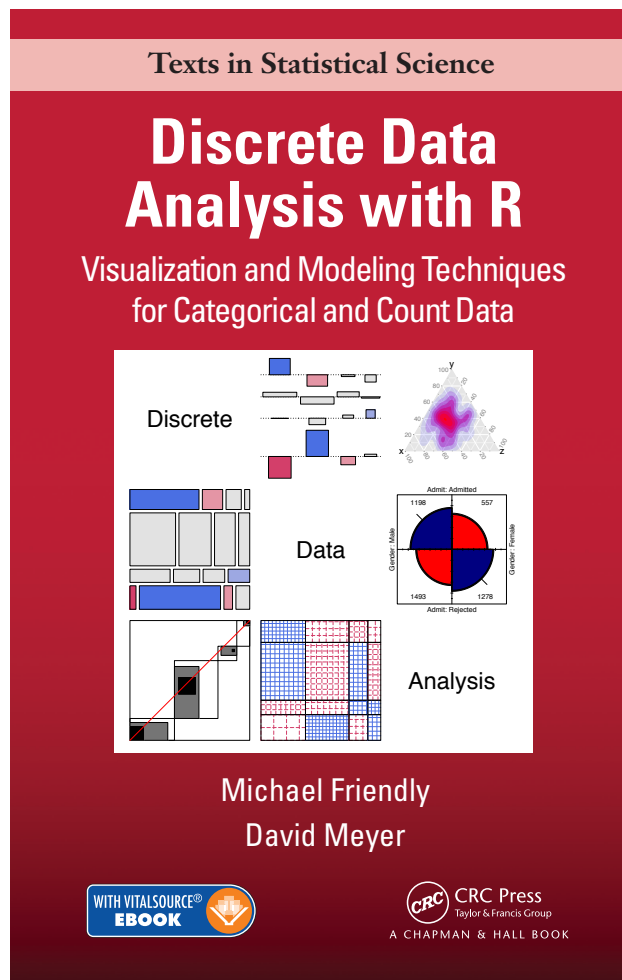


# Discrete Data Analysis with R: Solutions and Hints to Exercises

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

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## **This document**

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 and commentary are indicated with the ★ symbol, and with text in this font.

Instructors should recognize that many questions are open-ended or admit to different approaches. In many cases we simply present one reasonable approach.

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

For the most part, R code in answers indicates required packages with `library()` or `require()`. This document assumes, however, that the following packages are loaded: **AER**, **car**, **effects**, **MASS** **vcd**, **vcdExtra**.

## Chapter 1 Introduction

★ These questions are all conceptual, or based on judgment. No individual 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.

Some other sources that students might consult are:

- The Gallery of Data Visualization, <http://datavis.ca/gallery/>. A categorized collection of some of the best and worst of statistical graphics.
- Junk Charts, <http://junkcharts.typepad.com/>, a blog by Kaiser Fung. There is also a list of related blogs on graphics and data visualization at [http://junkcharts.typepad.com/junk\\_charts/other-graphics-blogs.html](http://junkcharts.typepad.com/junk_charts/other-graphics-blogs.html).
- Flowing Data, <http://flowingdata.com/>, by Nathan Yau. An eclectic collection of examples and blog posts encompassing a wide range from information visualization to statistical graphics.

**Exercise 1.1** A web page, “The top ten worst graphs,” [http://www.biostat.wisc.edu/~kbroman/topten\\_worstgraphs/](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](http://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 substantive 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.

- (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))

"Alcohol" "Income" "Status" "Urban" "City" "NonCity"
"<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

```



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 `strctable()` 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 `strctable()` have `as.matrix()` methods that convert their result to a matrix.

★

