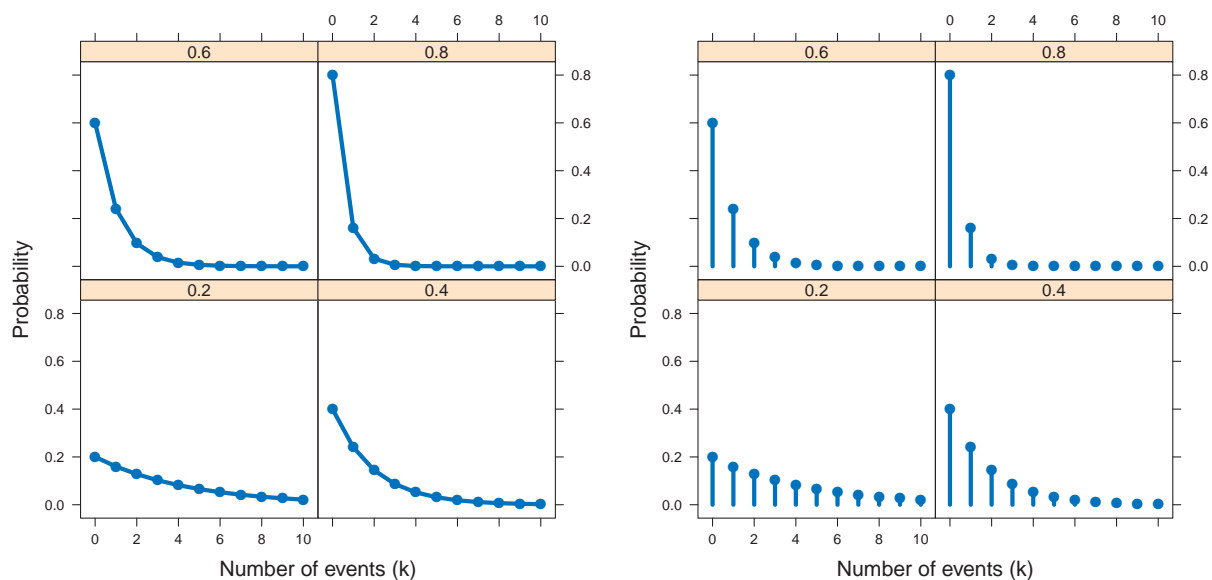
(b) Also with `xyplot()`, produce one version of a multi-line plot in a single panel that you think shows well how these distributions change with the probability p of success.

★

```
> geomplt<-xyplot(prob ~ k , data = geom_df, groups = p,
+                 type = c("b"), pch = 16, lwd = 4, cex = 1.25, col = mycol,
+                 xlab = list("Number of events (k)", cex = 1.25),
+                 ylab = list("Probability", cex = 1.25))
> library(directlabels)
> direct.label(geomplt, list("top.points", cex = 1.25, dl.trans(y = y + 0.1)))
```
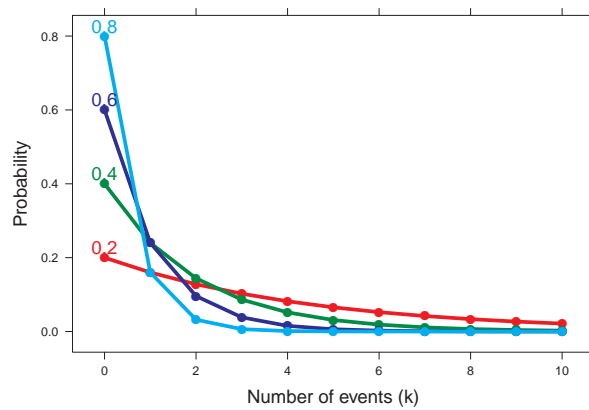

(c) Do the same in a multi-panel version, conditional on p.

★

```
> xyplot(prob ~ k | p , data = geom_df, type = c("b"),
+        pch = 16, lwd = 4, cex = 1.25,
+        xlab = list("Number of events (k)", cex = 1.1), layout = c(4,1),
+        ylab = list("Probability", cex = 1.25))
```
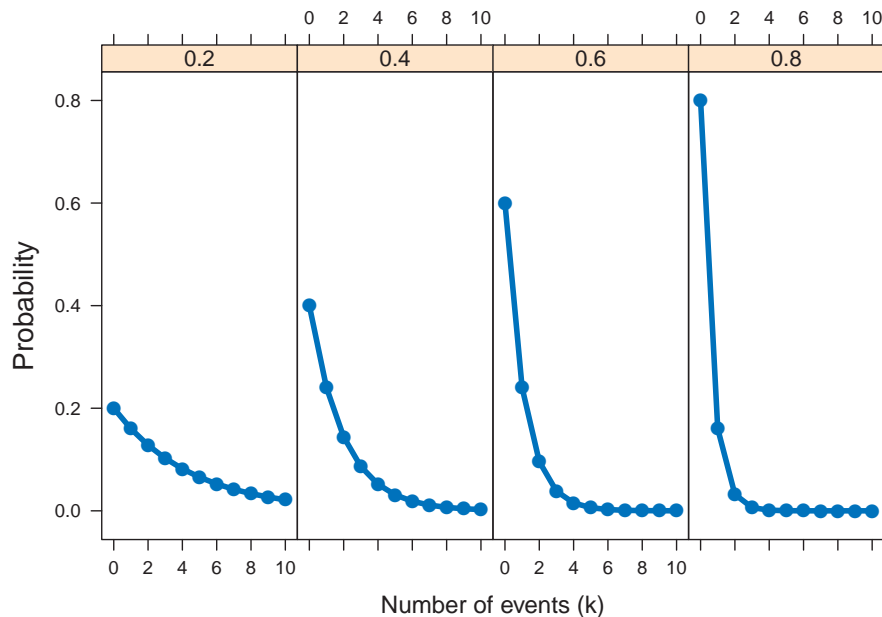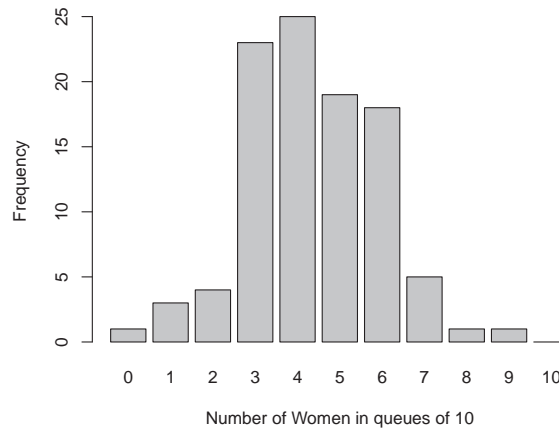

Exercise 3.3 Use the data set *WomenQueue* to:

(a) Produce plots analogous to those shown in Section 3.1 (some sort of bar graph of frequencies).

★

```
> data("WomenQueue", package = "vcd")
> barplot(WomenQueue, xlab="Number of Women in queues of 10", ylab= "Frequency")
```


(b) Check for goodness-of-fit to the binomial distribution using the goodfit() methods described in Section 3.3.2.
★ Note that with goodfit(), you should specify $n = 10$ for the binomial distribution as the size parameter.

```
> library(vcd)
> gf.women <- goodfit(WomenQueue, type = "binomial", par=list(size=10))
> summary(gf.women)

 Goodness-of-fit test for binomial distribution

                    X^2 df P(> X^2)
Likelihood Ratio 8.651  8  0.37259
```

(c) Make a reasonable plot showing departure from the binomial distribution.
★ The simplest plot is the hanging rootogram. An alternative plot is a "binomialness" plot produced by distplot().

```
> plot(gf.women, xlab = "Queue Length")
> distplot(WomenQueue, type = "binomial", size=10, xlab = "Queue Length")
```
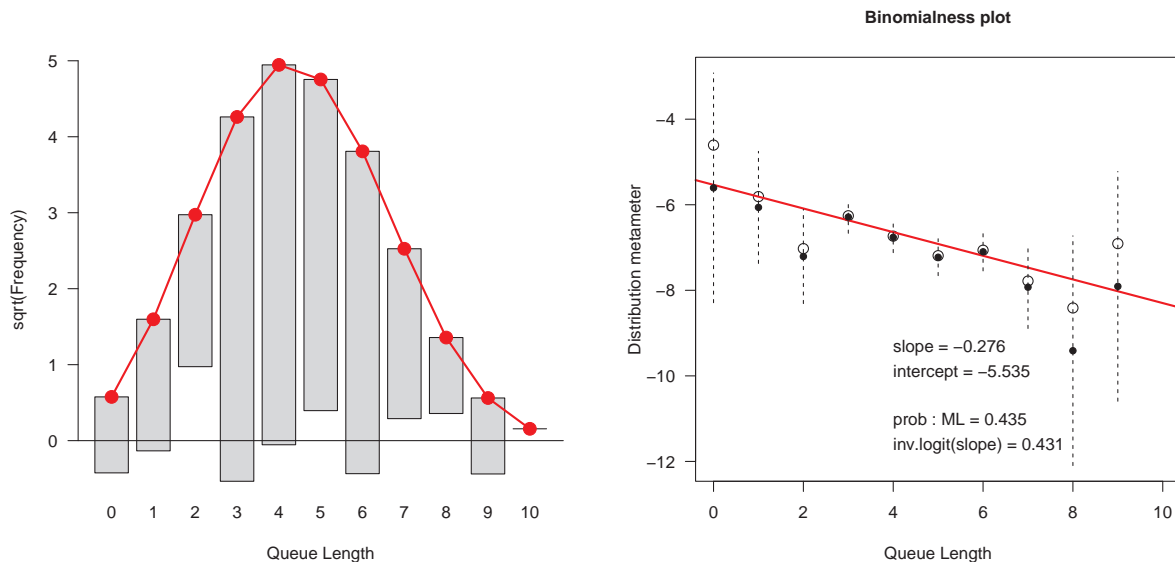

(d) Suggest some reasons why the number of women in queues of length 10 might depart from a binomial distribution, $\text{Bin}(n = 10, p = 1/2)$.
```

★

- Perhaps women (or men) are more prevalent in these queues, so $p \neq 1/2$.
- People often join lines in groups, so the observations are unlikely to be independent.

**Exercise 3.4** Continue Example 3.13 on the distribution of male children in families in Saxony by fitting a binomial distribution, $\mathrm{Bin}(n = 12, p = \frac{1}{2})$, specifying equal probability for boys and girls. [*Hint*: you need to specify both size and prob values for goodfit().]

(a) Carry out the GOF test for this fixed binomial distribution. What is the ratio of $\chi^2/df$? What do you conclude?
★ Note that you need to specify both $n$ and $p$ as fixed parameters here.

```
> Saxony_gf <-goodfit(Saxony, type = "binomial", par=list(size=12, prob=.5))
> ss <-summary(Saxony_gf)

 Goodness-of-fit test for binomial distribution

                   X^2 df   P(> X^2)
Pearson         249.20 12 2.0133e-46
Likelihood Ratio 205.41 12 2.4936e-37

>   #The ratio of Chi-square/df
> ss[,"X^2"] / ss[,"df"]

        Pearson Likelihood Ratio
         20.766           17.117
```

The binomial model fits very badly.

(b) Test the additional lack of fit for the model $\mathrm{Bin}(n = 12, p = \frac{1}{2})$ compared to the model $\mathrm{Bin}(n = 12, p = \hat{p})$ where $\hat{p}$ is estimated from the data.
★

```
> Saxony_gf2 <- goodfit(Saxony, type = "binomial", par=list(size=12))
> summary(Saxony_gf2)

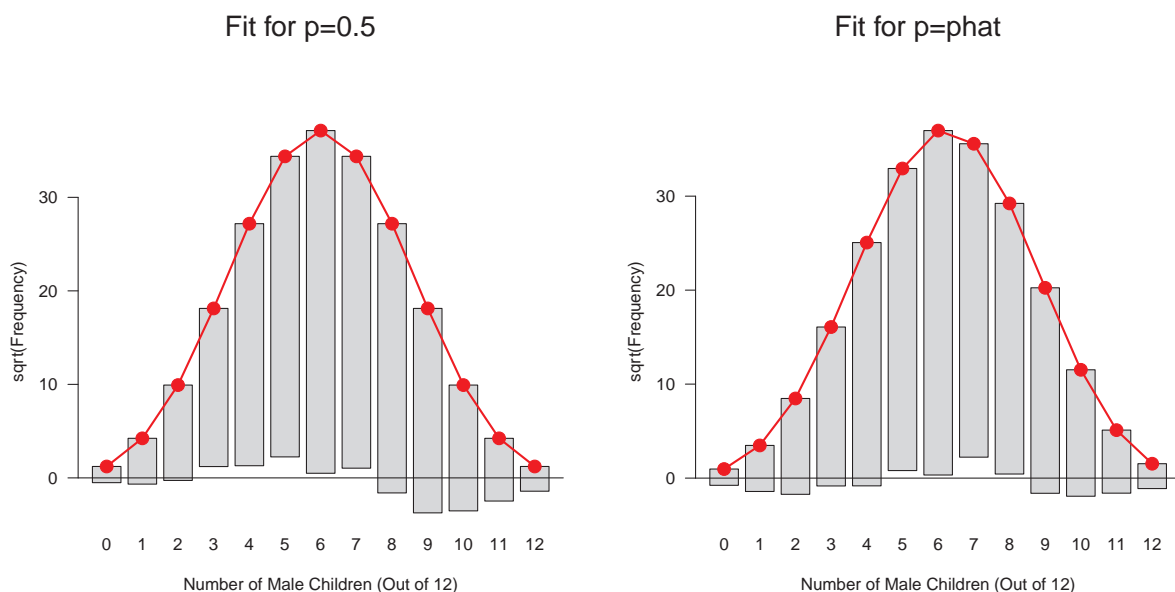 Goodness-of-fit test for binomial distribution

                   X^2 df   P(> X^2)
Likelihood Ratio 97.007 11 6.9782e-16
```

This fits much better, but still not a good fit.

(c) Use the plot.gootfit() method to visualize these two models.
★

```
> plot(Saxony_gf, main = "Fit for p=0.5", xlab = "Number of Male Children (Out of 12)")
> plot(Saxony_gf2, main = "Fit for p=phat", xlab = "Number of Male Children (Out of 12)")
```

Exercise 3.5 For the *Federalist* data, the examples in Section 3.3.1 and Section 3.3.2 showed the negative bino-mial to provide an acceptable fit. Compare this with the simpler special case of geometric distribution, corresponding to $n = 1$.

(a) Use `goodfit()` to fit the geometric distribution. [Hint: use `type="nbinomial"`, but specify `size=1` as a parameter.]
★

```
> fdfit1 <- goodfit(Federalist, type = "binomial", par = list(size=6))
> fdfit1

Observed and fitted values for binomial distribution
with parameters estimated by `ML'

 count observed      fitted pearson residual
     0      156 1.3072e+02          2.21074
     1       63 9.6362e+01         -3.39860
     2       29 2.9597e+01         -0.10972
     3        8 4.8483e+00          1.43139
     4        4 4.4673e-01          5.31624
     5        1 2.1954e-02          6.60094
     6        1 4.4953e-04         47.14399

> fdfit2 <- goodfit(Federalist, type = "nbinomial", par = list(size=1))
> fdfit2

Observed and fitted values for nbinomial distribution
with parameters estimated by `ML with size fixed'

 count observed      fitted pearson residual
     0      156 158.16590        -0.172219
     1       63  62.68326         0.040006
     2       29  24.84221         0.834194
     3        8   9.84530        -0.588102
     4        4   3.90182         0.049702
     5        1   1.54635        -0.439353
     6        1   0.61284        -0.015044
```

(b) Compare the negative binomial and the geometric models statistically, by a likelihood-ratio test of the difference between these two models.
★

```
> summary(fdfit1)

 Goodness-of-fit test for binomial distribution

                    X^2 df    P(> X^2)
Likelihood Ratio 49.026  5 2.1927e-09
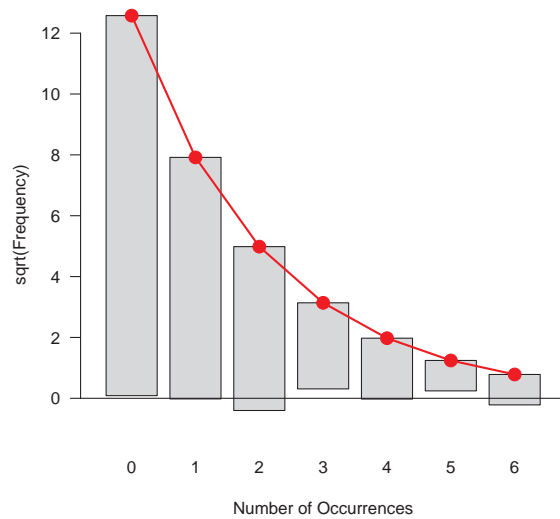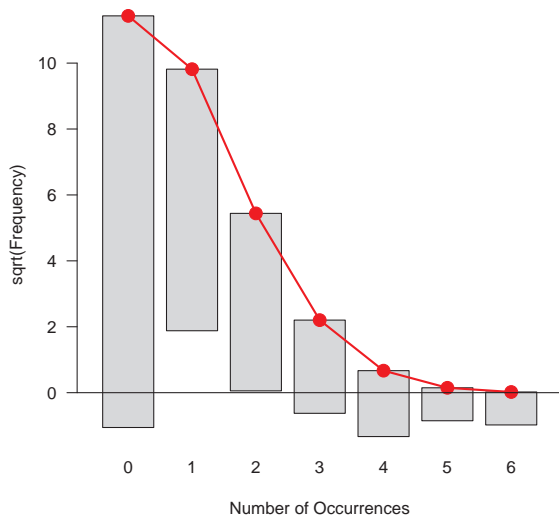
> summary(fdfit2)

 Goodness-of-fit test for nbinomial distribution

                   X^2 df P(> X^2)
Likelihood Ratio 2.2941  5  0.80713
```

(c) Compare the negative binomial and the geometric models visually by hanging rootograms or other methods.
★ Hanging rootograms:

```
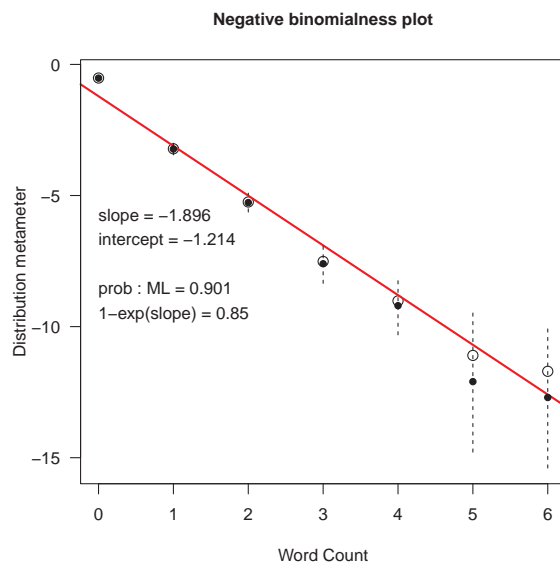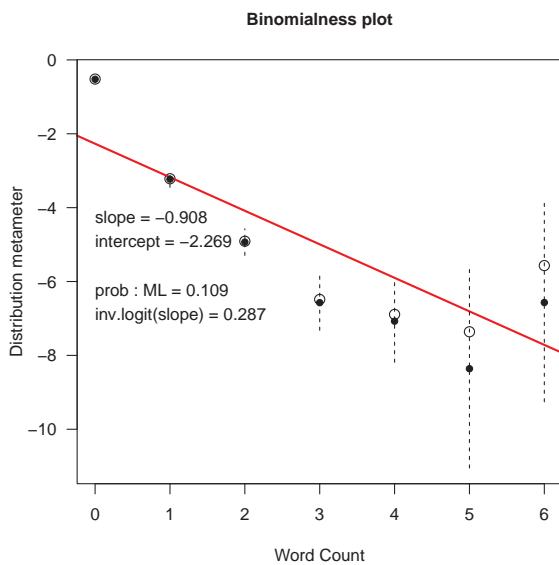> plot(fdfit1)
> plot(fdfit2)
```

Distribution-ness plots:

```
> distplot(Federalist, type = "binomial", size=6, xlab = "Word Count")
> distplot(Federalist, type = "nbinomial", size=6, xlab = "Word Count")
```


Exercise 3.6 Mosteller and Wallace (1963, Table 2.4) give the frequencies, n_k, of counts $k = 0, 1, \ldots$ of other selected marker words in 247 blocks of text known to have been written by Alexander Hamilton. The data below show the occurrences of the word *upon*, that Hamilton used much more than did James Madison.