```
> ucb.tab2 <- as.matrix(structable(Dept ~ Admit + Gender, data = UCBAmissions))
> 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  $4 \times 4$  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			
left	gender	1	2	3	4
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)
+ })
```

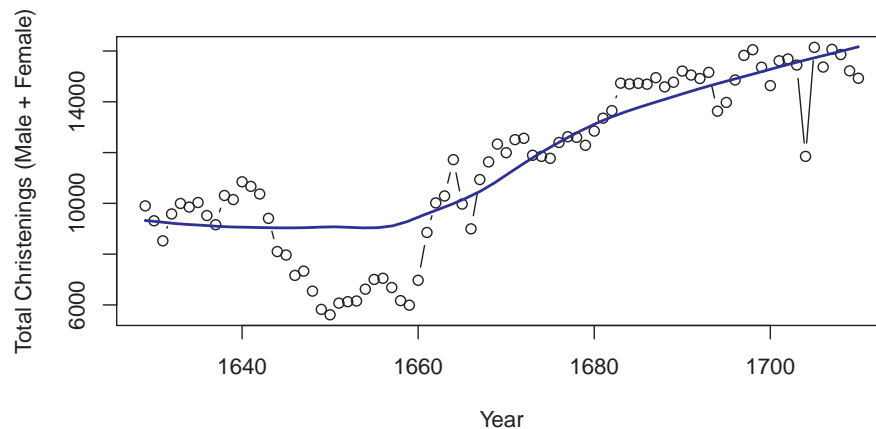


The plot is similar to Figure 3.1 in the text. If it is easier to think in terms of probability of a male birth, plotting that directly may be preferable.

- (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)
+ })
```



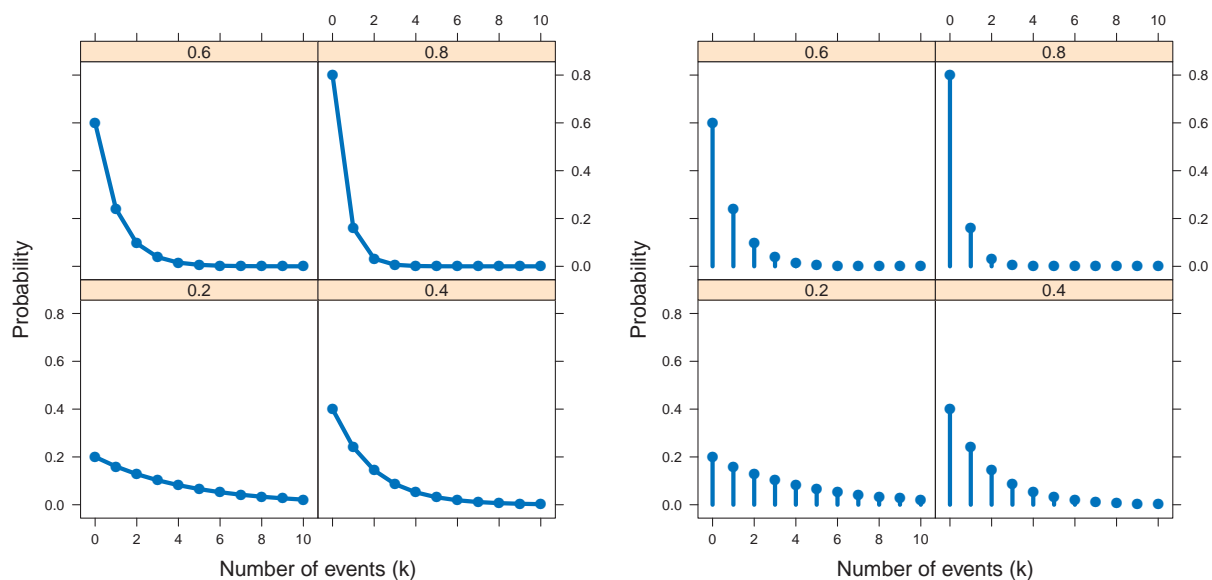
There was a large decline in births between 1640–1660, corresponding to years of plague in England.