```
> count <- 0 : 5
> Freq <- c(129, 83, 20, 9, 5, 1)
```

(a) Read these data into R and construct a one-way table of frequencies of counts or a matrix or data frame with frequencies in the first column and the corresponding counts in the second column, suitable for use with `goodfit()`.
★ `goodfit()` requires its first argument to be either a one-way table (from `xtabs()`), or a data.frame with frequencies in the *first* column and the corresponding counts in the second column. Both of the following forms will work.

15

```
> count <- 0:5
> Freq <- c(129, 83, 20, 9, 5, 1)
> sum(Freq)   # check N

[1] 247

> (Upon <- data.frame(Freq, count))           # as a data.frame

  Freq count
1  129     0
2   83     1
3   20     2
4    9     3
5    5     4
6    1     5

> (Upon.tab <- xtabs(Freq ~ count, data=Upon))   # one-way table

count
  0   1   2   3   4   5
129  83  20   9   5   1
```

(b) Fit and plot the Poisson model for these frequencies.
★

```
> (up0 <- goodfit(Upon, type="poisson"))

Observed and fitted values for poisson distribution
with parameters estimated by `ML'

 count observed     fitted pearson residual
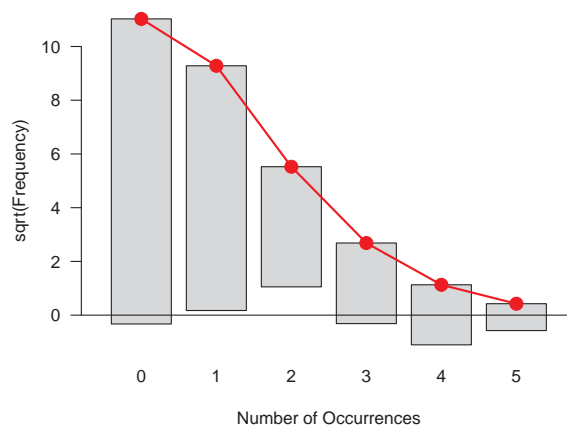     0      129 121.61816          0.66937
     1       83  86.16671         -0.34115
     2       20  30.52465         -1.90494
     3        9   7.20892          0.66708
     4        5   1.27688          3.29481
     5        1   0.18094          1.75800

> summary(up0)

 Goodness-of-fit test for poisson distribution

                    X^2 df P(> X^2)
Likelihood Ratio 13.139  4 0.010617

> plot(up0)
```


(c) Fit and plot the negative binomial model for these frequencies.
★

```
> (up1 <- goodfit(Upon, type="nbinomial"))

Observed and fitted values for nbinomial distribution
with parameters estimated by `ML'

 count observed     fitted pearson residual
     0      129 131.65936         -0.231767
```

```
   1       83  73.89421           1.059285
   2       20  28.41547          -1.578705
   3        9   9.25319          -0.083233
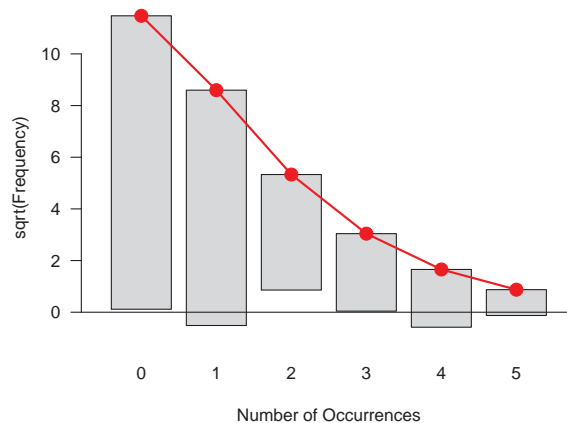   4        5   2.74068           1.364738
   5        1   0.76332          -0.036432
> summary(up1)

 Goodness-of-fit test for nbinomial distribution

                     X^2 df P(> X^2)
Likelihood Ratio 6.0306  3  0.11013

> plot(up1)
```


(d) What do you conclude?

★ The negative binomial model fits better than the Poisson.

Exercise 3.7 The data frame *Geissler* in the vcdExtra package contains the complete data from Geissler's (1889) tabulation of family sex composition in Saxony. The table below gives the number of boys in families of size 11.

boys	0	1	2	3	4	5	6	7	8	9	10	11
Freq	8	72	275	837	1,540	2,161	2,310	1,801	1,077	492	93	24

(a) Read these data into R.

★ See Exercise 2.6, which calculates `sax11` in the form of a data frame.

(b) Following Example 3.13, use `goodfit()` to fit the binomial model and plot the results. Is there an indication that the binomial does not fit these data?

★ The binomial distribution fits badly, where the extremes are under-fitted, and the middle values are over-fitted.

```
> sax11.tab <- xtabs(Freq ~ boys, data=sax11)
> goodfit(sax11.tab, type="binomial", par=list(size=11))

Observed and fitted values for binomial distribution
with parameters estimated by `ML'

 count observed      fitted pearson residual
    0         8     3.5616           2.3518
    1        72    41.9479           4.6400
    2       275   224.5724           3.3650
    3       837   721.3629           4.3055
    4      1540  1544.7559          -0.1210
    5      2161  2315.6023          -3.2128
    6      2310  2479.3627          -3.4013
    7      1801  1896.2173          -2.1866
    8      1077  1015.1593           1.9409
    9       492   362.3173           6.8130
   10        93    77.5881           1.7497
   11        24     7.5523           5.9850

> summary(goodfit(sax11.tab, type="binomial", par=list(size=11)))
```

```
Goodness-of-fit test for binomial distribution

                    X^2 df   P (> X^2)
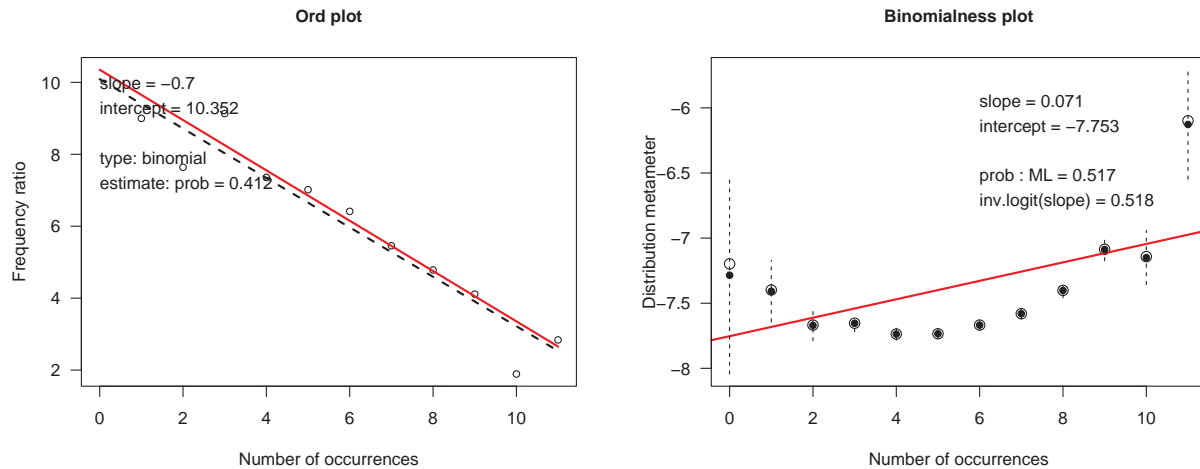Likelihood Ratio 148.09 10  9.2126e-27
```

(c) Diagnose the form of the distribution using the methods described in Section 3.4.

★ The Ord plot indicates that the closest distribution according to its heuristics is the binomial; the binomialness distribution plot, however, shows this is not an acceptable model, as was also seen in the text for families of size 12.

```
> Ord_plot(sax11.tab)
> distplot(sax11.tab, type="binomial", size=11)
```


Ord plot   **Binomialness plot**

(d) Try fitting the negative binomial distribution, and use `distplot()` to diagnose whether the negative binomial is a reasonable fit. **TODO**: Something wrong here.

★

```
> goodfit(sax11.tab, type="nbinomial", par=list(size=11))

Observed and fitted values for nbinomial distribution
with parameters estimated by `ML with size fixed'

 count observed   fitted pearson residual
     0        8   109.12            -9.6801
     1       72   409.11           -16.6667
     2      275   836.63           -19.4171
     3      837  1235.67           -11.3414
     4     1540  1474.07             1.7171
     5     2161  1507.26            16.8389
     6     2310  1369.95            25.3981
     7     1801  1133.97            19.8082
     8     1077   869.62             7.0323
     9      492   625.73            -5.3462
    10       93   426.55           -16.1500
    11       24   277.55           -25.3999
```

Exercise 3.8 The data frame *Bundesliga* gives a similar data set to that for UK soccer scores (*UKSoccer*) examined in Example 3.9, but over a wide range of years. The following lines calculate a two-way table, `BL1995`, of home-team and away-team goals for the 306 games in the year 1995.

```
> data("Bundesliga", package = "vcd")
> BL1995 <- xtabs(~ HomeGoals + AwayGoals, data = Bundesliga,
+                 subset = (Year == 1995))
> BL1995

         AwayGoals
HomeGoals  0  1  2  3  4  5  6
        0 26 16 13  5  0  1  0
        1 19 58 20  5  4  0  1
        2 27 23 20  5  1  1  1
        3 14 11 10  4  2  0  0
```

```
   4  3  5  3  0  0  0  0
   5  4  1  0  1  0  0  0
   6  1  0  0  1  0  0  0
```

(a) As in , find the one-way distributions of `HomeGoals`, `AwayGoals`, and `TotalGoals` = `HomeGoals` +
`AwayGoals`.
★ There are several ways to do this, but as illustrated in the text for Example 3.9, create the one-way
variables in a `data.frame`, and then use `xtabs()` to get their marginal distributions.

```
> BL.df <- as.data.frame(BL1995, stringsASFactors=FALSE)
> BL.df <- within(BL.df, {
+   HomeGoals <- as.numeric(HomeGoals)
+   AwayGoals <- as.numeric(AwayGoals)
+   TotalGoals <- HomeGoals + AwayGoals
+   })
>    # marginal distributions
> (BL.home <- xtabs(Freq ~ HomeGoals, data=BL.df))

HomeGoals
  1   2   3   4   5   6   7
 61 107  78  41  11   6   2

> (BL.away <- xtabs(Freq ~ AwayGoals, data=BL.df))

AwayGoals
  1   2   3   4   5   6   7
 94 114  66  21   7   2   2

> (BL.total <- xtabs(Freq ~ TotalGoals, data=BL.df))

TotalGoals
 2  3  4  5  6  7  8  9 10 11 12 13 14
26 35 98 62 39 29 10  4  2  1  0  0  0
```

(b) Use `goodfit()` to fit and plot the Poisson distribution to each of these. Does the Poisson seem to provide a
reasonable fit?
★ The Poisson distribution has a bad fit for all of these.

```
> summary(goodfit(BL.home))

 Goodness-of-fit test for poisson distribution

                     X^2 df    P(> X^2)
Likelihood Ratio 70.722  5 7.2516e-14

> summary(goodfit(BL.away))

 Goodness-of-fit test for poisson distribution

                     X^2 df    P(> X^2)
Likelihood Ratio 97.973  5 1.4131e-19
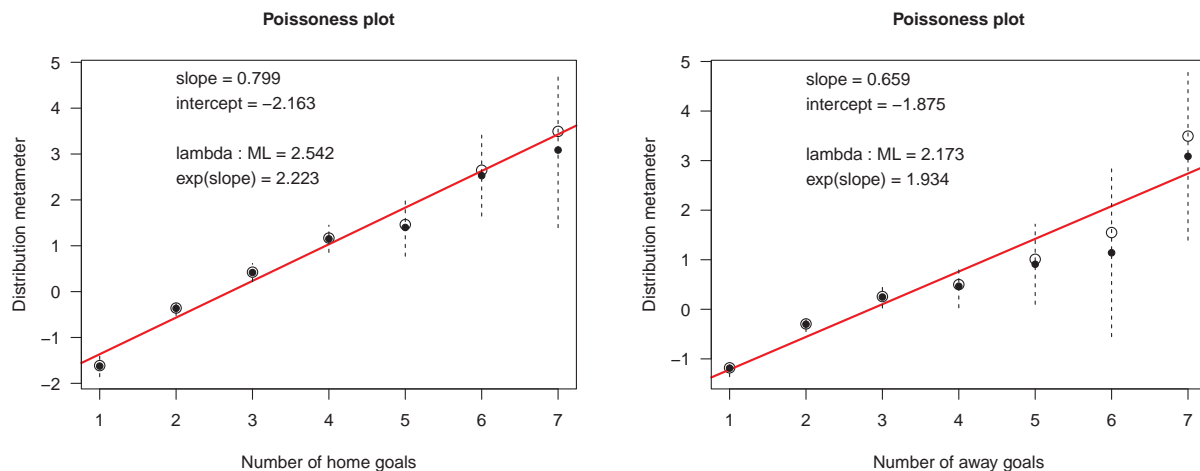
> summary(goodfit(BL.total))

 Goodness-of-fit test for poisson distribution

                     X^2 df    P(> X^2)
Likelihood Ratio 72.558  8 1.5185e-12
```

(c) Use `distplot()` to assess fit of the Poisson distribution.
★ The distribution plots for home goals looks better than that for away goals, which shows a systematic
departure from the red line.

```
> distplot(BL.home, xlab="Number of home goals")
> distplot(BL.away, xlab="Number of away goals")
```

Poissoness plot (left)

slope = 0.799
intercept = −2.163

lambda : ML = 2.542
exp(slope) = 2.223

Distribution metameter / Number of home goals

Poissoness plot (right)

slope = 0.659
intercept = −1.875

lambda : ML = 2.173
exp(slope) = 1.934

Distribution metameter / Number of away goals

(d) What circumstances of scoring goals in soccer might cause these distributions to deviate from Poisson distributions?

★ The Poisson distribution relies on (a) independent events with (b) constant probabilities. The probability of scoring a goal is almost certainly not constant over all pairs of teams.

Exercise 3.9 ⋆ Repeat the exercise above, this time using the data for all years in which there was the standard number (306) of games, that is for `Year>1965`, tabulated as shown below.

```
> BL <- xtabs(~ HomeGoals + AwayGoals, data = Bundesliga,
+              subset = (Year > 1965))
> BL

         AwayGoals
HomeGoals    0    1    2    3    4    5    6    7    8    9
       0   868  590  458  206   88   22   12    2    0    0
       1  1049 1550  589  360  121   34    8    6    1    1
       2  1039 1144  810  228   95   26   10    2    1    0
       3   712  793  392  187   43    8    5    2    0    0
       4   346  388  245   73   26    2    3    0    0    0
       5   128  164  106   34    2    2    1    0    0    0
       6    61   63   38   10    0    2    0    0    0    0
       7    20   16   12    4    3    0    0    0    0    0
       8     2    4    3    0    1    0    0    0    0    0
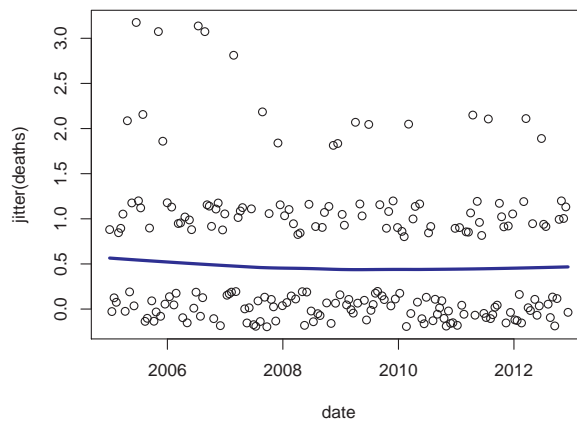       9     2    2    1    0    0    0    0    0    0    0
      10     2    0    0    0    0    0    0    0    0    0
      11     1    2    0    0    0    0    0    0    0    0
      12     1    0    0    0    0    0    0    0    0    0
```

★ The steps are similar to those in the previous problem, but now there are more years, and the range of both home goals and away goals is larger.

Exercise 3.10 Using the data *CyclingDeaths* introduced in Example 3.6 and the one-way frequency table `CyclingDeaths.tab = table(CyclingDeaths$deaths)`,

(a) Make a sensible plot of the number of deaths over time. For extra credit, add a smoothed curve (e.g., using `lines(lowess(...))`).
★ The number of deaths in a given fortnight are discrete, taking values $0:3$. A barplot, using `plot(deaths ~ date, type="h", data=CyclingDeaths)` is one option. Perhaps slightly better is to jitter the number of deaths.

```
> data("CyclingDeaths", package="vcdExtra")
> CyclingDeaths.tab <- table(CyclingDeaths$deaths)
> plot(jitter(deaths) ~ date, data=CyclingDeaths)
> with(CyclingDeaths, {lines(lowess(date, deaths), lwd=3, col="blue")})
```

(b) Test the goodness of fit of the table `CyclingDeaths.tab` to a Poisson distribution statistically using `goodfit()`.
★

```
> gf <- goodfit(CyclingDeaths.tab)
> gf

Observed and fitted values for poisson distribution
with parameters estimated by `ML'

 count observed    fitted pearson residual
     0      114 117.9464          -0.36338
     1       75  66.9119           0.98877
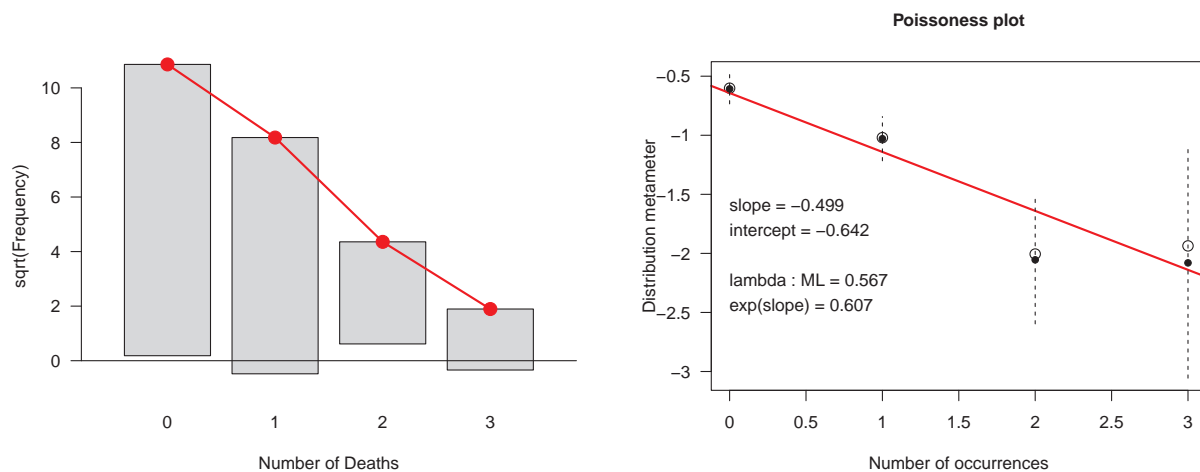     2       14  18.9798          -1.14306
     3        5   3.5891           0.41084

> summary(gf)

 Goodness-of-fit test for poisson distribution

                   X^2 df P(> X^2)
Likelihood Ratio 4.1517  2  0.12545
```

(c) Continue this analysis using a `rootogram()` and `distplot()`.
★

```
> plot(gf, xlab="Number of Deaths")
> distplot(CyclingDeaths.tab)
```


(d) Write a one-paragraph summary of the results of these analyses and your conclusions.
★

Exercise 3.11 * The one-way table, *Depends*, in vcdExtra and shown below gives the frequency distribution of the number of dependencies declared in $4,983$ R packages maintained on the CRAN distribution network on January 17, 2014. That is, there were 986 packages that had no dependencies, $1,347$ packages that depended on one other package, ... up to 2 packages that depended on 14 other packages.

Depends	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14
# Pkgs	986	1,347	993	685	375	298	155	65	32	19	9	4	9	4	2

(a) Make a bar plot of this distribution.
★

```
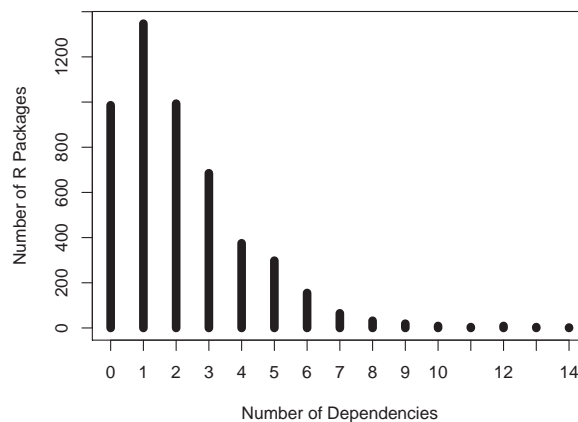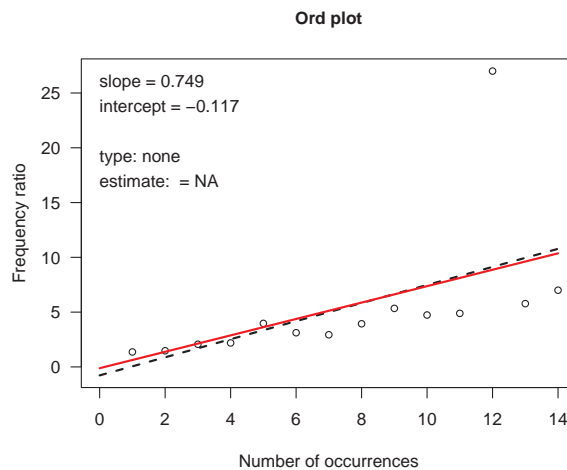> data("Depends", package="vcdExtra")
> plot(Depends, xlab="Number of Dependencies", ylab="Number of R Packages", lwd=8)
```


(b) Use Ord_plot() to see if this method can diagnose the form of the distribution.
★ This turns out to be a case where the Ord plot method, as implemented in Ord_plot() does not determine the form of the distribution. According to Table 3.11, the log series distribution is the only one with positive slope b and negative intercept a, but this requires $a = -b$.

```
> Ord_plot(Depends)
```


(c) Try to fit a reasonable distribution to describe dependencies among R packages.
★ Among the distributions described in Chapter 3 and implemented in the vcd package the negative binomial may be the best to try.

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```
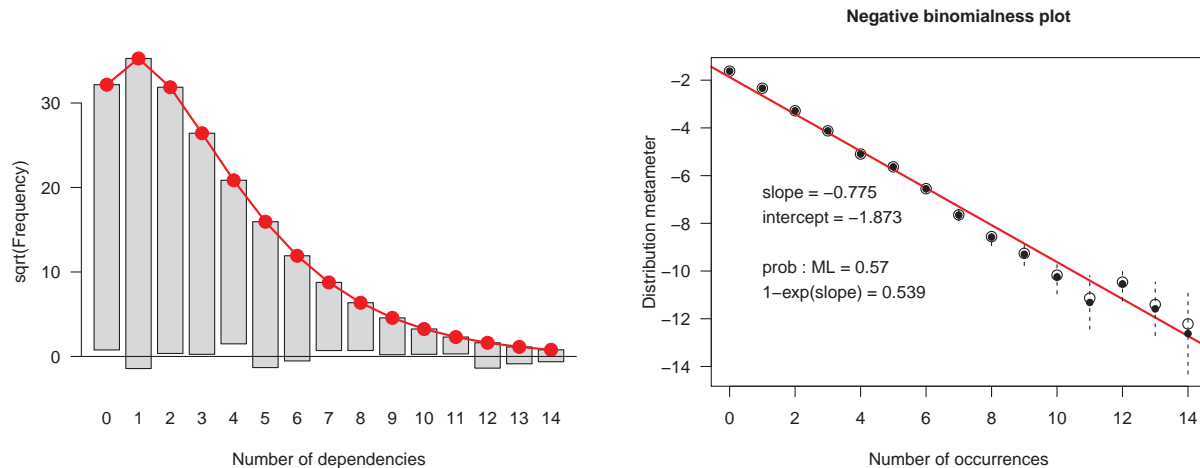> dep.gf <- goodfit(Depends, type="nbinomial")
> summary(dep.gf)

 Goodness-of-fit test for nbinomial distribution

                  X^2 df   P(> X^2)
Likelihood Ratio 49.081 12 2.0243e-06

> plot(dep.gf, xlab="Number of dependencies")
> distplot(Depends, type="nbinomial")
```


So, this does not fit well, particularly for the packages with many dependencies, but it is not altogether terrible. The remaining differences come from further heterogeneity for which we haven't got any covariates in the data set. For example, the age of the package would seem like a natural candidate: older packages probably have fewer dependencies.

Exercise 3.12 * How many years does it take to get into the baseball Hall of Fame? The Lahman (Friendly, 2014b) package provides a complete record of historical baseball statistics from 1871 to the present. One table, *HallOfFame*, records the history of players nominated to the Baseball Hall of Fame, and those eventually inducted. The table below, calculated in help(HallOfFame, package="Lahman"), records the distribution of the number of years taken (from first nomination) for the 109 players in the Hall of Fame to be inducted (1936–present). Note that years==0 does not, and cannot, occur in this table, so the distribution is restricted to positive counts. Such distributions are called *zero-truncated distribution*s. Such distributions are like the ordinary ones, but with the probability of zero being zero. Thus the other probabilities are scaled up (i.e., divided by $1 - \Pr(Y = 0)$) so they sum to 1.

years	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
inducted	46	10	8	7	8	4	2	4	6	3	3	1	4	1	2

(a) For the Poisson distribution, show that the zero-truncated probability function can be expressed in the form

$$\Pr\{X = k \mid k > 0\} = \frac{1}{1 - e^{-\lambda}} \times \frac{e^{-\lambda} \lambda^k}{k!} \qquad k = 1, 2, \ldots$$

★ The standard Poisson distribution has the probability mass function

$$\Pr\{X = k\} = \frac{e^{-\lambda} \lambda^k}{k!} \quad k = 1, 2, \ldots .$$

For this, $\Pr\{X = 0\} = e^{-\lambda}$. The formula given in the problem scales the standard probability to account for zero-truncation, i.e., by the factor $\frac{1}{1 - \Pr\{X=0\}}$.

(b) Show that the mean is $\lambda/(1 - \exp(-\lambda))$.

★

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(c) Enter these data into R as a one-way table, and use `goodfit()` to fit the standard Poisson distribution, as if you hadn't encountered the problem of zero truncation.
★ The rootogram below shows why zero truncation needs to be taken into account.

```
> years <- 1:15
> inducted <- c(46, 10,  8,  7,  8,  4,  2,  4,  6,  3,  3,  1,  4,  1,  2)
> HOF.df <- data.frame(years, inducted)
> HOF.tab <- xtabs(inducted ~ years, data=HOF.df)
> goodfit(HOF.tab)

Observed and fitted values for poisson distribution
with parameters estimated by `ML'

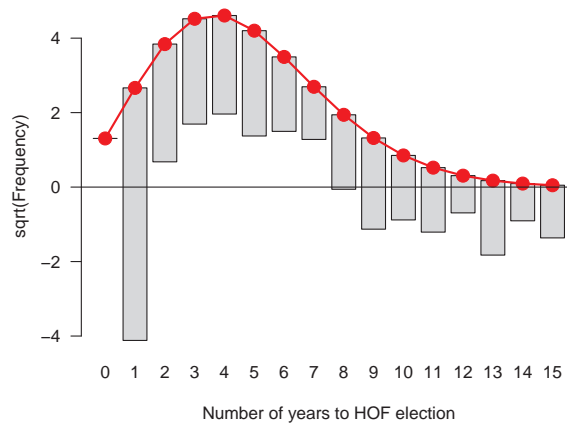 count observed      fitted pearson residual
     0        0  1.7081050         -1.30694
     1       46  7.0988218         14.60056
     2       10 14.7512214         -1.23706
     3        8 20.4351783         -2.75082
     4        7 21.2319627         -3.08866
     5        8 17.6478516         -2.29660
     6        4 12.2239706         -2.35221
     7        2  7.2574819         -1.95157
     8        4  3.7702285          0.11833
     9        6  1.7409924          3.22782
    10        3  0.7235500          2.67623
    11        3  0.2733679          5.21498
    12        1  0.0946756          2.94229
    13        4  0.0302668         22.81803
    14        1  0.0089848         10.45503
    15        2  0.0024894         34.54549

> summary(HOF.tab)

Number of cases in table: 109
Number of factors: 1

> plot(goodfit(HOF.tab), xlab='Number of years to HOF election')
```


Though not asked in the problem, the zero-truncated Poisson distribution can be fit using `vglm()` in the VGAM (Yee, 2015) package.

```
> library(VGAM)
> hof.tpois0 <- vglm(years ~ 1, family=pospoisson, data=HOF.df, weights=inducted)
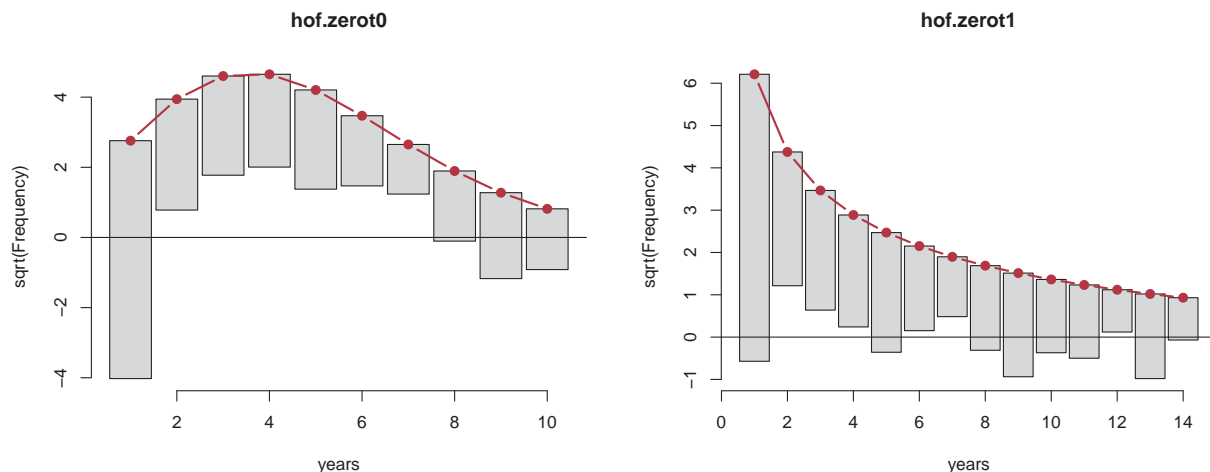> hof.tpois0

Call:
vglm(formula = years ~ 1, family = pospoisson, data = HOF.df,
    weights = inducted)

Coefficients:
(Intercept)
     1.4076

Degrees of Freedom: 15 Total; 14 Residual
Log-likelihood: -339.31
```

Models for count data, taking account of excess zeros or zero truncation are examined in more detail in Chapter 11. There, we use the countreg (Zeileis and Kleiber, 2014) package, that provides a `zerotrunc()` function for these problems. The zero truncated negative binomial provides a better fit than the zero truncated Poisson, but that is not great either.

```
> library(countreg)
> hof.zerot0 <- zerotrunc(years ~ 1, weights = inducted, data=HOF.df)
> hof.zerot1 <- zerotrunc(years ~ 1, weights = inducted, dist="negbin")
> countreg::rootogram(hof.zerot0)
> countreg::rootogram(hof.zerot1)
```


Chapter 4

Two-Way Contingency Tables

Exercise 4.1 The data set `fat`, created below, gives a 2×2 table recording the level of cholesterol in diet and the presence of symptoms of heart disease for a sample of 23 people.

```
> fat <- matrix(c(6, 4, 2, 11), 2, 2)
> dimnames(fat) <- list(diet = c("LoChol", "HiChol"),
+                        disease = c("No", "Yes"))
```

(a) Use `chisq.test(fat)` to test for association between diet and disease. Is there any indication that this test may not be appropriate here?
★

(b) Use a fourfold display to test this association visually. Experiment with the different options for standardizing the margins, using the `margin` argument to `fourfold()`. What evidence is shown in different displays regarding whether the odds ratio differs significantly from 1?
★

(c) `oddsratio(fat, log = FALSE)` will give you a numerical answer. How does this compare to your visual impression from fourfold displays?
★

(d) With such a small sample, Fisher's exact test may be more reliable for statistical inference. Use `fisher.test(fat)`, and compare these results to what you have observed before.
★

(e) Write a one-paragraph summary of your findings and conclusions for this data set.
★

Exercise 4.2 The data set *Abortion* in vcdExtra gives a $2 \times 2 \times 2$ table of opinions regarding abortion in relation to sex and status of the respondent. This table has the following structure:

```
> data("Abortion", package = "vcdExtra")
> str(Abortion)

 table [1:2, 1:2, 1:2] 171 152 138 167 79 148 112 133
 - attr(*, "dimnames")=List of 3
  ..$ Sex             : chr [1:2] "Female" "Male"
  ..$ Status          : chr [1:2] "Lo" "Hi"
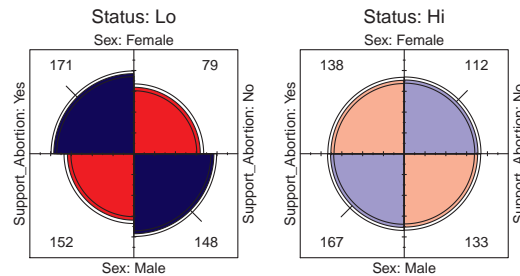  ..$ Support_Abortion: chr [1:2] "Yes" "No"
```

(a) Taking support for abortion as the outcome variable, produce fourfold displays showing the association with sex, stratified by status.
★

```
> data("Abortion", package="vcdExtra")
> structable(Abortion)

                     Status   Lo   Hi
Sex     Support_Abortion
Female  Yes                  171  138
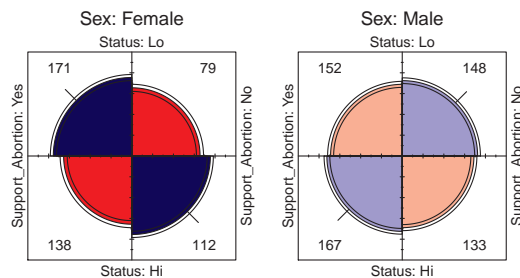        No                    79  112
Male    Yes                  152  167
        No                   148  133

> Abortion2<-aperm(Abortion, c(1,3,2))
> fourfold(Abortion2)
```


(b) Do the same for the association of support for abortion with status, stratified by sex.
★

```
> Abortion3<-aperm(Abortion, c(2,3,1))
> fourfold(Abortion3)
```

(c) For each of the problems above, use `oddsratio()` to calculate the numerical values of the odds ratio, as stratified in the question.

★

```
>       # Sex by support for abortion, stratified by status
> summary(oddsratio(Abortion2))

z test of coefficients:

                      Estimate Std. Error z value Pr(>|z|)
Female:Male/Yes:No|Lo   0.7455     0.1784    4.18  2.9e-05 ***
Female:Male/Yes:No|Hi  -0.0189     0.1723   -0.11     0.91
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>       # Status by support for abortion, stratified by sex
> summary(oddsratio(Abortion3))

z test of coefficients:

                    Estimate Std. Error z value Pr(>|z|)
Lo:Hi/Yes:No|Female    0.563      0.186    3.03   0.0025 **
Lo:Hi/Yes:No|Male     -0.201      0.164   -1.23   0.2199
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(d) Write a brief summary of how support for abortion depends on sex and status.
★ Regardless of status, more women say no to abortion and more men say yes. Regardless of gender, more low status say no and more high status say yes.

Exercise 4.3 The *JobSat* table on income and job satisfaction created in Example 2.5 is contained in the vcdExtra package.

(a) Carry out a standard χ^2 test for association between income and job satisfaction. Is there any indication that this test might not be appropriate? Repeat this test using `simulate.p.value = TRUE` to obtain a Monte Carlo test that does not depend on large sample size. Does this change your conclusion?
★

(b) Both variables are ordinal, so CMH tests may be more powerful here. Carry out that analysis. What do you conclude?
★

Exercise 4.4 The *Hospital* data in vcd gives a 3×3 table relating the length of stay (in years) of 132 long-term schizophrenic patients in two London mental hospitals with the frequency of visits by family and friends.

(a) Carry out a χ^2 test for association between the two variables.
★

```
> data("Hospital", package="vcd")
> chisq.test(Hospital)

Pearson's Chi-squared test

data:  Hospital
X-squared = 35.2, df = 4, p-value = 4.3e-07
```

(b) Use `assocstats()` to compute association statistics. How would you describe the strength of association here?
★

```
> assocstats(Hospital)

                    X^2 df    P(> X^2)
Likelihood Ratio 38.353  4 9.4755e-08
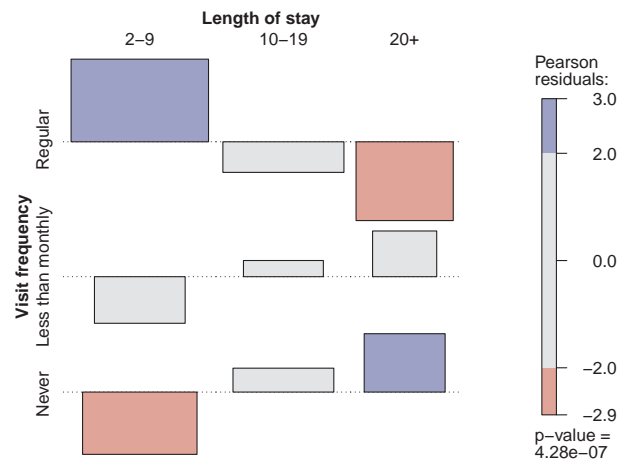Pearson          35.171  4 4.2842e-07

Phi-Coefficient   : NA
Contingency Coeff.: 0.459
Cramer's V        : 0.365
```

By the contingency coefficient, there is moderately strong association between the length of stay long-term schizophrenic patients and the frequency of visits by family and friends.

(c) Produce an association plot for these data, with visit frequency as the vertical variable. Describe the pattern of the relation you see here.
★

```
> assoc(Hospital, shade=TRUE)
```


(d) Both variables can be considered ordinal, so `CMHtest()` may be useful here. Carry out that analysis. Do any of the tests lead to different conclusions?
★

```
> CMHtest(Hospital)

Cochran-Mantel-Haenszel Statistics for Visit frequency by Length of stay

               AltHypothesis Chisq Df     Prob
cor         Nonzero correlation  29.1  1 6.74e-08
rmeans  Row mean scores differ  34.4  2 3.40e-08
cmeans  Col mean scores differ  29.6  2 3.72e-07
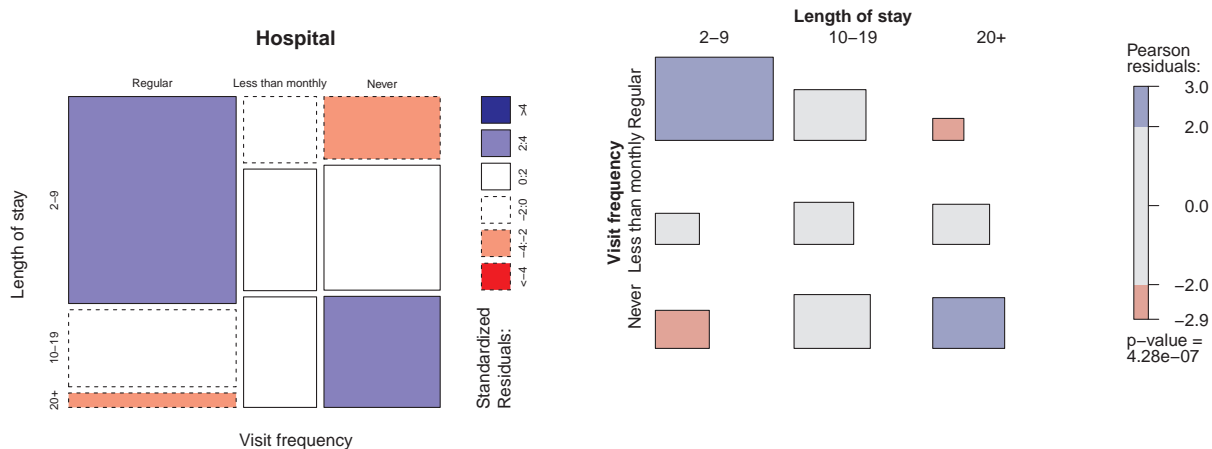general    General association  34.9  4 4.86e-07
```

The results of all four tests lead to the same conclusion that there is a significant association between the visit frequency and the length of stay. The test for non-zero correlation, trteating both variables as ordinal, has the largest ratio of χ^2/df.

Exercise 4.5 Continuing with the *Hospital* data:

(a) Try one or more of the following other functions for visualizing two-way contingency tables with this data: `plot()`, `tile()`, `mosaic()`, and `spineplot()`. [For all except `spineplot()`, it is useful to include the argument `shade=TRUE`].

★

```
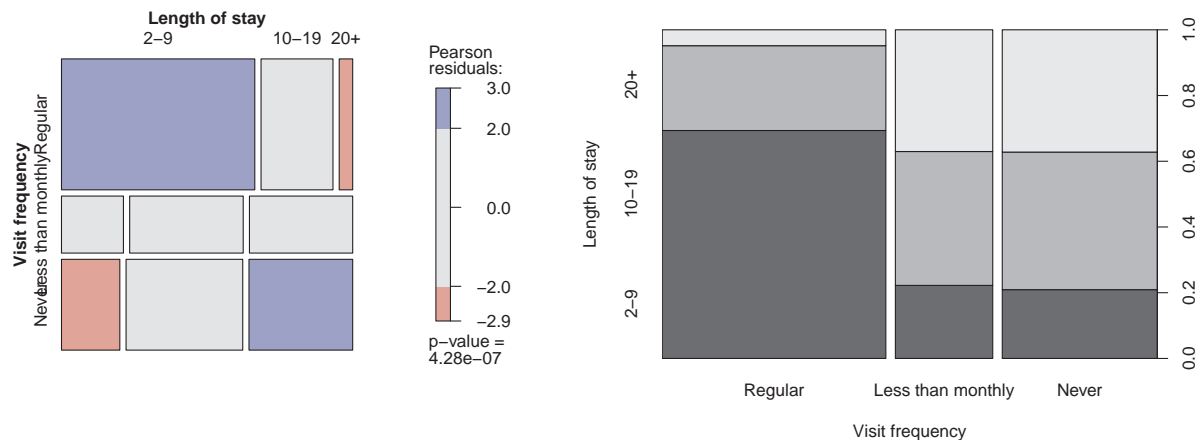> plot(Hospital, shade=TRUE)
> tile(Hospital, shade=TRUE)
```


★

```
> mosaic(Hospital, shade=TRUE)
> spineplot(Hospital)
```


(b) Comment on the differences among these displays for understanding the relation between visits and length of stay.

★

Exercise 4.6 The two-way table `Mammograms` in vcdExtra gives ratings on the severity of diagnosis of 110 mammograms by two raters.

(a) Assess the strength of agreement between the raters using Cohen's κ, both unweighted and weighted.
★ Both unweighted and weighted κ indicate substantial agreement. Fleiss-Cohen weights give greater weight to the "near-misses," so gives a larger value.