**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  $k = 0, 1, \dots, 10$ .

- (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))
```



- (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.

★

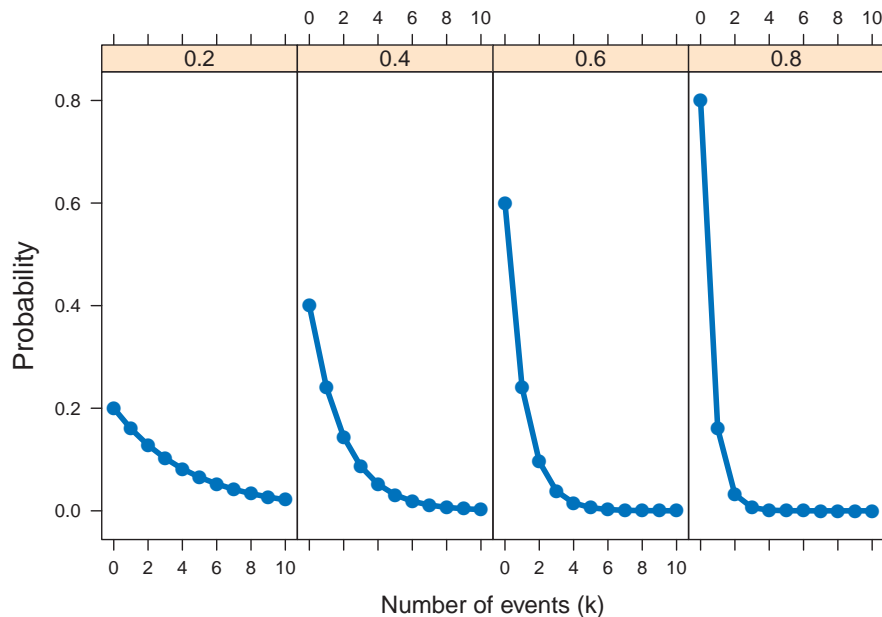
```
> geomplt<-xyplot(prob ~ k, data = geom_df, groups = p,
+               type = c("b"), pch = 16, lwd = 4, cex = 1.25, col = mycol,
+               xlab = list("Number of events (k)", cex = 1.25),
+               ylab = list("Probability", cex = 1.25))
> library(directlabels)
> direct.label(geomplt,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

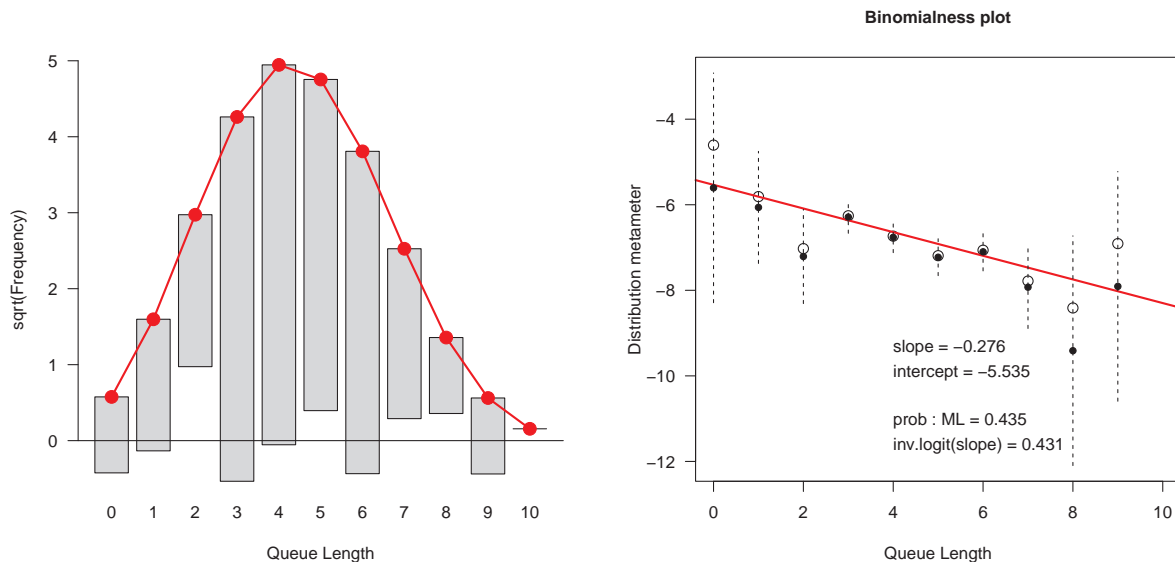
```
> library(vcd)
> gf.women <- goodfit(WomenQueue, type = "binomial", par=list(size=10))
> summary(gf.women)
```

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,  $\text{Bin}(n = 12, p = \frac{1}{2})$ , 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  $\text{Bin}(n = 12, p = \frac{1}{2})$  compared to the model  $\text{Bin}(n = 12, p = \hat{p})$  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