```
> Kappa(Mammograms)
           value     ASE      z Pr(>|z|)
```

```
Unweighted 0.371 0.0603  6.15 7.56e-10
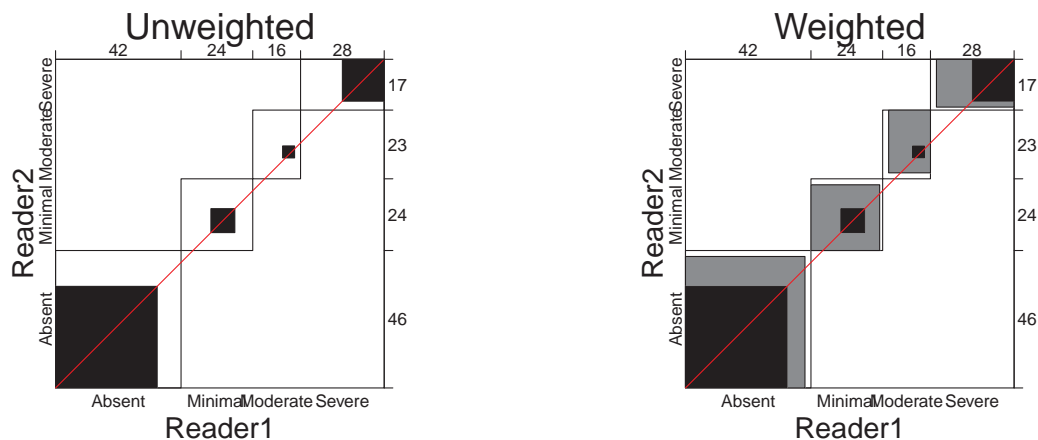Weighted   0.596 0.0492 12.11 8.90e-34

> Kappa(Mammograms, weights= "Fleiss-Cohen")

           value    ASE      z Pr(>|z|)
Unweighted 0.371 0.0603  6.15 7.56e-10
Weighted   0.764 0.0400 19.12 1.67e-81
```

(b) Use `agreementplot()` for a graphical display of agreement here.
★ The default for `agreementplot()` shows the weighted display, so you can use `weights=1` for the unweighted version.

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


(c) Compare the Kappa measures with the results from `assocstats()`. What is a reasonable interpretation of each of these measures?
★ The contingency coefficient and Cramer's V assess only association, so these could be large when there is little agreement. The values of these statistics are not directly comparable.

```
> assocstats(Mammograms)

                    X^2 df    P(> X^2)
Likelihood Ratio 92.619  9 4.4409e-16
Pearson          83.516  9 3.2307e-14

Phi-Coefficient   : NA
Contingency Coeff.: 0.657
Cramer's V        : 0.503
```

Exercise 4.7 Agresti and Winner (1997) gave the data in Table 4.1 on the ratings of 160 movies by the reviewers Gene Siskel and Roger Ebert for the period from April 1995 through September 1996. The rating categories were Con ("thumbs down"), Mixed, and Pro ("thumbs up").

Table 4.1: Movie ratings by Siskel & Ebert, April 1995–September 1996. *Source*: Agresti and Winner (1997)

		Ebert			
		Con	Mixed	Pro	Total
	Con	24	8	13	45
Siskel	Mixed	8	13	11	32
	Pro	10	9	64	83
	Total	42	30	88	160

(a) Assess the strength of agreement between the raters using Cohen's κ, both unweighted and weighted.
★

```
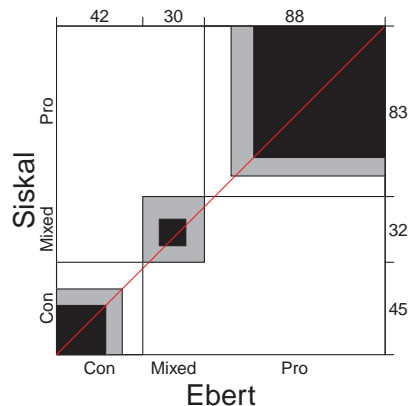> ratings <- matrix(
+ c(
+    24,   8, 13,
+     8, 13, 11,
+    10,   9, 64
+ ), 3, 3, byrow=TRUE)
> dimnames(ratings) <- list(Siskal=c("Con", "Mixed", "Pro"),
+                           Ebert =c("Con", "Mixed", "Pro"))
> Kappa(ratings)

          value    ASE    z Pr(>|z|)
Unweighted 0.389 0.0598 6.50 7.87e-11
Weighted   0.427 0.0635 6.72 1.78e-11
```

(b) Use `agreementplot()` for a graphical display of agreement here.
★ The agreement plot shows that both Siskal and Ebert most commonly gave "thumbs up" ratings where they largely agreed. Their ratings differed most when one of them gave a Mixed rating.

```
> agreementplot(ratings)
```


(c) Assess the hypothesis that the ratings are *symmetric* around the main diagonal, using an appropriate χ^2 test. *Hint*: Symmetry for a square table T means that $t_{ij} = t_{ji}$ for $i \neq j$. The expected frequencies under the hypothesis of symmetry are the average of the off-diagonal cells, $E = (T + T^\mathsf{T})/2$.
★

```
> T <- (ratings + t(ratings))/2
> (Chisq <- sum((ratings - T)^2 / T))

[1] 0.5913

> df <- nrow(T) * (nrow(T)-1) /2
> pchisq(Chisq,df, lower.tail = FALSE)

[1] 0.89842
```

(d) Compare the results with the output of `mcnemar.test()`.
★

```
> mcnemar.test(ratings)

        McNemar's Chi-squared test

data:  ratings
McNemar's chi-squared = 0.591, df = 3, p-value = 0.9
```

Exercise 4.8 For the *VisualAcuity* data set:

(a) Use the code shown in the text to create the table form, `VA.tab`.
★

```
> data("VisualAcuity", package = "vcd")
> VA <- xtabs(Freq ~ right + left + gender, data = VisualAcuity)
> dimnames(VA)[1:2] <- list(c("high", 2, 3, "low"))
> names(dimnames(VA))[1:2] <- paste(c("Right", "Left"), "eye grade")
```

(b) Perform the CMH tests for this table.
★

```
> CMHtest(VA)

$`gender:male`
Cochran-Mantel-Haenszel Statistics for Right eye grade by Left eye grade
in stratum gender:male

                AltHypothesis Chisq Df Prob
cor        Nonzero correlation  1555  1   0
rmeans  Row mean scores differ  1556  3   0
cmeans  Col mean scores differ  1557  3   0
general     General association  3303  9   0


$`gender:female`
Cochran-Mantel-Haenszel Statistics for Right eye grade by Left eye grade
in stratum gender:female

                AltHypothesis Chisq Df Prob
cor        Nonzero correlation  3691  1   0
rmeans  Row mean scores differ  3709  3   0
cmeans  Col mean scores differ  3724  3   0
general     General association  8096  9   0
```

(c) Use the `woolf_test()` described in Section 4.3.2 to test whether the association between left and right eye acuity can be considered the same for men and women.
★ The Woolf test gives no evidence that the association differs for men and women.

```
> woolf_test(VA)

Woolf-test on Homogeneity of Odds Ratios (no 3-Way assoc.)

data:  VA
X-squared = 0.0892, df = 1, p-value = 0.77
```

Exercise 4.9 The graph in Figure 4.23 may be misleading, in that it doesn't take into account of the differing capacities of the 18 life boats on the *Titanic*, given in the variable `cap` in the `Lifeboats` data.

(a) Calculate a new variable, `pctloaded`, as the percentage loaded relative to the boat capacity.
★

```
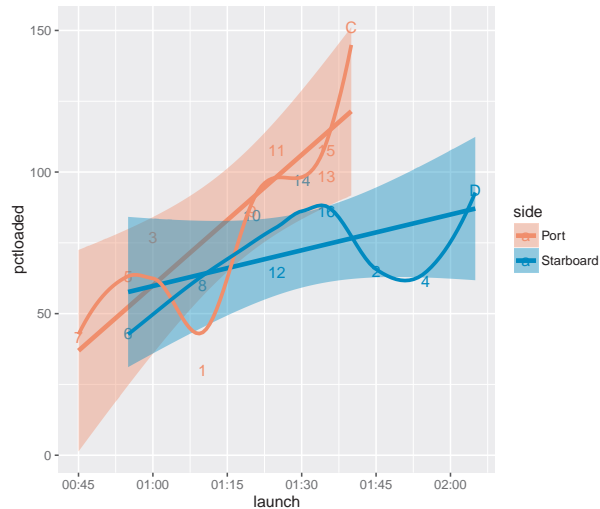> Lifeboats$pctloaded <- with(Lifeboats, 100*total/cap)
```

(b) Produce a plot similar to Figure 4.23, showing the changes over time in this measure.
★ Boats on the port side began loading earlier, but were initally less than half full. Boats launched from the starbord side were more consistent over time. With percent loaded (0–100) as the response, a linear model is only a rough approximation.

```
> library(ggplot2)
> AES <- aes(x = launch, y = pctloaded, colour = side, label = boat)
> ggplot(data = Lifeboats, mapping = AES) +
+     geom_text() +
+     geom_smooth(method = "lm", aes(fill = side), size = 1.5) +
+     geom_smooth(method = "loess", aes(fill = side), se = FALSE,
+                 size = 1.2)
```

Test a model allowing different slopes and intercepts for port and starboard sides:

```
> summary(lm(pctloaded ~ side * as.numeric(launch), data=Lifeboats))

Call:
lm(formula = pctloaded ~ side * as.numeric(launch), data = Lifeboats)

Residuals:
   Min     1Q Median     3Q    Max
-45.34 -11.78   0.34  11.46  29.61

Coefficients:
                                Estimate Std. Error t value Pr(>|t|)
(Intercept)                     4.67e+07   1.10e+07    4.24  0.00083 ***
sideStarboard                  -3.39e+07   1.48e+07   -2.29  0.03800 *
as.numeric(launch)              2.56e-02   6.05e-03    4.24  0.00083 ***
sideStarboard:as.numeric(launch) -1.86e-02  8.12e-03   -2.29  0.03800 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 20.2 on 14 degrees of freedom
Multiple R-squared:  0.602,Adjusted R-squared:  0.517
F-statistic: 7.06 on 3 and 14 DF,  p-value: 0.004
```

Chapter 5

Mosaic Displays for n-Way Tables

Exercise 5.1 The data set *criminal* in the package logmult (Bouchet-Valat, 2015) gives the 4×5 table below of the number of men aged 15–19 charged with a criminal case for whom charges were dropped in Denmark from 1955–1958.

```
> data("criminal", package = "logmult")
> criminal

      Age
Year    15  16  17  18  19
  1955 141 285 320 441 427
  1956 144 292 342 441 396
  1957 196 380 424 462 427
  1958 212 424 399 442 430
```

(a) Use `loglm()` to test whether there is an association between `Year` and `Age`. Is there evidence that dropping of charges in relation to age changed over the years recorded here?

★ There is a significant association between `Year` and `Age`, so the row profiles of proportions differ over year.

```
> loglm(~Year + Age, data=criminal)
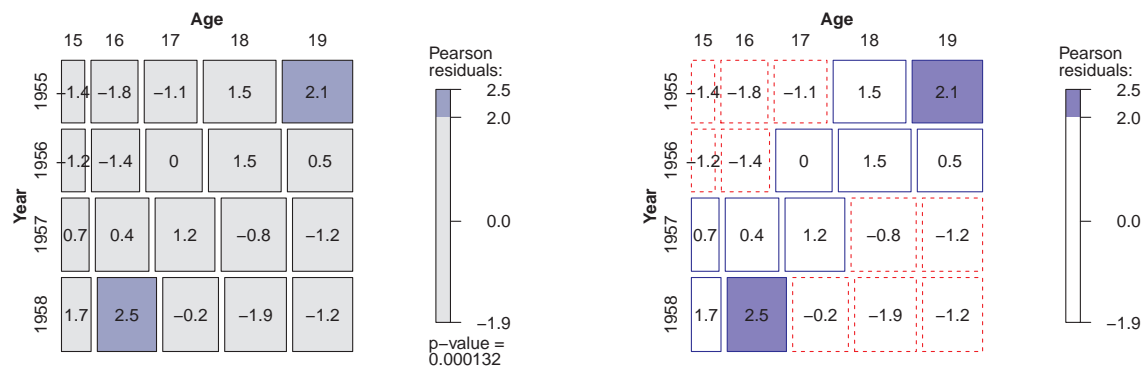
Call:
loglm(formula = ~Year + Age, data = criminal)

Statistics:
                      X^2 df    P(> X^2)
Likelihood Ratio 38.245 12 0.00014004
Pearson          38.410 12 0.00013155
```

(b) Use `mosaic()` with the option `shade=TRUE` to display the pattern of signs and magnitudes of the residuals. Compare this with the result of `mosaic()` using "Friendly shading," from the option `gp=shading_Friendly`. Describe verbally what you see in each regarding the pattern of association in this table.
★ It is helpful here to display all the residual contributions to association in the mosaic display using `labeling=labeling_residuals`.

```
> mosaic(criminal, shade=TRUE, labeling=labeling_residuals, suppress=0)
> mosaic(criminal, gp=shading_Friendly, labeling=labeling_residuals, suppress=0)
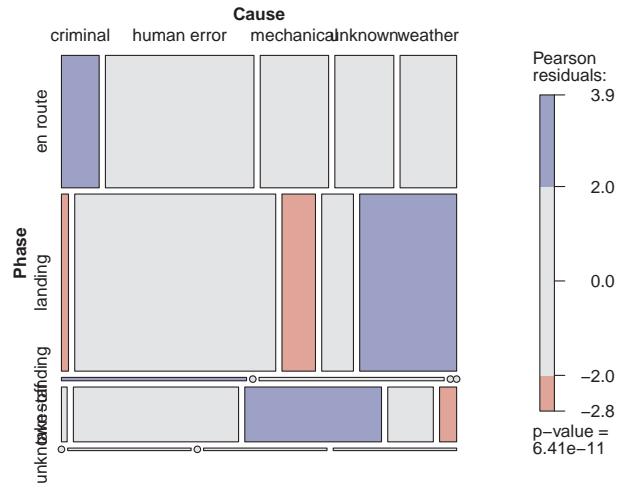```



Although only two residuals exceed the default $|r_{ij}| > 2$ threshold for shading, there is clearly a systematic association between year and age shown by the signs of the residuals.
The Friendly shading option here gives a better picture of the pattern of associations, showing positive and negative residuals in the diagonally opposite corners of the plot. See Exercise 6.2 for further analysis of this data.

**Exercise 5.2** The data set *AirCrash* in vcdExtra gives a database of all crashes of commercial airplanes between 1993–2015, classified by `Phase` of the flight and `Cause` of the crash. How can you best show is the nature of the association between these variables in a mosaic plot? Start by making a frequency table, `aircrash.tab`:

```
> data("AirCrash", package = "vcdExtra")
> aircrash.tab <- xtabs(~ Phase + Cause, data = AirCrash)
```

(a) Make a default mosaic display of the data with `shade=TRUE` and interpret the pattern of the high-frequency cells.
★

```
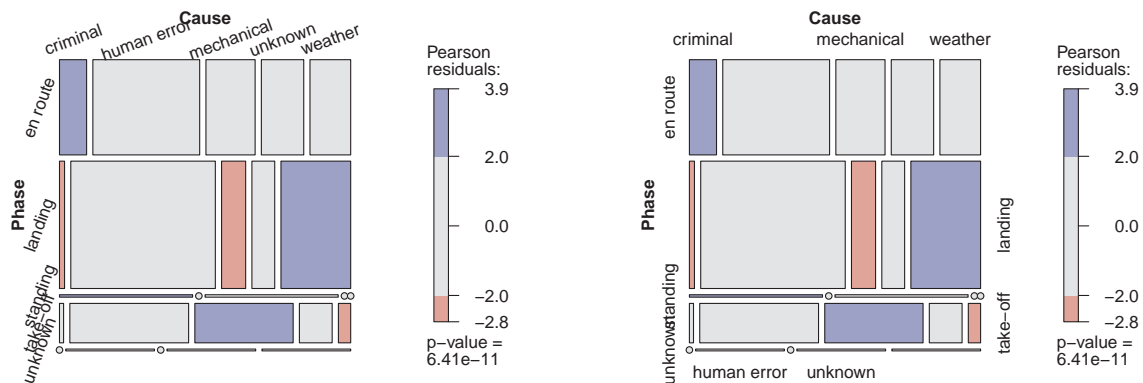>   mosaic(aircrash.tab, shade=TRUE)
```

Four cells stand out as having greater than expected frequencies, if Phase and Cause were indepen-
dent. Both take-off and en-route are positively associated with criminal activities. Crashes in landing
are more associated with weather. It is difficult to interpret the unknown cells.

(b) The default plot has overlapping labels due to the uneven marginal frequencies relative to the lengths of the
category labels. Experiment with some of the `labeling_args` options (`abbreviate`, `rot_labels`,
etc.) to see if you can make the plot more readable. *Hint*: a variety of these are illustrated in Section 4.1 of
`vignette("strucplot")`
★ Here are two alternatives that reduce the overplotting of labels:

```
> mosaic(aircrash.tab, shade=TRUE, rot_labels=c(20,90,0,70))
> mosaic(aircrash.tab, shade=TRUE, alternate_labels=TRUE)
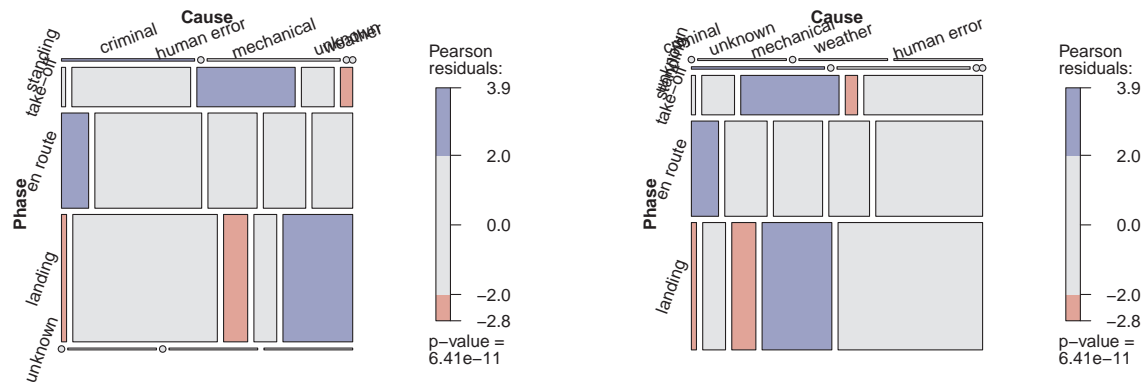```



(c) The levels of `Phase` and `Cause` are ordered alphabetically (because they are factors). Experiment with other
orderings of the rows/columns to make interpretation clearer, e.g., ordering `Phase` temporally or ordering both
factors by their marginal frequency.
★ Ordering by `Phase` is slightly easier to interpret. Ordering both variables by marginal frequencies

is also slightly better than the default, except that it leads to more overplotting of the labels.

```
> # reorder Phase temporarally
> roworder <- c(3, 4, 1, 2, 5)
> mosaic(aircrash.tab[roworder,], shade=TRUE, rot_labels=c(20,90,0,70))
>
> # marginal frequencies
> roworder <- order(rowSums(aircrash.tab))
> colorder <- order(colSums(aircrash.tab))
> mosaic(aircrash.tab[roworder, colorder], shade=TRUE, rot_labels=c(20,90,0,70))
```


The best general approach, as was illustrated in Figure 1.10, uses **effect ordering** to order the factors according to their associations. One easy method for this (Friendly and Kwan, 2003) is to order the factor levels according to their scores on the first dimension of a correspondence analysis solution as illustrated below. This maximizes an opposite corner pattern of the residuals.

```
> library(ca)
> aircrash.ca <- ca(aircrash.tab)
> aircrash.ca

 Principal inertias (eigenvalues):
            1        2        3         4
Value      0.123002 0.051548 0.01234  0.000562
Percentage 65.62%   27.5%    6.58%    0.3%
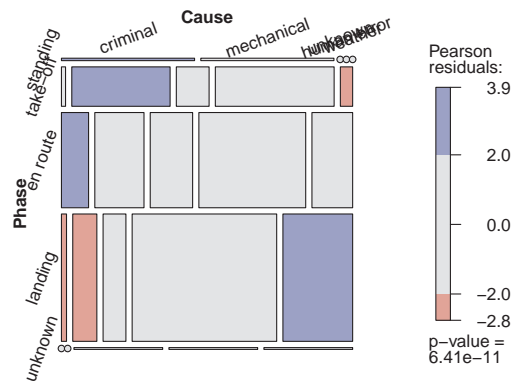

 Rows:
         en route    landing   standing   take-off    unknown
Mass     0.357631    0.478360  0.009112   0.148064    0.006834
ChiDist  0.282474    0.324494  2.292345   0.612039    0.872559
Inertia  0.028536    0.050370  0.047880   0.055463    0.005203
Dim. 1  -0.646053    0.910702 -5.413140  -1.099071    1.091749
Dim. 2  -0.630689   -0.073348 -4.720748   2.090502   -0.859449


 Columns:
         criminal human error mechanical  unknown    weather
Mass     0.052392    0.47153  0.168565    0.11845    0.189066
ChiDist  1.122062    0.17033  0.598187    0.33281    0.426378
Inertia  0.065962    0.01368  0.060317    0.01312    0.034372
Dim. 1  -2.308247    0.44543 -1.488701   -0.40903    1.112281
Dim. 2  -3.396324    0.24831  1.252718   -0.10358   -0.730118

> # reorder by CA coordinates on Dim 1
> roworder <- order(aircrash.ca$rowcoord[,"Dim1"])
> colorder <- order(aircrash.ca$colcoord[,"Dim1"])
> aircrash.tab[roworder, colorder]

            Cause
Phase     criminal mechanical unknown human error weather
  standing        2          2       0           0       0
  take-off        1         24       8          29       3
  en route       16         29      25          63      24
  landing         4         19      18         114      55
  unknown         0          0       1           1       1
```

```
> mosaic(aircrash.tab[roworder, colorder], shade=TRUE, rot_labels=c(20,90,0,70))
```


Exercise 5.3 The Lahman package contains comprehensive data on baseball statistics for Major League Baseball from 1871 through 2012. For all players, the *Master* table records the handedness of players, in terms of throwing (L, R) and batting (B, L, R), where B indicates "both." The table below was generated using the following code:

```
> library(Lahman)
> data("Master", package = "Lahman")
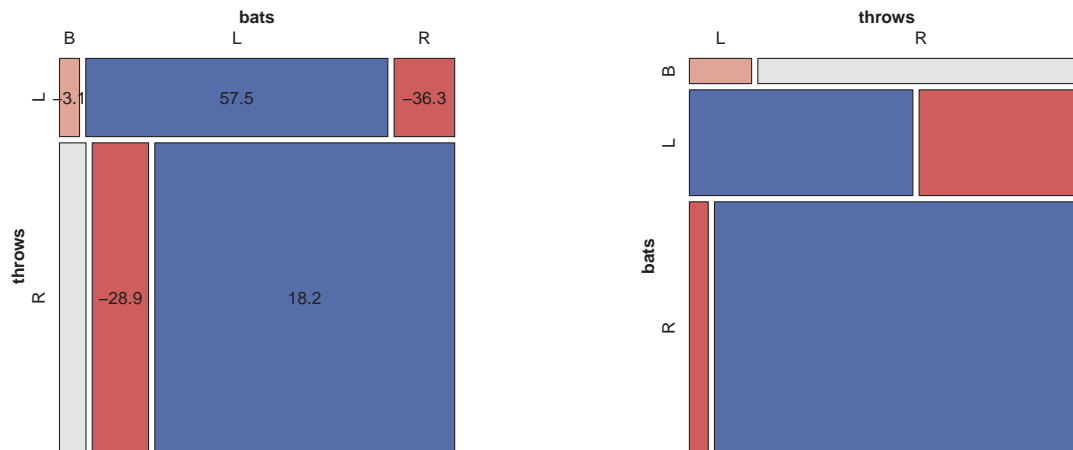> basehands <- with(Master, table(throws, bats))
```

	Bats		
Throws	B	L	R
L	177	2640	527
R	924	1962	10442

- Use the code above, or else enter these data into a frequency table in R.
  ★ These notes use a later version of the Lahman package (v. 4.0-1) with the code above, so the numbers used in the plots don't correspond to those in the table. The current version of the table is shown below.

```
> basehands

      bats
throws    B    L    R
     L  182 2742   550
     R  956 2031 10814
```

- Construct mosaic displays showing the relation of batting and throwing handedness, split first by batting and then by throwing.
  ★ By default, a two-way contingency table is split first by the row variable, then by the column variable. So, to split the other way, you can use t() on the table argument.

```
> mosaic(basehands, shade=TRUE, labeling=labeling_residuals(), legend=FALSE)
> mosaic(t(basehands), direction=c("h", "v"), shade=TRUE, legend=FALSE)
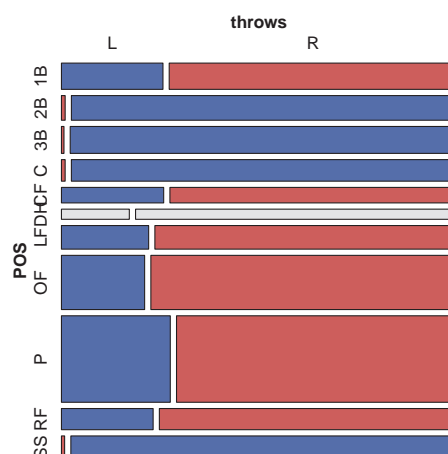```

- From these displays, what can be said about players who throw with their left or right hands in terms of their batting handedness?

  ★ Players who throw with their left or right hands are most likely to bat in the same way. From the values of the cell residuals, left handers are more likely to be uni-handers than righties.

**Exercise 5.4** ⋆ A related analysis concerns differences in throwing handedness among baseball players according to the fielding position they play. The following code calculates such a frequency table.

```
> library(Lahman)
> MasterFielding <- data.frame(merge(Master, Fielding, by = "playerID"))
> throwPOS <- with(MasterFielding, table(POS, throws))
```

(a) Make a mosaic display of throwing hand vs. fielding position.

   ★ There is clearly a very strong association between throwing hand and fielding position. A peculiarity of the data is that designated hitters (DH) do not play a fielding position, but instead fill in for the pitcher in the batting order, so throwing hand is not really relevant here. This position might arguably be deleted from this analysis

```
> mosaic(throwPOS, shade=TRUE, legend=FALSE)
```


(b) Calculate the percentage of players throwing left-handed by position. Make a sensible graph of this data.

   ★ A barplot is simple and reasonable here. However, the levels of fielding position are ordered alphabetically, which makes interpretation harder. Sorting by `pctLeft` is better.

```
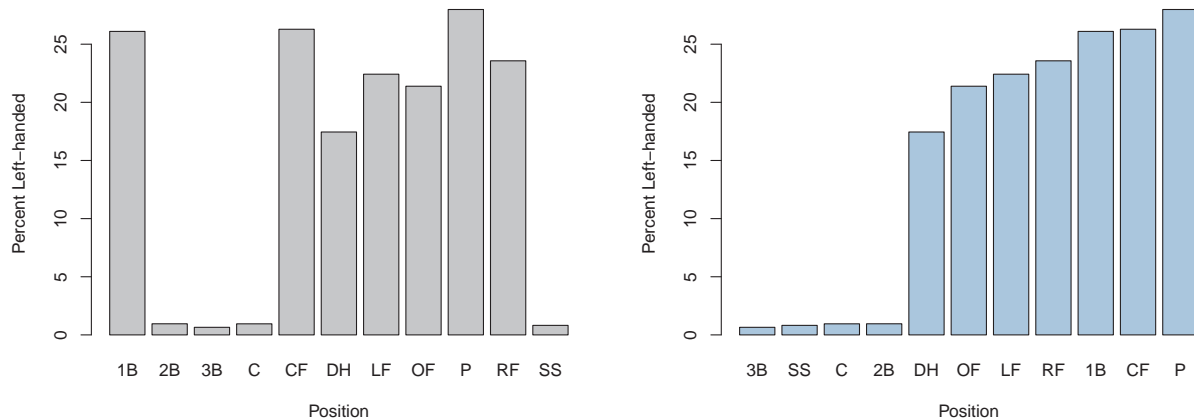> pctLeft <- 100 * throwPOS[,1] / rowSums(throwPOS)
> pctLeft

      1B       2B       3B        C       CF       DH       LF       OF        P       RF
26.09995  0.95479  0.65037  0.95194 26.28438 17.44900 22.41938 21.38510 27.98363 23.57075
      SS
 0.81835

> ord <- order(pctLeft)
> barplot(pctLeft, xlab="Position", ylab="Percent Left-handed")
> barplot(pctLeft[ord], xlab="Position", ylab="Percent Left-handed", col="lightblue")
```


(c) Re-do the mosaic display with the positions sorted by percentage of left-handers.
★

```
> mosaic(throwPOS[ord,], shade=TRUE, legend=FALSE)
```


(d) Is there anything you can say about positions that have very few left-handed players?
★ All infield positions except for 1st base have a very small percentage of players who throw left-handed. Given the marginal distributions of handeness and position, outfielders, pitchers and 1st basemen are more likely to throw left-handed than if these variables were independent.

Exercise 5.5 For the *Bartlett* data described in Example 5.12, fit the model of no three-way association, H_4 in Table 5.2.

(a) Summarize the goodness of fit for this model, and compare to simpler models that omit one or more of the two-way terms.

39

★

(b) Use a mosaic-like display to show the lack of fit for this model.

★

Exercise 5.6 Red core disease, caused by a fungus, is not something you want if you are a strawberry. The data set *jansen.strawberry* from the **agridat** (Wright, 2015) package gives a frequency data frame of counts of damage from this fungus from a field experiment reported by Jansen (1990). See the help file for details. The following lines create a $3 \times 4 \times 3$ table of crossings of 3 male parents with 4 (different) female parents, recording the number of plants in four blocks of 9 or 10 plants each showing red core disease in three ordered categories, C1, C2, or C3.

```
> data("jansen.strawberry", package = "agridat")
>
> dat <- jansen.strawberry
> dat <- transform(dat, category = ordered(category,
+                                          levels = c('C1','C2','C3')))
> levels(dat$male) <- paste0("M", 1:3)
> levels(dat$female) <- paste0("F", 1:4)
>
> jansen.tab <- xtabs(count ~ male + female + category, data = dat)
> names(dimnames(jansen.tab)) <- c("Male parent", "Female parent",
+                                  "Disease category")
> ftable(jansen.tab)
```

(a) Use `pairs(jansen.tab, shade=TRUE)` to display the pairwise associations among the three variables. Describe how disease category appears to vary with male and female parent. Why is there no apparent association between male and female parent?

★

(b) As illustrated in Figure 5.6, use `mosaic()` to prepare a 3-way mosaic plot with the tiles colored in increasing shades of some color according to disease category. Describe the pattern of category C3 in relation to male and female parent. (Hint: the `highlighting` arguments are useful here.)

★

(c) With `category` as the response variable, the minimal model for association is [MF][C], or ~ `1*2 + 3`. Fit this model using `loglm()` and display the residuals from this model with `mosaic()`. Describe the pattern of lack of fit of this model.

★

Exercise 5.7 The data set *caith* in **MASS** (Ripley, 2015) gives another classic 4×5 table tabulating hair color and eye color, this for people in Caithness, Scotland, originally from Fisher (1940). The data is stored as a data frame of cell frequencies, whose rows are eye colors and whose columns are hair colors.

```
> data("caith", package = "MASS")
> caith

       fair red medium dark black
blue    326  38    241  110     3
light   688 116    584  188     4
medium  343  84    909  412    26
dark     98  48    403  681    85
```

(a) The `loglm()` and `mosaic()` functions don't understand data in this format, so use `Caith <- as.matrix(caith)` to convert to array form. Examine the result, and use
`names(dimnames(Caith))<-c()` to assign appropriate names to the row and column dimensions.

★

(b) Fit the model of independence to the resulting matrix using `loglm()`.

★

(c) Calculate and display the residuals for this model.

★

(d) Create a mosaic display for this data.

★

Exercise 5.8 The *HairEyePlace* data in **vcdExtra** gives similar data on hair color and eye color, for both Caithness and Aberdeen as a $4 \times 5 \times 2$ table.

(a) Prepare separate mosaic displays, one for each of Caithness and Aberdeen. Comment on any difference in the pattern of residuals.

★

(b) Construct conditional mosaic plots, using the formula `~ Hair + Eye | Place` and both `mosaic()` and `cotabplot()`. It is probably more useful here to suppress the legend in these plots. Comment on the difference in what is shown in the two displays.

★

Exercise 5.9 Bertin (1983, pp. 30–31) used a 4-way table of frequencies of traffic accident victims in France in 1958 to illustrate his scheme for classifying data sets by numerous variables, each of which could have various types and could be assigned to various visual attributes. His data are contained in *Accident* in **vcdExtra**, a frequency data frame representing his $5 \times 2 \times 4 \times 2$ table of the variables `age`, `result` (died or injured), `mode` of transportation, and `gender`.

```
> data("Accident", package = "vcdExtra")
> str(Accident, vec.len=2)

'data.frame': 80 obs. of  5 variables:
 $ age   : Ord.factor w/ 5 levels "0-9"<"10-19"<..: 5 5 5 5 5 ...
 $ result: Factor w/ 2 levels "Died","Injured": 1 1 1 1 1 ...
 $ mode  : Factor w/ 4 levels "4-Wheeled","Bicycle",..: 4 4 2 2 3 ...
 $ gender: Factor w/ 2 levels "Female","Male": 2 1 2 1 2 ...
 $ Freq  : int  704 378 396 56 742 ...
```

(a) Use `loglm()` to fit the model of mutual independence, `Freq ~ age+mode+gender+result` to this data set.

★

(b) Use `mosaic()` to produce an interpretable mosaic plot of the associations among all variables under the model of mutual independence. Try different orders of the variables in the mosaic. (*Hint*: the `abbreviate` component of the `labeling_args` argument to `mosaic()` will be useful to avoid some overlap of the category labels.)

★

(c) Treat `result` (`"Died"` vs. `"Injured"`) as the response variable, and fit the model `Freq ~ age*mode*gender + result` that asserts independence of `result` from all others jointly.

★

(d) Construct a mosaic display for the residual associations in this model. Which combinations of the predictor factors are more likely to result in death?

★

Exercise 5.10 The data set *Vietnam* in **vcdExtra** gives a $2 \times 5 \times 4$ contingency table in frequency form reflecting a survey of student opinion on the Vietnam War at the University of North Carolina in May 1967. The table variables are sex, year in school, and response, which has categories: (A) Defeat North Vietnam by widespread bombing and land invasion; (B) Maintain the present policy; (C) De-escalate military activity, stop bombing and begin negotiations; (D) Withdraw military forces immediately. How does the chosen response vary with sex and year?

```
> data("Vietnam", package = "vcdExtra")
> str(Vietnam)

'data.frame': 40 obs. of  4 variables:
 $ sex     : Factor w/ 2 levels "Female","Male": 1 1 1 1 1 1 1 1 1 1 1 ...
 $ year    : int  1 1 1 1 2 2 2 2 3 3 ...
 $ response: Factor w/ 4 levels "A","B","C","D": 1 2 3 4 1 2 3 4 1 2 ...
 $ Freq    : int  13 19 40 5 5 9 33 3 22 29 ...
```

(a) With `response` (R) as the outcome variable and `year` (Y) and `sex` (S) as predictors, the minimal baseline loglinear model is the model of joint independence, [R][YS]. Fit this model, and display it in a mosaic plot.

★

(b) Construct conditional mosaic plots of the `response` versus `year` separately for males and females. Describe the associations seen here.

★

(c) Follow the methods shown in Example 5.10 to fit separate models of independence for the levels of `sex`, and the model of conditional independence, $R \perp Y \mid S$. Verify that the decomposition of G^2 in Eqn. (5.6) holds for these models.

★

(d) Construct a useful 3-way mosaic plot of the data for the model of conditional independence.

★

Exercise 5.11 Consider the models for 4-way tables shown in Table 5.3.

(a) For each model, give an independence interpretation. For example, the model of mutual independence corresponds to $A \perp B \perp C \perp D$.

★

(b) Use the functions shown in the table together with `loglin2formula()` to print the corresponding model formulas for each.

★

Exercise 5.12 The dataset *Titanic* classifies the 2,201 pasengers and crew of the *Titanic* by `Class` (1st, 2nd, 3rd, Crew), `Sex`, `Age`, and `Survived`. Treating `Survived` as the response variable,

(a) Fit and display a mosaic plot for the baseline model of joint independence, [CGA][S]. Describe the remaining pattern of associations.

★

(b) Do the same for a "main effects" model that allows two-way associations between each of C, G, and A with S.

★

(c) What three-way association term should be added to this model to allow for greater survival among women and children? Does this give an acceptable fit?

★

(d) Test and display models that allow additional three-way associations until you obtain a reasonable fit.

★

Chapter 6

Correspondence Analysis

These solutions use an updated version of the `ca` package, v. 0.64 or greater.

Exercise 6.1 The *JobSat* data in **vcdExtra** gives a 4×4 table recording job satisfaction in relation to income.

(a) Carry out a simple correspondence analysis on this table. How much of the inertia is accounted for by a one-dimensional solution? How much by a two-dimensional solution?
    ★ The 1D solution accounts for 76.4

```
> data("JobSat", package="vcdExtra")
> library(ca)
> jobsat.ca <- ca(JobSat)
>     # just show the scree plot
> summary(jobsat.ca, rows=FALSE, columns=FALSE)

Principal inertias (eigenvalues):
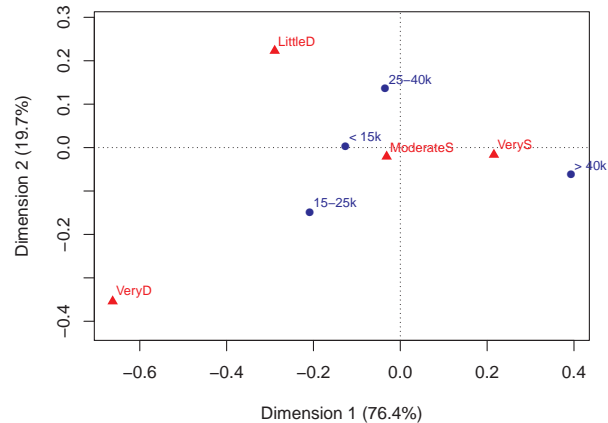
 dim    value       %    cum%   scree plot
 1      0.047496   76.4   76.4  ********************
 2      0.012248   19.7   96.1  *****
 3      0.002397    3.9  100.0  *
        --------  -----
 Total: 0.062141 100.0
```

(b) Plot the 2D CA solution. To what extent can you consider the association between job satisfaction and income "explained" by the ordinal nature of these variables?