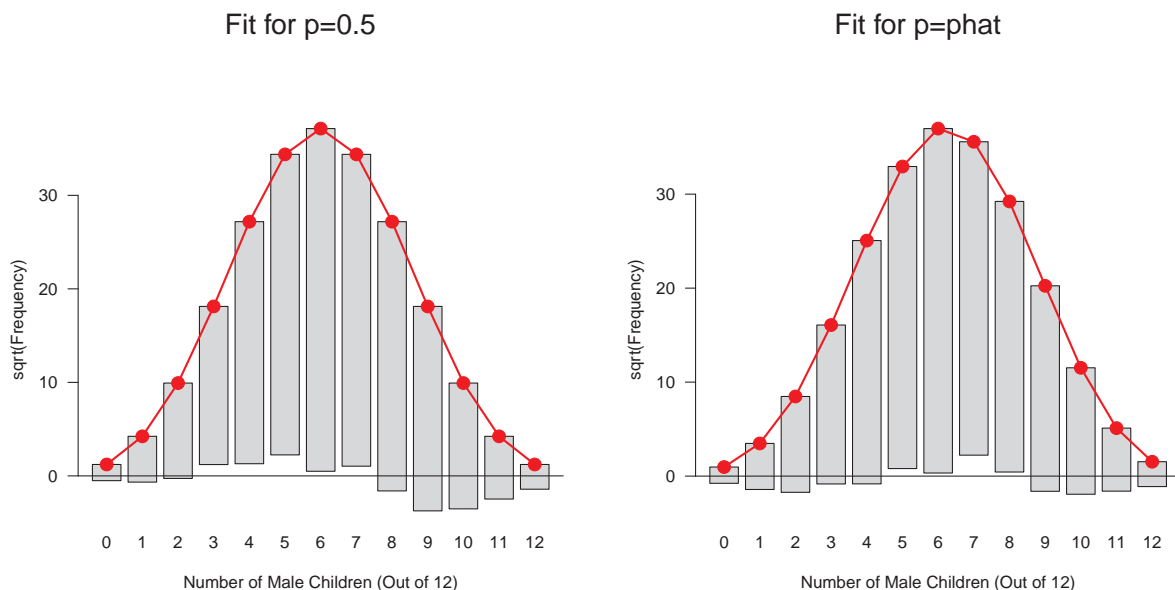
              X^2 df    P(> X^2)
Likelihood Ratio 97.007 11 6.9782e-16
```

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 binomial 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:

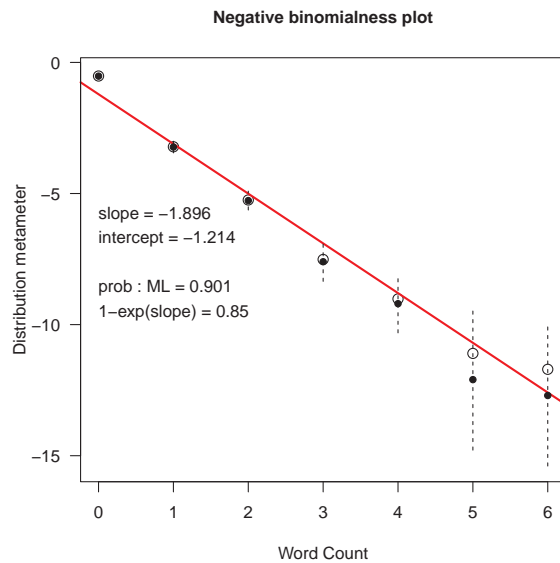
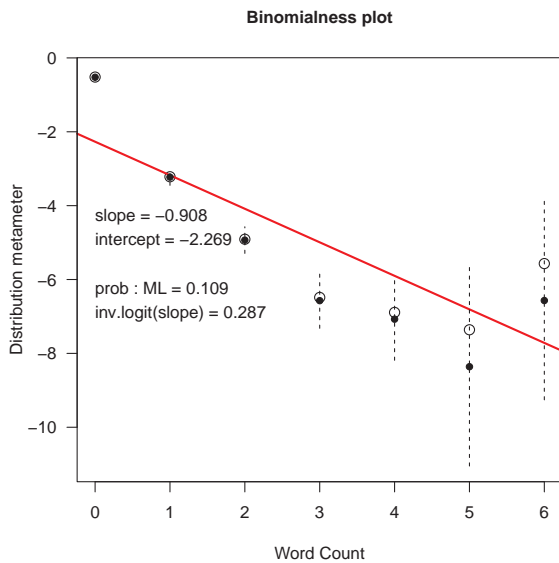
```
> plot(fdfit1)
> plot(fdfit2)
```





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  $k = 0, 1, \dots$  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.