★

```
> plot(jobsat.ca)
```


Job `satisfaction` is ordered as expected by its ordinal levels along Dimension 1. The levels of `income` in this plot do not appear to be ordered according to the quantitative levels they represent.

Exercise 6.2 Refer to Exercise 5.1 in Chapter 5. Carry out a simple correspondence analysis on the 4×5 table `criminal` from the logmult package.

(a) What percentages of the Pearson χ^2 for association are explained by the various dimensions?

★

```
> data("criminal", package = "logmult")
> criminal.ca <- ca(criminal)
>       # just show the scree plot
> summary(criminal.ca, rows=FALSE, columns=FALSE)

Principal inertias (eigenvalues):

 dim    value       %    cum%   scree plot
 1      0.004939  90.3   90.3   ***********************
 2      0.000491   9.0   99.3   **
 3      3.8e-050   0.7  100.0
        --------  -----
 Total: 0.005468 100.0
```

(b) Plot the 2D correspondence analysis solution. Describe the pattern of association between year and age.

★

```
> plot(criminal.ca, lines=TRUE)
```

The category points for both year and age vary systematically over Dimension 1. There were more younger men in later years, and more older in earlier years.

Exercise 6.3 Refer to Exercise 5.2 for a description of the `AirCrash` data from the vcdExtra package. Carry out a simple correspondence analysis on the 5×5 table of `Phase` of the flight and `Cause` of the crash.

(a) What percentages of the Pearson χ^2 for association are explained by the various dimensions?
★ `aircrash.tab` was calculated in Exercise 5.2.

```
> aircrash.tab

          Cause
Phase        criminal  human error  mechanical  unknown  weather
  en route        16           63          29        25       24
  landing          4          114          19        18       55
  standing         2            0           2         0        0
  take-off         1           29          24         8        3
  unknown          0            1           0         1        1

> aircrash.ca <- ca(aircrash.tab)
>       # just show the scree plot
> summary(aircrash.ca, rows=FALSE, columns=FALSE)
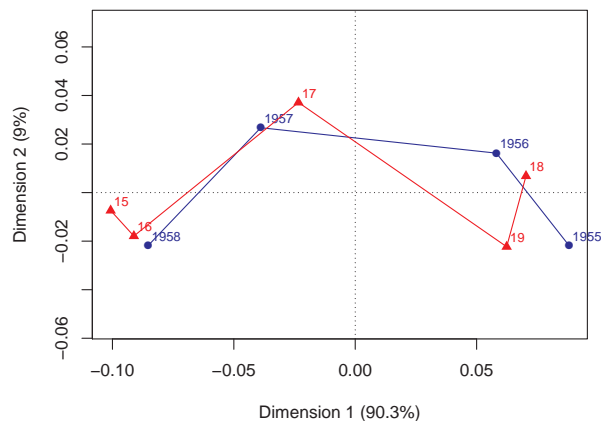
Principal inertias (eigenvalues):

 dim     value       %    cum%    scree plot
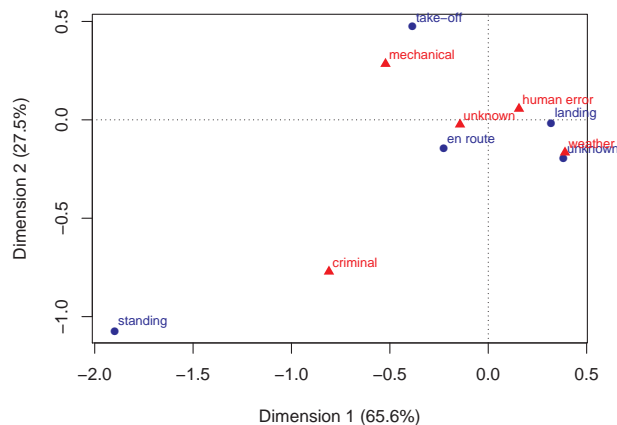 1       0.123002  65.6   65.6    ****************
 2       0.051548  27.5   93.1    *******
 3       0.012340   6.6   99.7    **
 4       0.000562   0.3  100.0
         --------  -----
 Total: 0.187452 100.0
```

(b) Plot the 2D correspondence analysis solution. Describe the pattern of association between phase and cause. How would you interpret the dimensions?
★

```
> plot(aircrash.ca)
```

Dimension 1 (65.6%)

Dimension 1 largely distinguishes standing from landing, where the main causes are human error and weather problems. Dimension 2 largely distinguishes standing from take-off, where mechanical problems are more prevalent.

(c) The default plot method uses `map="symmetric"` with points for both rows and columns. Try using `map="symbiplot"` with vectors (`arrows=`) for either rows or columns. (Read `help(plot.ca)` for a description of these options.)
★

```
> plot(aircrash.ca, map="symbiplot", arrows=c(FALSE, TRUE))
```


Dimension 1 (65.6%)

Exercise 6.4 The data set `caith` in MASS gives a classic table tabulating hair color and eye color of people in Caithness, Scotland, originally from Fisher (1940).

(a) Carry out a simple correspondence analysis on this table. How many dimensions seem necessary to account for most of the association in the table?
★

```
> data("caith", package="MASS")
> caith.ca <- ca(caith)
> summary(caith.ca, rows=FALSE, columns=FALSE)
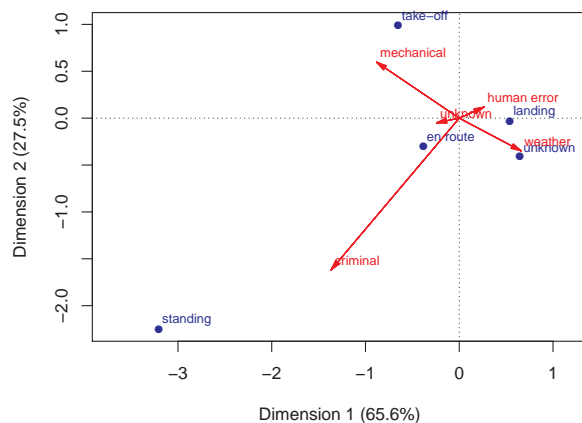
Principal inertias (eigenvalues):

 dim    value      %    cum%   scree plot
 1     0.199245  86.6  86.6   **********************
 2     0.030087  13.1  99.6   ***
```

```
 3      0.000859   0.4 100.0
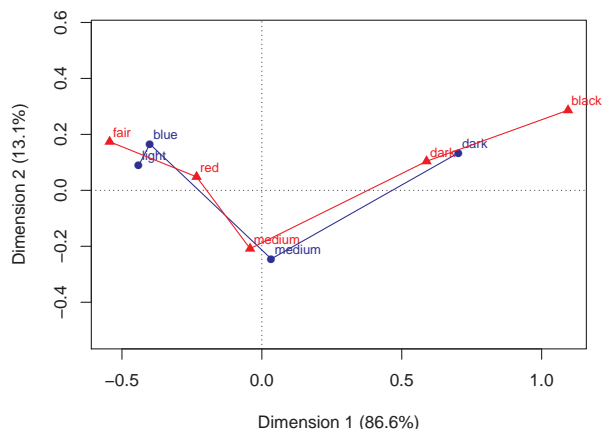        -------- -----
Total: 0.230191 100.0
```

One could argue that a 1D solution is adequate here. The 2D solution is essentially complete.

(b) Plot the 2D solution. The interpretation of the first dimension should be obvious; is there any interpretation for the second dimension?

★

```
> plot(caith.ca, lines=TRUE)
```


Dimension 1 is the obvious light–dark dimension for hair color and eye color (but not that blue and light eyes have quite similar positions). Dimension 2 could be called "extremes vs. middle", but in CA results with largely 1D association, this effect is common, often called the "horseshoe" or "arch" effect.

Exercise 6.5 The same data, plus a similar table for Aberdeen, are given as a three-way table as *HairEyePlace* in vcdExtra.

(a) Carry out a similar correspondence analysis to the last exercise for the data from Aberdeen. Comment on any differences in the placement of the category points.

★

(b) Analyze the three-way table, stacked to code hair color and place interactively, i.e., for the loglinear model [Hair Place][Eye]. What does this show?

★

Exercise 6.6 The data set *Gilby* in vcdExtra gives a classic (but now politically incorrect) 6×4 table of English schoolboys classified according to their clothing and their teacher's rating of "dullness" (lack of intelligence).

(a) Compute and plot a correspondence analysis for this data. Write a brief description and interpretation of these results.

★

```
> data("Gilby", package="vcdExtra")
> gilby.ca <- ca(Gilby)
> summary(gilby.ca)

Principal inertias (eigenvalues):

 dim    value      %    cum%   scree plot
 1      0.079346  78.3  78.3   ********************
 2      0.020118  19.9  98.1   *****
 3      0.001881   1.9 100.0
        -------- -----
Total: 0.101346 100.0


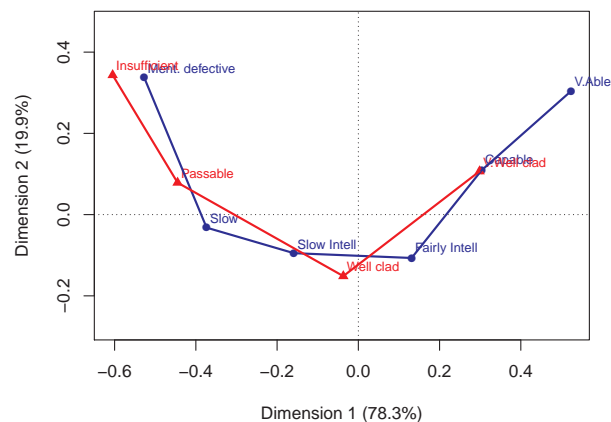Rows:
```

```
        name   mass  qlt   inr     k=1 cor ctr     k=2 cor ctr
1 | Mntd |     75  996  292 | -527 707 264 |  337 289 426 |
2 | Slow |    127  943  187 | -374 936 223 |  -32   7   7 |
3 | SlwI |    236  938   85 | -159 691  75 |  -95 247 106 |
4 | FrlI |    310  999   88 |  131 601  67 | -107 398 176 |
5 | Cpbl |    217 1000  223 |  304 885 253 |  109 115 129 |
6 | VAbl |     34  990  125 |  524 740 118 |  304 250 157 |

Columns:
        name   mass  qlt   inr     k=1 cor ctr     k=2 cor ctr
1 | VWll |    369 1000  366 |  299 886 414 |  107 113 208 |
2 | Wllc |    435  989  106 |  -37  56   8 | -151 934 496 |
3 | Pssb |    154  976  317 | -445 946 383 |   79  30  47 |
4 | Insf |     42  955  212 | -605 722 195 |  344 233 248 |
> plot(gilby.ca, lines="TRUE", lwd=2)
```


The association between clothing and dullness is largely one dimensional, but there is a moderately large horseshoe effect. On Dimension 1, the categories of both variables are approximately equally spaced.

(b) Make an analogous mosaic plot of this table. Interpret this in relation to the correspondence analysis plot. ★

```
> mosaic(Gilby, shade=TRUE, labeling=labeling_residuals)
```


The mosaic nearly shows the opposite corner pattern associated with a unidimensional association of two ordered variables, but the largest residuals are not systematically confined to the diagonally opposite cells. The mosaic shows the marginal frequencies of dullness and the cell frequencies by the

47

area of the tiles, while this information is not available in the CA plot.

Exercise 6.7 For the mental health data analyzed in Example 6.2, construct a shaded sieve diagram and mosaic plot. Compare these with the correspondence analysis plot shown in Figure 6.2. What features of the data and the association between SES and mental health status are shown in each?

★

Exercise 6.8 Simulated data are often useful to help understand the connections between data, analysis methods, and associated graphic displays. Section 6.3.1 illustrated interactive coding in R, using a simulated 4-way table of counts of pets, classified by age, color, and sex, but with no associations because the counts had a constant Poisson mean, $\lambda = 15$.

(a) Re-do this example, but in the call to `rpois()`, specify a non-negative vector of Poisson means to create some associations among the table factors.
★ First, create a data.frame of the factor levels. Then you can use these variables to create the Poisson means in a way that varies across some of the category combinations to create associations. Here we try to creates associations between Pet and Color (more black dogs than other combinations) and between Age and Sex (more young male pets). These cell means are then used in the call to `rpois()`.

```
> dim <- c(3, 2, 2, 2)
> factors <- expand.grid(Pet=c("dog","cat","bird"),
+                        Age=c("young","old"),
+                        Color=c("black", "white"),
+                        Sex=c("male", "female"))
> means <-
+ with(factors, {
+        20 +
+        ifelse(Pet=="dog", 10, 0) +
+        ifelse((Pet=="dog" & Color=="black"), 10, -10) +
+        ifelse((Age=="young" & Sex=="male"), 5, -5)
+        })
>
> set.seed(1234)
> tab <- array(rpois(prod(dim), means), dim=dim)
> dimnames(tab) <- list(Pet=c("dog","cat","bird"),
+                       Age=c("young","old"),
+                       Color=c("black", "white"),
+                       Sex=c("male", "female"))
```

(b) Use CA methods to determine if and how the structure you created in the data appears in the results.
★

Exercise 6.9 The `TV` data was analyzed using CA in Example 6.4, ignoring the variable `Time`. Carry out analyses of the 3-way table, reducing the number of levels of `Time` to three hourly intervals as shown below.

```
> data("TV", package="vcdExtra")
> # reduce number of levels of Time
> TV.df <- as.data.frame.table(TV)
> levels(TV.df$Time) <- rep(c("8", "9", "10"), c(4, 4, 3))
> TV3 <- xtabs(Freq ~ Day + Time + Network, TV.df)
> structable(Day ~ Network + Time, TV3)
```

		Day Monday	Tuesday	Wednesday	Thursday	Friday
Network	Time					
ABC	8	536	861	744	735	1119
	9	1401	1205	1022	682	907
	10	910	1044	668	349	711
CBS	8	1167	646	550	680	509
	9	967	959	409	385	544
	10	789	798	324	270	426
NBC	8	858	1090	512	1927	823
	9	946	890	831	1858	590
	10	825	588	869	2101	585

(a) Use the stacking approach (Section 6.3) to perform a CA of the table with `Network` and `Time` coded interactively. You can create this using the `as.matrix()` method for a "structable" object.

```
> TV3S <- as.matrix(structable(Day ~ Network + Time, TV3), sep=":")
```

★

```
> TV3S.ca <-ca(TV3S)
> TV3S

            Day
Network:Time Monday Tuesday Wednesday Thursday Friday
     ABC:8    536     861       744      735   1119
     ABC:9   1401    1205      1022      682    907
     ABC:10   910    1044       668      349    711
     CBS:8   1167     646       550      680    509
     CBS:9    967     959       409      385    544
     CBS:10   789     798       324      270    426
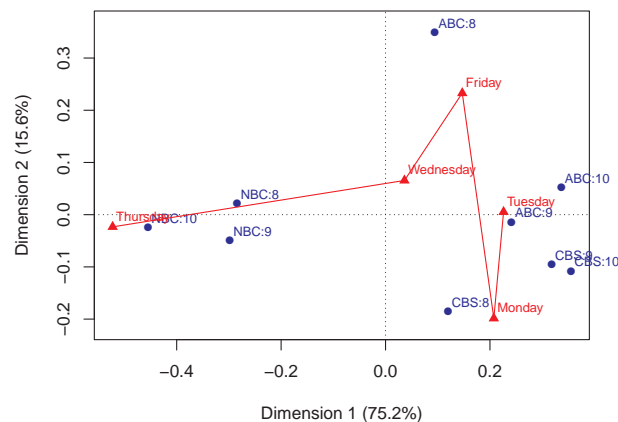     NBC:8    858    1090       512     1927    823
     NBC:9    946     890       831     1858    590
     NBC:10   825     588       869     2101    585
```

(b) What loglinear model is analyzed by this approach?

★ The model is the joint independence model, [Day][Network Time], asserting that the frequencies of watching the combinations of networks in different time slots do not vary with day of the week.

(c) Plot the 2D solution. Compare this to the CA plot of the two-way table in Figure 6.4.

★

```
> plot(TV3S.ca, lines=c(FALSE, TRUE))
```


Overall, the plot is somewhat similar to that of Figure 6.4 except for the (arbitrary) reversal of Dimension 1. The category points for NBC cluster near Thursday, while those for ABC and CBS are at the other end of that dimension and Dimension 2 is related to the difference in viewership to those channels.

(d) Carry out an MCA analysis using `mjca()` of the three-way table `TV3`. Plot the 2D solution, and compare this with both the CA plot and the solution for the stacked three-way table.

★ The MCA analysis differs in that it includes all pairwise associations of Day, Time and Network rather than just the joint independence model analyzed by the stacking approach.

```
> TV3.mca <- mjca(TV3)
> plot(TV3.mca, collabels="level")
```

The default plot is somewhat difficult to read because the factor points s aren't distinguished by color or shape. A customized plot can be constructed as follows (as illustrated in the text, e.g., for Figure 6.10). (The `multilines()` function is new in the ca (Greenacre and Nenadic, 2014) package, v. 0.64.)

```
> res <- plot(TV3.mca, labels=0, pch='.', cex.lab=1.2)
> coords <- data.frame(res$cols, TV3.mca$factors)
> nlev <- rle(as.character(coords$factor))$lengths
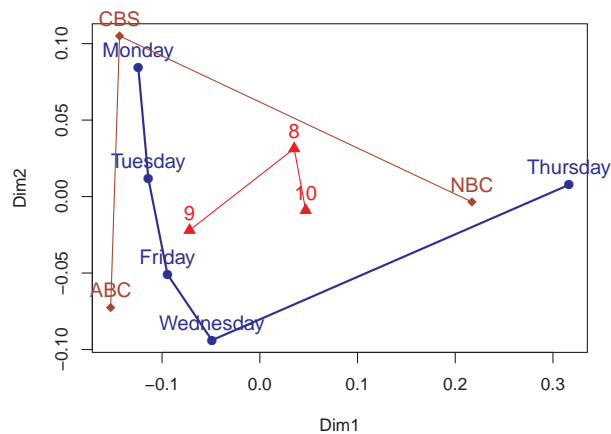> fact <- unique(as.character(coords$factor))
>
> cols <- c("blue", "red", "brown")
> lwd <- 2
> plot(Dim2 ~ Dim1, type='n', data=coords)
> points(coords[,1:2], pch=rep(16:18, nlev), col=rep(cols, nlev), cex=1.2)
> text(coords[,1:2], labels=coords$level, col=rep(cols, nlev), pos=3, cex=1.2, xpd=TRUE)
> multilines(coords[, c("Dim1", "Dim2")], group=coords$factor, col=cols, lwd=lwd)
```


Exercise 6.10 Refer to the MCA analysis of the `PreSex` data in Example 6.8. Use the stacking approach to analyze the stacked table with the combinations of premarital and extramarital sex in the rows and the combinations of gender and marital status in the columns. As suggested in the exercise above, you can use `as.matrix(structable())` to create the stacked table.

```
> presexS<- as.matrix(structable(PremaritalSex + ExtramaritalSex ~ Gender + Marital, PreSex), sep=":")
> presexS
                   PremaritalSex:ExtramaritalSex
Gender:MaritalStatus Yes:Yes Yes:No No:Yes No:No
      Women:Divorced      17      54     36   214
```

50

```
        Women:Married          4      25      4    322
        Men:Divorced          28      60     17     68
        Men:Married           11      42      4    130
```

(a) What loglinear model is analyzed by this approach? Which associations are included and which are excluded in this analysis?

★ The model is that of independence between the combinations of the row variables and the column variables, i.e., [Pre Extra][Gender Marital]. The associations that remain indicate how the combinations of pre- and extra-marital sex are related to the the combinations of gender and marital status. The association between pre-marital sex and extra-marital sex is excluded, as is the association between gender and marital status.

(b) Plot the 2D CA solution for this analysis. You might want to draw lines connecting some of the row points or column points to aid in interpretation.