```

> 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'

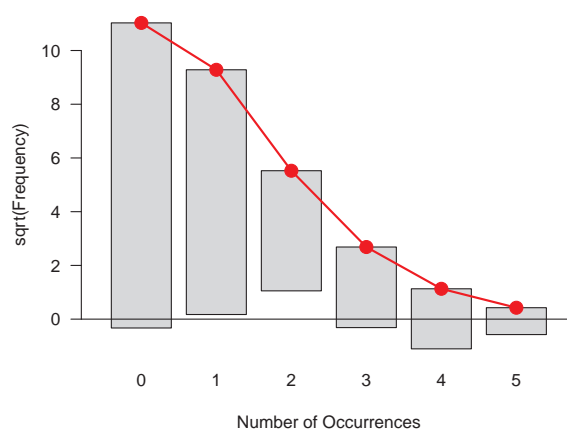
count observed      fitted pearson residual
0          129 121.61816      0.66937
1           83  86.16671     -0.34115
2           20  30.52465     -1.90494
3            9   7.20892     0.66708
4            5   1.27688     3.29481
5            1   0.18094     1.75800

> 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)
```

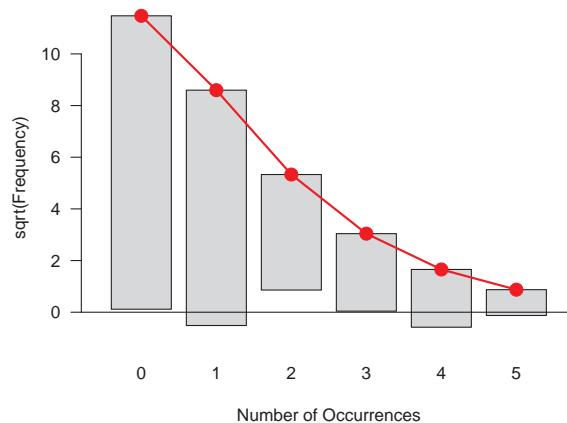
Goodness-of-fit test for nbinomial distribution

```

              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

```

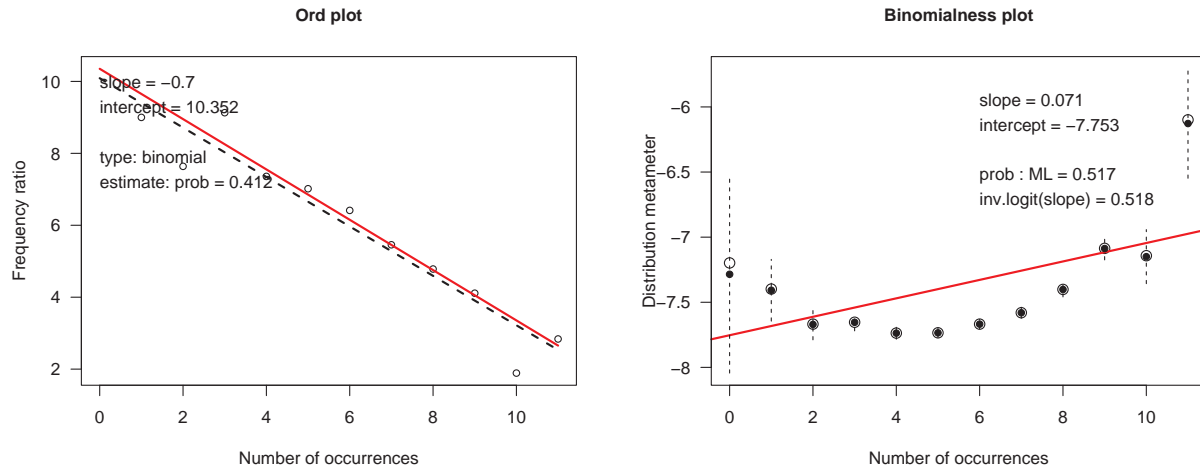
- (c) Diagnose the form of the distribution using the methods described in Section 3.4.

★ 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 (Figure 3.22).

```

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

```



- (d) Try fitting the negative binomial distribution, and use `distplot()` to diagnose whether the negative binomial is a reasonable fit.

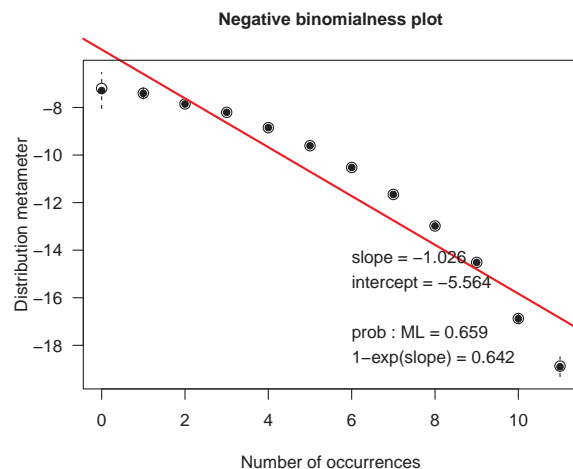
```

> distplot(sax11.tab, type = "nbinomial", size = 11)
> 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



The negative binomial is not a good choice either, as can be seen by the size of the residuals. In fact, the **double binomial distribution** will fit well, as illustrated in Example 3.23.

**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
```

HomeGoals	AwayGoals						
	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))

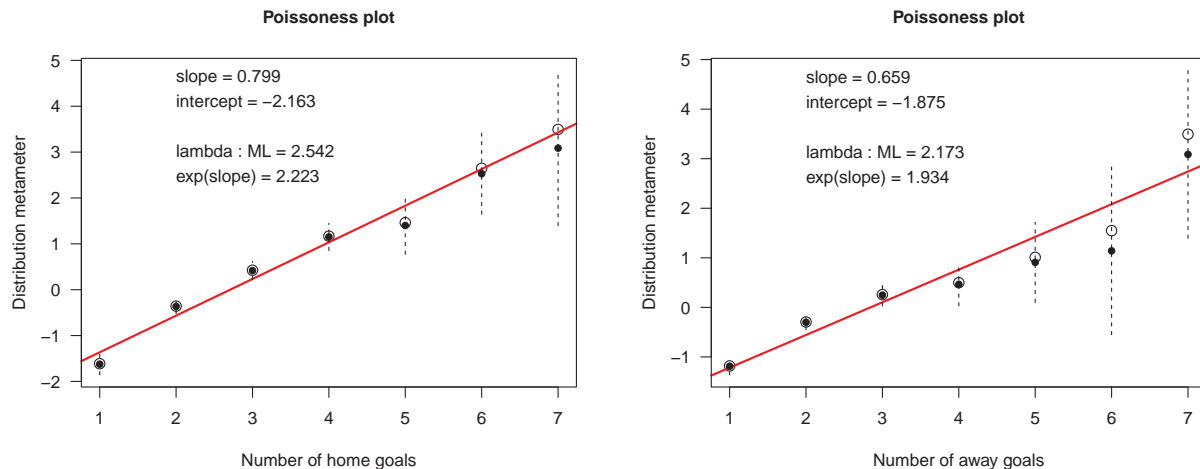
Goodness-of-fit test for poisson distribution

            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")
```



- (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

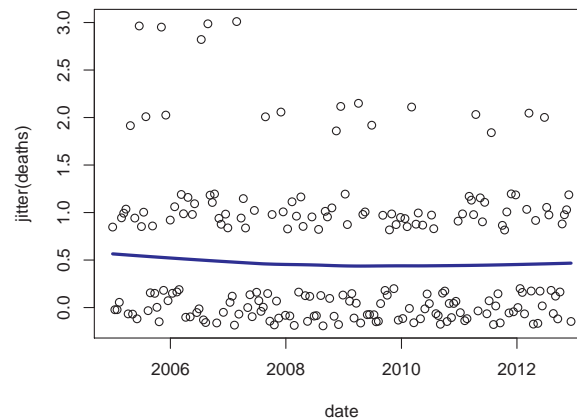
★ The steps are similar to those in the previous problem, but now there are more years, and the range of both home goals and away goals is larger.