★ The 2D solution accounts for 99.1% of association between these sets of variables.

```
> presexS.ca <- ca(presexS)
> summary(presexS.ca)

Principal inertias (eigenvalues):

 dim     value       %    cum%    scree plot
 1       0.153126  86.7   86.7    **********************
 2       0.021929  12.4   99.1    ***
 3       0.001552   0.9  100.0
        --------  -----
 Total: 0.176606 100.0


Rows:
    name    mass  qlt   inr     k=1 cor ctr      k=2 cor ctr
1 | WmnD |   310  995    90 |     84 138  14 |   210 857 622 |
2 | WmnM |   343  995   376 |   -437 984 427 |   -46  11  34 |
3 | MnDv |   167  996   494 |    715 978 558 |   -97  18  72 |
4 | MnMr |   181  878    39 |     24  15   1 |  -182 863 273 |

Columns:
    name    mass  qlt   inr     k=1  cor ctr      k=2 cor ctr
1 | YsYs |    58  979   250 |    850  948 274 |  -152  30  61 |
2 | YesN |   175  989   296 |    530  937 320 |  -124  51 122 |
3 | NoYs |    59 1000   209 |    567  514 124 |   552 486 817 |
4 | NoNo |   708 1000   245 |   -247 1000 283 |    -3   0   0 |
```

Here is one version of a plot, drawing lines connecting the pairs of Gender and Marital status.

```
> res <- plot(presexS.ca)
> # join pairs of column points
> lines(res$cols[1:2,], col="red")
> lines(res$cols[3:4,], col="red")
> lines(res$cols[c(1,3),], col="red")
> lines(res$cols[c(2,4),], col="red")
```

(c) How does this analysis differ from the MCA analysis shown in Figure 6.10?

★ The MCA analysis treats all four factors individually, analyzing all bivariate associations. The stacked approach here treats them in two sets, analyzing only the associations *between* sets.

Exercise 6.11 Refer to Exercise 5.10 for a description of the `Vietnam` data set in vcdExtra.

(a) Using the stacking approach, carry out a correspondence analysis corresponding to the loglinear model [R][YS], which asserts that the response is independent of the combinations of year an sex.

★

(b) Construct an informative 2D plot of the solution, and interpret in terms of how the response varies with year for males and females.

★

(c) Use `mjca()` to carry out an MCA on the three-way table. Make a useful plot of the solution and interpret in terms of the relationship of the response to year and sex.

★

Exercise 6.12 Refer to Exercise 5.9 for a description of the `Accident` data set in vcdExtra. The data set is in the form of a frequency data frame, so first convert to table form.

```
> accident.tab <- xtabs(Freq ~ age + result + mode + gender, data=Accident)
```

(a) Use `mjca()` to carry out an MCA on the four-way table `accident.tab`.

★

```
> accident.mca <- mjca(accident.tab)
> summary(accident.mca)
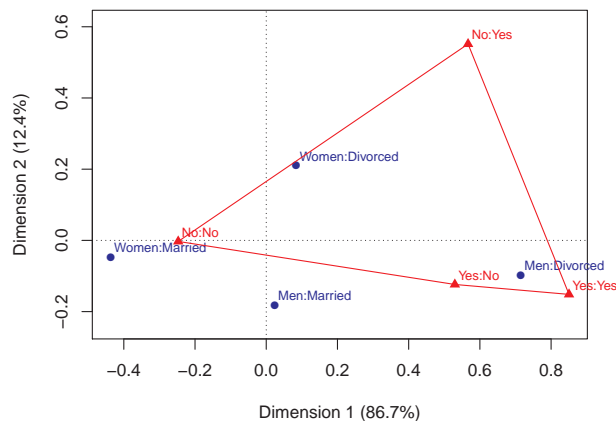
Principal inertias (eigenvalues):

 dim    value      %    cum%   scree plot
 1     0.025429  46.5   46.5   ****************
 2     0.011848  21.7   68.1   *******
 3     0.001889   3.5   71.6   *
 4     0.000491   0.9   72.5
       --------  -----
 Total: 0.054700


Columns:
              name    mass  qlt  inr    k=1  cor ctr    k=2  cor ctr
 1 |       age:0-9 |    13  672  107 |   551  561 152 |  -246  111  65 |
 2 |      age:10-19 |   49  678   91 |    40   13   3 |   292  665 354 |
 3 |      age:20-29 |   56  784   85 |  -215  747 102 |   -48   37  11 |
 4 |      age:30-49 |   76  546   75 |  -103  396  32 |   -63  149  26 |
 5 |        age:50+ |   56  687   85 |   196  616  84 |   -67   72  21 |
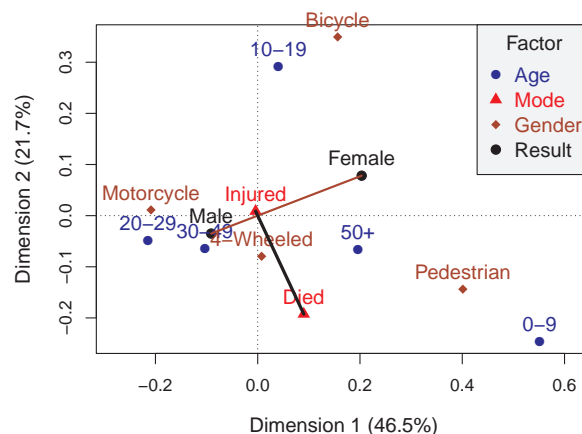 6 |    result:Died |   11  515  100 |    90   92   3 |  -192  422  34 |
```

52

```
7  |   result:Injured |  239  515    5 |   -4   92    0 |    9 422    2 |
8  |   mode:4-Wheeled |   81  230   73 |    8    2    0 |  -80 228   43 |
9  |      mode:Bicycle |   31  762   98 |  156  127   30 |  349 635  320 |
10 |   mode:Motorcycle |   99  686   70 | -209 684  170 |   11    2    1 |
11 |  mode:Pedestrian |   38  677  100 |  401 600  241 | -144   77   66 |
12 |    gender:Female |   77  788   77 |  203 686  126 |   78 101   40 |
13 |      gender:Male |  173  788   35 |  -91 686   56 |  -35 101   18 |
```

The adjusted inertias indicate that a 2D solution accounts for only 68.1% of the pairwise associations. The qualities (`qlt`) of the factor levels indicate that the categories are only moderately well-represented in a 2D plot.

(b) Construct an informative 2D plot of the solution, and interpret in terms of how the variable `result` varies in relation to the other factors.
★ Here, the plot becomes too messy to if we connect all factor levels with lines.

```
> res <- plot(accident.mca, labels=0, pch='.', cex.lab=1.2) #makes plot with no labels or points
> coords <- data.frame(res$cols, accident.mca$factors) #to extract factor names & levels
> cols <- c("blue", "red", "brown", "black")
> nlev <- accident.mca$levels.n
>
> points(coords[,1:2], pch=rep(16:19, nlev), col=rep(cols, nlev), cex=1.2)
> text(coords[,1:2], label=coords$level, col=rep(cols, nlev), pos=3, cex=1.2, xpd=TRUE)
> lines(Dim2 ~ Dim1, data=coords, subset=factor=="gender", lty=1, lwd=2, col="brown")
> lines(Dim2 ~ Dim1, data=coords, subset=factor=="result", lty=1, lwd=3, col="black")
>
> legend("topright", legend=c("Age", "Mode", "Gender", "Result"),
+        title="Factor", title.col="black",
+        col=cols, text.col=cols, pch=16:19,
+        bg="gray95", cex=1.2)
```


In the figure above, one interpretation of the dimensions is in terms of the age categories: Dimension 1 for young adults vs. old and young, Dimension 2 for teenage vs. the rest. In these terms, Dimension 1 shows associations among males, aged 20–49, riding a motorcycle or 4-wheeled vehicle and more likely to be injured, vs. females, either old or very young, as pedestrians and more likely to have died. Dimension 2 contrasts bicycle accidents involving youth aged 10–19 who are more likely to be just injured against the other categories.

Exercise 6.13 The *UCBAdmissions* data was featured in numerous examples in Chapter 4 (e.g., Example 4.11, Example 4.15) and Chapter 5 (e.g., Example 5.14, Example 5.18).

(a) Use `mjca()` to carry out an MCA on the three-way table `UCBAdmissions`.
★

```
> ucb.mca <- mjca(UCBAdmissions)
> summary(ucb.mca)

Principal inertias (eigenvalues):
```

```
dim    value      %    cum%    scree plot
1      0.114945  80.5  80.5    ************************
2      0.005694   4.0  84.5    *
3      00000000   0.0  84.5
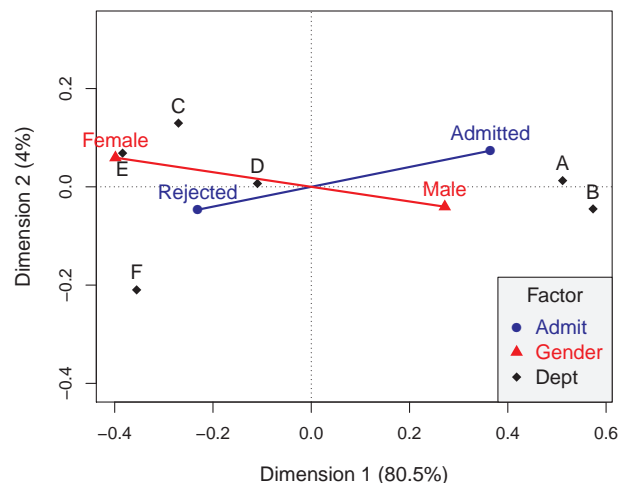4      00000000   0.0  84.5
5      00000000   0.0  84.5
       --------  -----
Total: 0.142840


Columns:
               name    mass  qlt  inr    k=1 cor ctr     k=2 cor ctr
1  | Admit:Admitted |   129  911   93 |  365 875 150 |   74  36 123 |
2  | Admit:Rejected |   204  911   59 | -231 875  95 |  -47  36  78 |
3  |  Gender:Female |   135  863   95 | -399 845 187 |   59  19  84 |
4  |    Gender:Male |   198  863   65 |  272 845 127 |  -40  19  57 |
5  |         Dept:A |    69  838  117 |  512 837 156 |   13   1   2 |
6  |         Dept:B |    43  829  124 |  573 824 123 |  -45   5  15 |
7  |         Dept:C |    68  731  108 | -270 594  43 |  130 137 199 |
8  |         Dept:D |    58  832  106 | -110 828   6 |    7   3   0 |
9  |         Dept:E |    43  812  117 | -384 787  55 |   69  25  35 |
10 |         Dept:F |    53  737  116 | -355 547  58 | -210 190 406 |
```

(b) Plot the 2D MCA solution in a style similar to that shown in Figure 6.10 and Figure 6.11
★

```
> op <- par(mar=c(5,4,1,1)+.1)
> res <- plot(ucb.mca, labels=0, pch='.', cex.lab=1.2)
>
> coords <- data.frame(res$cols, ucb.mca$factors)
> cols <- c("blue", "red", "black")
> nlev <- ucb.mca$levels.n
> pos <- rep(3, nrow(coords)); pos[9]<-1
>
> points(coords[,1:2], pch=rep(16:18, nlev), col=rep(cols, nlev), cex=1.2)
> text(coords[,1:2], labels=coords$level, col=rep(cols, nlev), pos=pos, cex=1.2, xpd=TRUE)
>
> lines(Dim2 ~ Dim1, data=coords, subset=factor=="Admit", lty=1, lwd=2, col=cols[1])
> lines(Dim2 ~ Dim1, data=coords, subset=factor=="Gender", lty=1, lwd=2, col=cols[2])
>
> legend("bottomright", legend=c("Admit", "Gender", "Dept"),
+        title="Factor", title.col="black",
+        col=cols, text.col=cols, pch=16:18,
+        bg="gray95", cex=1.2)
> par(op)
```


(c) Interpret the plot. Is there some interpretation for the first dimension? What does the plot show about the relation of admission to the other factors?
★ The first dimension largely corresponds to Admission, showing the overall association of Males more likely to be admitted, Females more likely to be rejected. Note that the departments, labeled A–F, were actually ordered by overall rate of admission, but this ordering does not appear along Dimension 1 in the plot

Chapter 7

Logistic Regression Models

Exercise 7.1 Arbuthnot's data on the sex ratio of births in London was examined in Example 3.1. Use a binomial logistic regression model to assess whether the proportion of male births varied with the variables `Year`, `Plague`, and `Mortality` in the *Arbuthnot* data set. Produce effect plots for the terms in this model. What do you conclude?

★ For the binomial logistic model, use `cbind(Males, Females)` for the response variable in the model.

```
> data(Arbuthnot, package="HistData")
> arbuth.mod <- glm(cbind(Males, Females) ~ Year + Plague + Mortality,
+                   data=Arbuthnot, family=binomial)
> summary(arbuth.mod)

Call:
glm(formula = cbind(Males, Females) ~ Year + Plague + Mortality,
    family = binomial, data = Arbuthnot)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-3.184  -0.996  -0.005   0.850   3.714

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.07e-02   3.09e-01   -0.13    0.895
Year         8.28e-05   1.93e-04    0.43    0.668
Plague       1.91e-06   1.13e-06    1.68    0.093 .
Mortality   -1.86e-06   9.26e-07   -2.01    0.045 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 169.74  on 81  degrees of freedom
Residual deviance: 156.31  on 78  degrees of freedom
AIC: 963.8

Number of Fisher Scoring iterations: 3

> LRstats(arbuth.mod)

Likelihood summary table:
           AIC BIC LR Chisq Df Pr(>Chisq)
arbuth.mod 964 973      156 78    3.6e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The effects of `Year` and `Plague` are small and non-significant. The Male/Female proportion appears to decrease with increasing `Mortality`.

```
> library(effects)
> arbuth.eff <- allEffects(arbuth.mod)
> plot(arbuth.eff, ylab="Males/Females", rows=1, cols=3)
```

Year effect plot · **Plague effect plot** · **Mortality effect plot**

In the plots for `Plague` and `Mortality`, it is apparent that both are extremely skewed. One alternative is to represent these as `log(Plague+1)` and `log(Mortality)` in the model. Overall, these effects are quite small, but the main effects model `arbuth.mod` is better than the null model.

```
>    # compare with null model
> arbuth.mod0 <- glm(cbind(Males, Females) ~ 1,
+                    data=Arbuthnot, family=binomial)
> anova(arbuth.mod0, arbuth.mod, test="Chisq")
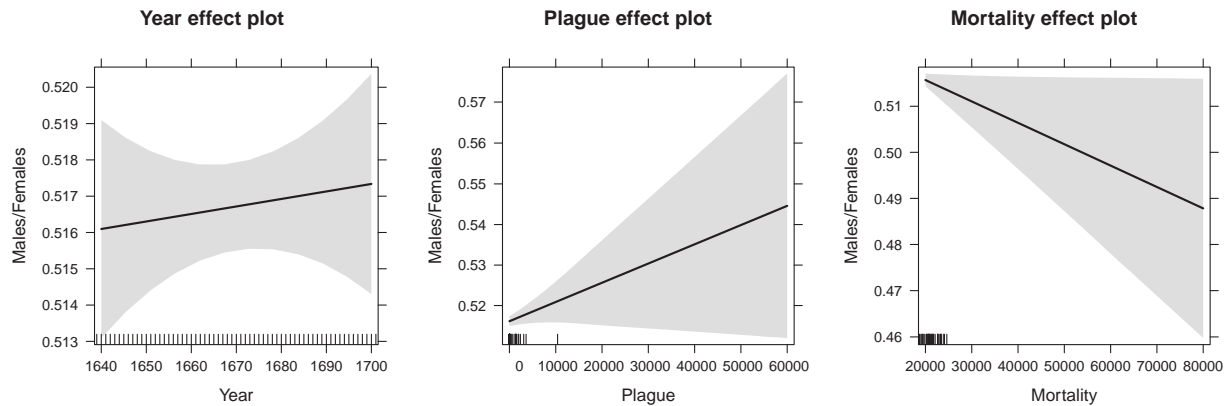
Analysis of Deviance Table

Model 1: cbind(Males, Females) ~ 1
Model 2: cbind(Males, Females) ~ Year + Plague + Mortality
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1        81        170
2        78        156  3     13.4   0.0038 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Exercise 7.2 For the Donner Party data in *Donner*, examine Grayson's 1990 claim that survival in the Donner Party was also mediated by the size of the family unit. This takes some care, because the `family` variable in the *Donner* data is a simplified grouping based on the person's name and known alliances among families from the historical record. Use the following code to compute a `family.size` variable from each individual's last name:

```
> data("Donner", package="vcdExtra")
> Donner$survived <-factor(Donner$survived, labels=c("no", "yes"))
> # use last name for family
> lname <-strsplit(rownames(Donner), ",")
> lname <-sapply(lname, function(x) x[[1]])
> Donner$family.size <-as.vector(table(lname)[lname])
```

(a) Choose one of the models (`donner.mod4`, `donner.mod6`) from Example 7.9 that include the interaction of age and sex and nonlinear terms in age. Fit a new model that adds a main effect of `family.size`. What do you conclude about Grayson's claim?
★

```
> library(car)
> donner.mod4a <- glm(survived ~ poly(age,2) * sex + family.size, data=Donner, family=binomial)
> Anova(donner.mod4a)

Analysis of Deviance Table (Type II tests)

Response: survived
                LR Chisq Df Pr(>Chisq)
poly(age, 2)       14.94  2    0.00057 ***
sex                 4.24  1    0.03944 *
family.size        11.54  1    0.00068 ***
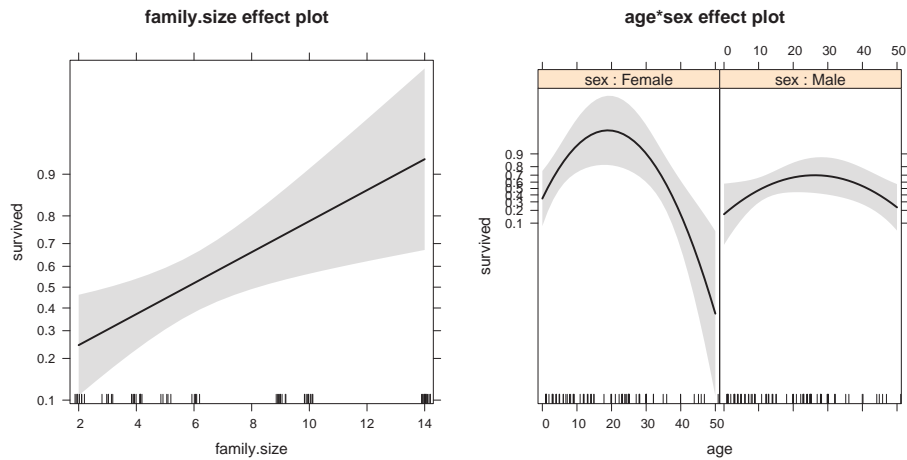poly(age, 2):sex   12.24  2    0.00220 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Family size seems to have an effect on survival.

(b) Produce an effect plot for this model.
★

```
> library(effects)
> donner.eff4a <- allEffects(donner.mod4a, xlevels=list(age=seq(0,50,5)))
> plot(donner.eff4a, ticks=list(n=8))
```


(c) Continue, by examining whether the effect of family size can be taken as linear, or whether a nonlinear term should be added.
★

```
> donner.mod4b <- glm(survived ~ poly(age,2) * sex + poly(family.size, 2), data=Donner, family=binomial)
> Anova(donner.mod4b)

Analysis of Deviance Table (Type II tests)

Response: survived
                   LR Chisq Df Pr(>Chisq)
poly(age, 2)          17.64  2    0.00015 ***
sex                    2.33  1    0.12688
poly(family.size, 2)  24.81  2    4.1e-06 ***
poly(age, 2):sex      12.25  2    0.00219 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> donner.eff4b <- allEffects(donner.mod4b, xlevels=list(age=seq(0,50,5)))
> plot(donner.eff4b, ticks=list(n=8))
```


Exercise 7.3 Use component+residual plots (Section 7.5.3) to examine the additive model for the *ICU* data given by

```
> icu.glm2 <- glm(died ~ age + cancer  + admit + uncons,
+                data=ICU, family=binomial)
```

(a) What do you conclude about the linearity of the (partial) relationship between age and death in this model?
★

(b) An alternative strategy is to allow some nonlinear relation for age in the model using a quadratic (or cubic) term like `poly(age, 2)` (or `poly(age, 3)`) in the model formula. Do these models provide evidence for a nonlinear effect of age on death in the ICU?
★

Exercise 7.4 Explore the use of other marginal and conditional plots to display the relationships among the variables predicting death in the ICU in the model `icu.glm2`. For example, you might begin with a marginal `gpairs()` plot showing all bivariate marginal relations, something like this:

```
> library(gpairs)
> gpairs(ICU[,c("died", "age", "cancer", "admit", "uncons")],
+    diag.pars=list(fontsize=16, hist.color="lightgray"),
+    mosaic.pars=list(gp=shading_Friendly,
+                     gp_args=list(interpolate=1:4)))
```

★

Exercise 7.5 The data set *Caesar* in **vcdExtra** gives a 3×2^3 frequency table classifying 251 women who gave birth by Caesarian section by `Infection` (three levels: none, Type 1, Type2) and `Risk`, whether `Antibiotics` were used, and whether the Caesarian section was `Planned` or not. `Infection` is a natural response variable. In this exercise, consider only the binary outcome of infection vs. no infection.