**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)

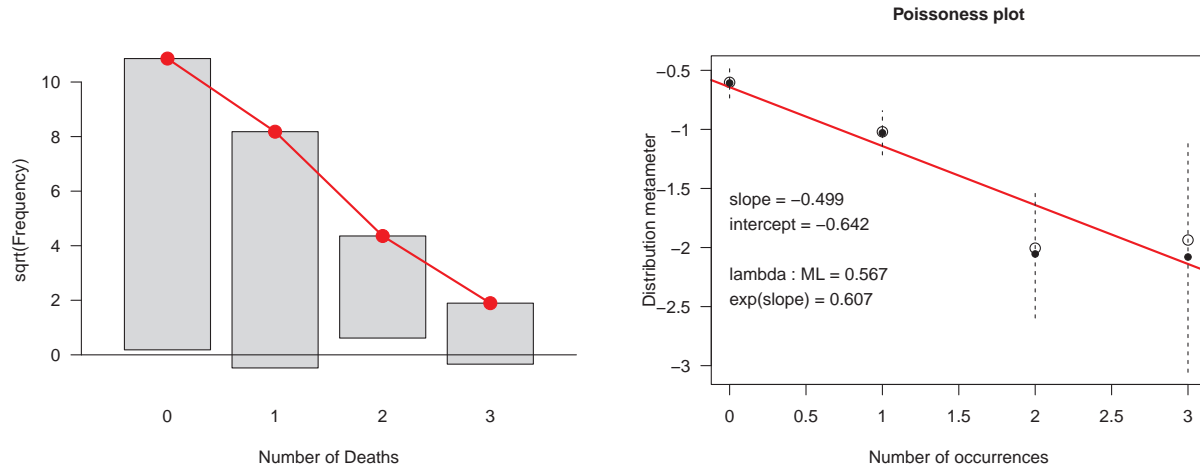
Goodness-of-fit test for poisson distribution

                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.

★

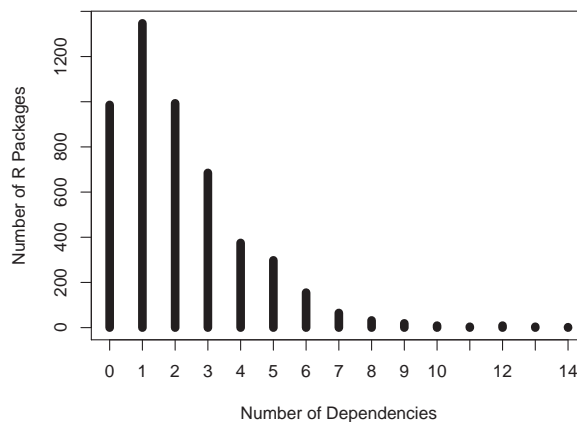
**Exercise 3.11** ★ The one-way table, *Depends*, in *vcdExtra* and shown below gives the frequency distribution of the number of dependencies declared in 4,983 R packages maintained on the CRAN distribution network on January 17, 2014. That is, there were 986 packages that had no dependencies, 1,347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

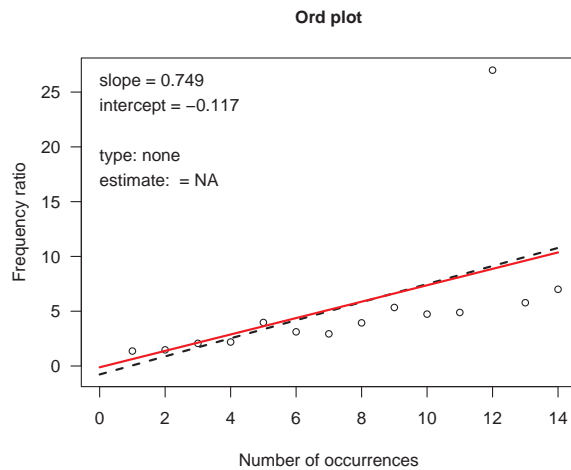


(b) Use `Ord_plot()` to see if this method can diagnose the form of the distribution.