```
> data("Caesar", package="vcdExtra")
> Caesar.df <- as.data.frame(Caesar)
> Caesar.df$Infect <- as.numeric(Caesar.df$Infection %in%
+                                 c("Type 1", "Type 2"))
```

(a) Fit the main-effects logit model for the binary response `Infect`. Note that with the data in the form of a frequency data frame you will need to use `weights=Freq` in the call to `glm()`. (It might also be convenient to reorder the levels of the factors so that `"No"` is the baseline level for each.)
★

(b) Use `summary()` or **car** (Fox and Weisberg, 2015)::`Anova()` to test the terms in this model.
★

(c) Interpret the coefficients in the fitted model in terms of their effect on the odds of infection.
★

(d) Make one or more effects plots for this model, showing separate terms, or their combinations.
★

Exercise 7.6 The data set *birthwt* in the MASS package gives data on 189 babies born at Baystate Medical Center, Springfield, MA during 1986. The quantitative response is `bwt` (birth weight in grams), and this is also recorded as `low`, a binary variable corresponding to `bwt < 2500` (2.5 Kg). The goal is to study how this varies with the available predictor variables. The variables are all recorded as numeric, so in R it may be helpful to convert some of these into factors and possibly collapse some low frequency categories. The code below is just an example of how you might do this for some variables.

```
> data("birthwt", package="MASS")
> birthwt <- within(birthwt, {
+    race <- factor(race, labels = c("white", "black", "other"))
+        ptd <- factor(ptl > 0)   # premature labors
+        ftv <- factor(ftv)       # physician visits
+        levels(ftv)[-(1:2)] <- "2+"
+        smoke <- factor(smoke>0)
+        ht <- factor(ht>0)
+        ui <- factor(ui>0)
+    })
```

(a) Make some exploratory plots showing how low birth weight varies with each of the available predictors. In some cases, it will probably be helpful to add some sort of smoothed summary curves or lines.
★

(b) Fit several logistic regression models predicting low birth weight from these predictors, with the goal of explaining this phenomenon adequately, yet simply.

★

(c) Use some graphical displays to convey your findings.

★

Exercise 7.7   Refer to Exercise 5.9 for a description of the `Accident` data. The interest here is to model the probability that an accident resulted in death rather than injury from the predictors `age`, `mode`, and `gender`. With `glm()`, and the data in the form of a frequency table, you can use the argument `weight=Freq` to take cell frequency into account.

(a) Fit the main effects model, `result=="Died" ~ age + mode + gender`. Use `car::Anova()` to assess the model terms.

★

(b) Fit the model that allows all two-way interactions. Use `anova()` to test whether this model is significantly better than the main effects model.

★

(c) Fit the model that also allows the three-way interaction of all factors. Does this offer any improvement over the two-way model?

★

(d) Interpret the results of the analysis using effect plots for the two-way model, separately for each of the model terms. Describe verbally the nature of the `age*gender` effect. Which mode of transportation leads to greatest risk of death?

★

Chapter 8

Models for Polytomous Responses

Exercise 8.1   For the women's labor force participation data (`Womenlf`), the response variable, `partic`, can be treated as ordinal by using

```
> Womenlf$partic <- ordered(Womenlf$partic,
+                          levels=c('not.work', 'parttime', 'fulltime'))
```

Use the methods in Section 8.1 to test whether the proportional odds model holds for these data.

★

Exercise 8.2   The data set `housing` in the MASS package gives a $3 \times 3 \times 4 \times 2$ table in frequency form relating (a) satisfaction (`Sat`) of residents with their housing (High, Medium, Low), (b) perceived degree of influence (`Infl`) they have on the management of the property (High, Medium, Low), (c) `Type` of rental (Tower, Atrium, Apartment, Terrace), and (d) contact (`Cont`) residents have with other residents (Low, High). Consider satisfaction as the ordinal response variable.

(a) Fit the proportional odds model with additive (main) effects of housing type, influence in management, and contact with neighbors to this data. (Hint: Using `polr()`, with the data in frequency form, you need to use the `weights` argument to supply the `Freq` variable.)

★

(b) Investigate whether any of the two-factor interactions among `Infl`, `Type`, and `Cont` add substantially to goodness of fit of this model. (Hint: use `stepAIC()`, with the scope formula `~ .^2` and `direction="forward"`.)

★

(c) For your chosen model from the previous step, use the methods of Section 8.1.5 to plot the probabilities of the categories of satisfaction.

★

(d) Write a brief summary of these analyses, interpreting *how* satisfaction with housing depends on the predictor variables.

★

Exercise 8.3 The data *TV* on television viewing was analyzed using correspondence analysis in Example 6.4, ignoring the variable `Time`, and extended in Exercise 6.9. Treating `Network` as a three-level response variable, fit a generalized logit model (Section 8.3) to explain the variation in viewing in relation to `Day` and `Time`. The *TV* data is a three-way table, so you will need to convert it to a frequency data frame first.

```
> data("TV", package="vcdExtra")
> TV.df <- as.data.frame.table(TV)
```

(a) Fit the main-effects model, `Network ~ Day + Time`, with `multinom()`. Note that you will have to supply the `weights` argument because each row of `TV.df` represents the number of viewers in the `Freq` variable.

★

(b) Prepare an effects plot for the fitted probabilities in this model.

★

(c) Interpret these results in comparison to the correspondence analysis in Example 6.4.

★

Exercise 8.4 * Refer to Exercise 5.10 for a description of the *Vietnam* data set in **vcdExtra**. The goal here is to fit models for the polytomous `response` varialble in relation to `year` and `sex`.

(a) Fit the proportional odds model to these data, allowing an interaction of `year` and `sex`.

★

(b) Is there evidence that the proportional odds assumption does not hold for this data set? Use the methods described in Section 8.1 to assess this.

★

(c) Fit the multinomial logistic model, also allowing an interaction. Use car::`Anova()` to assess the model terms.

★

(d) Produce an effect plot for this model and describe the nature of the interaction.

★

(e) Fit the simpler multinomial model in which there is no effect of year for females and the effect of year is linear for males (on the logit scale). Test whether this model is significantly worse than the general multinomial model with interaction.

★

Chapter 9

Loglinear and Logit Models for Contingency Tables

Exercise 9.1 Consider the data set *DaytonSurvey* (described in Example 2.6), giving results of a survey of use of alcohol (A), cigarettes (C), and marijuana (M) among high school seniors. For this exercise, ignore the variables `sex` and `race`, by working with the marginal table `Dayton.ACM`, a $2 \times 2 \times 2$ table in frequency data frame form.

```
> Dayton.ACM <- aggregate(Freq ~ cigarette + alcohol + marijuana,
+                         data=DaytonSurvey, FUN=sum)
```

(a) Use `loglm()` to fit the model of mutual independence, [A][C][M].

★

(b) Prepare mosaic display(s) for associations among these variables. Give a verbal description of the association between cigarette and alcohol use.

★

(c) Use `fourfold()` to produce fourfold plots for each pair of variables, AC, AM, and CM, stratified by the remaining one. Describe these associations verbally.

★

Exercise 9.2 Continue the analysis of the `DaytonSurvey` data by fitting the following models:

(a) Joint independence, [AC][M]

★

(b) Conditional independence, [AM][CM]

★

(c) Homogeneous association, [AC][AM][CM]

★

(d) Prepare a table giving the goodness-of-fit tests for these models, as well as the model of mutual independence, [A][C][M], and the saturated model, [ACM]. *Hint*: `anova()` and `LRstats()` are useful here. Which model appears to give the most reasonable fit?

★

Exercise 9.3 The data set `Caesar` in **vcdExtra** gives a 3×2^3 frequency table classifying 251 women who gave birth by Caesarian section by `Infection` (three levels: none, Type 1, Type2) and `Risk`, whether `Antibiotics` were used, and whether the Caesarian section was `Planned` or not. `Infection` is a natural response variable, but the table has quite a few zeros.

(a) Use `structable()` and `mosaic()` to see the locations of the zero cells in this table.

★

(b) Use `loglm()` to fit the baseline model [I][RAP]. Is there any problem due to zero cells indicated in the output?

★

(c) For the purpose of this excercise, treat all the zero cells as *sampling zeros* by adding 0.5 to all cells, e.g., `Caesar1 <- Caesar + 0.5`. Refit the baseline model.

★

(d) Now fit a "main effects" model [IR][IA][IP][RAP] that allows associations of `Infection` with each of the predictors.

★

Exercise 9.4 The `Detergent` in **vcdExtra** gives a $2^3 \times 3$ table classifying a sample of 1,008 consumers according to their preference for (a) expressed `Preference` for Brand "X" or Brand "M" in a blind trial, (b) `Temperature` of laundry water used, (c) previous use (`M_user`) of detergent Brand "M," and (d) the softness (`Water_softness`) of the laundry water used.

(a) Make some mosaic displays to visualize the associations among the table variables. Try using different orderings of the table variables to make associations related to `Preference` more apparent.

★

(b) Use a `doubledecker()` plot to visualize how `Preference` relates to the other factors.

★

(c) Use `loglm()` to fit the baseline model [P][TMW] for `Preference` as the response variable. Use a mosaic display to visualize the lack of fit for this model.

★

Chapter 10

Extending Loglinear Models

Exercise 10.1 Example 10.5 presented an analysis of the data on visual acuity for the subset of women in the `VisualAcuity` data. Carry out a parallel analysis of the models fit there for the `men` in this data set, given by:

```
> data("VisualAcuity", package="vcd")
> men <- subset(VisualAcuity, gender=="male", select=-gender)
```

★

Exercise 10.2 Table 10.1 gives a 4×4 table of opinions about premarital sex and whether methods of birth control should be made available to teenagers aged 14–16, from the 1991 General Social Survey (Agresti, 2013, Table 10.3). Both variables are ordinal, and their grades are represented by the case of the row and column labels.

Table 10.1: Opinions about premarital sex and availability of teenage birth control. *Source*: Agresti (2013, Table 10.3).

Premarital sex	Birth control			
	DISAGREE	disagree	agree	AGREE
WRONG	81	68	60	38
Wrong	24	26	29	14
wrong	18	41	74	42
OK	36	57	161	157

(a) Fit the independence model to these data using `loglm()` or `glm()`.
   ★
(b) Make a mosaic display showing departure from independence and describe verbally the pattern of association.
   ★
(c) Treating the categories as equally spaced, fit the $L \times L$ model of uniform association, as in Section 10.1. Test the difference against the independence model with a likelihood-ratio test.
   ★
(d) Fit the RC(1) model with `gnm()`, and test the difference of this against the model of uniform association.
   ★
(e) Write a brief summary of these results, including plots useful for explaining the relationships in this data set.
   ★

Exercise 10.3 For the data on attitudes toward birth control in Table 10.1,

(a) Calculate and plot the observed local log odds ratios.
   ★
(b) Also fit the R, C, and R+C models.
   ★
(c) Use the method described in Section 10.1.2 to visualize the structure of fitted local log odds ratios implied by each of these models, together with the RC(1) model.
   ★

Exercise 10.4 The data set *gss8590* in logmult gives a $4 \times 5 \times 4$ table of education levels and occupational categories for the four combinations of gender and race from the General Social Surveys, 1985–1990, as reported by Wong (2001, Table 2). Wong (2010, Table 2.3B) later used the subset pertaining to women to illustrate RC(2) models. This data is created below as `Women.tab`, correcting an inconsistency to conform with the 2010 table.

★

```
> data("gss8590", package="logmult")
> Women.tab <- margin.table(gss8590[,,c("White Women", "Black Women")], 1:2)
> Women.tab[2,4] <- 49
> colnames(Women.tab)[5] <- "Farm"
```

   (a) Fit the independence model, and also the RC(1) and RC(2) models using `rc()` with marginal weights, as illus-
       trated in Example 10.4. Summarize these statistical tests in a table.
       ★

   (b) Plot the solution for the RC(2) model with 68% confidence ellipses. What verbal labels would you use for the
       two dimensions?
       ★

   (c) Is there any indication that a simpler model, using integer scores for the row (Education) or column (Occupation)
       categories, or both, might suffice? If so, fit the analogous column effects, row effects, or $L \times L$ model, and
       compare with the models fit in part (a).
       ★

Chapter 11

Generalized Linear Models for Count Data

Exercise 11.1 Poole (1989) studied the mating behavior of elephants over 8 years in Amboseli National Park, Kenya.
A focal aspect of the study concerned the mating success of males in relation to age, since larger males tend to be
more successful in mating. Her data were used by Ramsey and Schafer (2002, Chapter 22) as a case study, and are
contained in the Sleuth2 (Ramsey et al., 2012) package (Ramsey et al., 2012) as *case2201*.

For convenience, rename this to `elephants`, and study the relation between `Age` (at the beginning of the study) and
number of successful `Matings` for the 41 adult male elephants observed over the course of this study, ranging in age
from 27–52.

```
> data("case2201", package="Sleuth2")
> elephants <- case2201
> str(elephants)

'data.frame':   41 obs. of  2 variables:
 $ Age    : num  27 28 28 28 28 29 29 29 29 29 ...
 $ Matings: num  0 1 1 1 3 0 0 0 2 2 ...
```

   (a) Create some exploratory plots of `Matings` against `Age` in the styles illustrated in this chapter. To do this
       successfully, you will have to account for the fact that `Matings` has a range of only 0–9, and use some smoothing
       methods to show the trend.
       ★

   (b) Repeat (a) above, but now plotting `log(Matings+1)` against `Age` to approximate a Poisson regression with a
       log link and avoid problems with the zero counts.
       ★

   (c) Fit a linear Poisson regression model for `Matings` against `Age`. Interpret the fitted model *verbally* from a
       graph of predicted number of matings and/or from the model coefficients. (*Hint*: Using `Age-27` will make the
       intercept directly interpretable.)
       ★

   (d) Check for nonlinearity in the relationship by using the term `poly(Age,2)` in a new model. What do you
       conclude?
       ★

   (e) Assess whether there is any evidence of overdispersion in these data by fitting analogous quasi-Poisson and
       negative-binomial models.
       ★

Exercise 11.2 The data set *quine* in MASS gives data on absenteeism from schools in rural New South Wales, Australia. 146 children were classified by ethnic background (Eth), age (Age, a factor), Sex, and Learner status (Lrn), and the number of days absent (Days) from school in a particular school year was recorded.

(a) Fit the all main-effects model in the Poisson family and examine the tests of these effects using summary() and car::Anova(). Are there any terms that should be dropped according to these tests?
★

(b) Re-fit this model as a quasi-Poisson model. Is there evidence of overdispersion? Test for overdispersion formally, using dispersiontest() from AER (Kleiber and Zeileis, 2015).
★

(c) Carry out the same significance tests and explain why the results differ from those for the Poisson model.
★

Exercise 11.3 The data set *AirCrash* in vcdExtra was analyzed in Exercise 5.2 and Exercise 6.3 in relation to the Phase of the flight and Cause of the crash. Additional variables include the number of Fatalities and Year. How does Fatalities depend on the other variables?

(a) Use the methods of this chapter to make some exploratory plots relating fatalities to each of the predictors.
★

(b) Fit a main effects poisson regression model for Fatalities, and make effects plots to visualize the model. Which phases and causes result in the largest number of fatalities?
★

(c) A linear effect of Year might not be appropriate for these data. Try using a natural spline term, ns(Year, df) to achieve a better, more adequate model.
★

(d) Use a model-building tool like add1() or MASS::stepAIC() to investigate whether there are important two-way interactions among the factors and your chosen effect for Year.
★

(e) Visualize and interpret your final model and write a brief summary to answer the question posed.
★

Exercise 11.4 Male double-crested cormorants use advertising behavior to attract females for breeding. The *Cormorants* data set in vcdExtra gives some results from a study by Meagan Mc Rae (2015) on counts of advertising males observed two or three times a week at six stations in a tree-nesting colony for an entire breeding season. The number of advertising birds was counted and these observations were classified by characteristics of the trees and nests. The goal was to determine how this behavior varies temporally over the season and spatially over observation stations, as well as with characteristics of nesting sites. The response variable is count and other predictors are shown below. See help(Cormorants, package="vcdExtra") for further details.

```
> data("Cormorants", package = "vcdExtra")
> car::some(Cormorants)

      category week station   nest height  density tree_health count
44         Pre    1      B2      no    mid      few     healthy     2
84         Pre    2      C4      no   high      few        dead     1
98         Pre    2      B1    full    mid      few     healthy     2
133        Pre    3      B1      no    mid      few        dead     2
159  Incubation   4      C2 partial    low      few        dead     1
176  Incubation   4      C4    full   high      few        dead     1
243  Incubation   6      C2    full    mid      few        dead     1
248  Incubation   6      C3      no   high     high        dead     1
315  Incubation   9      B2      no    mid moderate        dead     1
317  Incubation   9      B2      no   high moderate        dead     1
```

(a) Using the methods illustrated in this chapter, make some exploratory plots of the number of advertising birds against week in the breeding season, perhaps stratified by another predictor, like tree height, nest condition, or observation station. To see anything reasonable, you should plot count on a log (or square root) scale, jitter the points, and add smoothed curves. The variable category breaks the weeks into portions of the breeding season, so adding vertical lines separating those will be helpful for interpretation.
★

(b) Fit a main-effects Poisson GLM to these data and test the terms using `Anova()` from the **car** package.

★

(c) Interpret this model using an effects plot.

★

(d) Investigate whether the effect of `week` should be treated as linear in the model. You could try using a polynomial term like `poly(week, degree)` or perhaps better, using a natural spline term like `ns(week, df)` from the **splines** package.

★

(e) Test this model for overdispersion, using either a `quasipoisson` family or `dispersiontest()` in **AER**.

★

Exercise 11.5 For the *CodParasites* data, recode the `area` variable as an ordered factor as suggested in footnote 13. Test the hypotheses that prevalence and intensity of cod parasites is linearly related to area.

★

Exercise 11.6 In Example 11.10, we ignored other potential predictors in the *CodParasites* data: `depth`, `weight`, `length`, `sex`, `stage`, and `age`. Use some of the graphical methods shown in this case study to assess whether any of these are related to prevalence and intensity.

★

Exercise 11.7 The analysis of the *PhdPubs* data in the examples in this chapter were purposely left incomplete, going only as far as the negative binomial model.

(a) Fit the zero-inflated and hurdle models to this data set, considering whether the count component should be Poisson or negative-binomial, and whether the zero model should use all predictors or only a subset. Describe your conclusions from this analysis in a few sentences.

★

(b) Using the methods illustrated in this chapter, create some graphs summarizing the predicted counts and probabilities of zero counts for one of these models.

★

(c) For your chosen model, use some of the diagnostic plots of residuals and other measures shown in Section 11.6 to determine if your model solves any of the problems noted in Example 11.17 and Example 11.18, and whether there are any problems that remain.

★

Exercise 11.8 In Example 11.19 we used a simple analysis of $\log(y + 1)$ for the multivariate responses in the *NMES1988* data using a classical MLM (Eqn. (11.16)) as a rough approximation of a multivariate Poisson model. The HE plot in Figure 11.40 was given as a visual summary, but did not show the data. Examine why the MLM is not appropriate statistically for these data, as follows:

(a) Calculate residuals for the model `nmes.mlm` using

```
> resids <- residuals(nmes.mlm, type="deviance")
```

(b) Make univariate density plots of these residuals to show their univariate distributions. These should be approximately normal under the MLM. What do you conclude?

★

(c) Make some bivariate plots of these residuals. Under the MLM, each should be bivariate normal with elliptical contours and linear regressions. Add 2D density contours (`kde2d()`, or `geom_density2d()` in **ggplot2** (Wickham and Chang, 2015)) and some smoothed curve. What do you conclude?

★

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