★ 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)
```



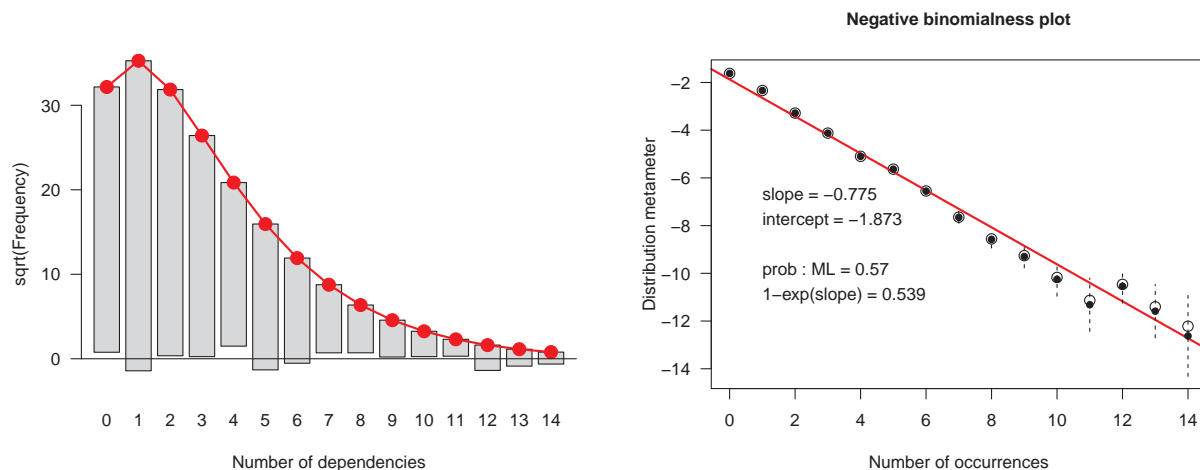
- (c) Try to fit a reasonable distribution to describe dependencies among R packages.  
 ★ Among the distributions described in Chapter 3 and implemented in the vcd package the negative binomial may be the best to try.

```
> 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 distributions**. 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

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

★ The standard Poisson distribution has the probability mass function

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

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  $\lambda/(1 - \exp(-\lambda))$ .

★

- (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)
```

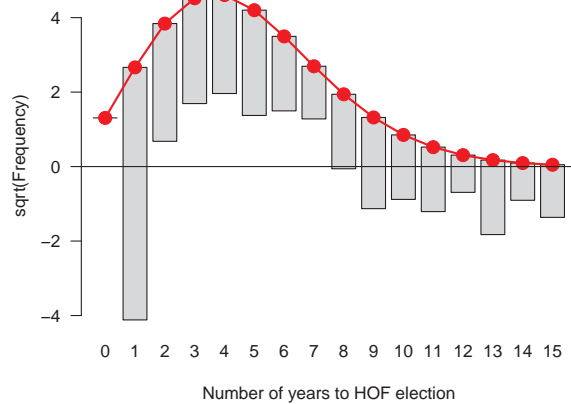
Observed and fitted values for poisson distribution  
with parameters estimated by 'ML'

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
```

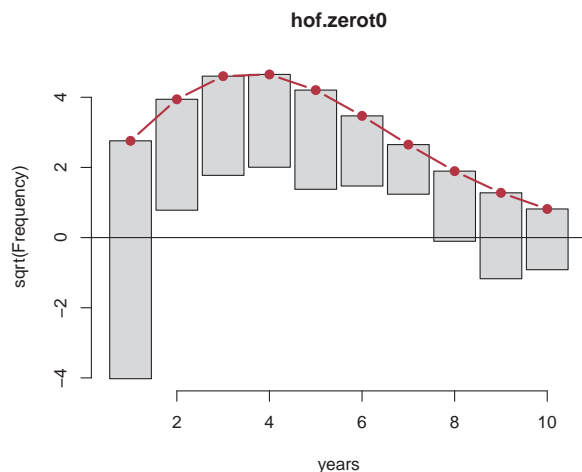
```
Call:
vglm(formula = years ~ 1, family = pospoisson, data = HOF.df,
      weights = inducted)
```

```
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  $2 \times 2$  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)

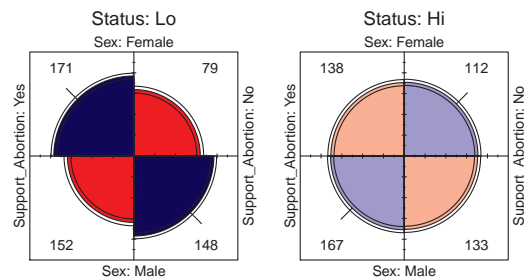
table [1:2, 1:2, 1:2] 171 152 138 167 79 148 112 133
- attr(*, "dimnames")=List of 3
..$ Sex          : chr [1:2] "Female" "Male"
..$ Status       : chr [1:2] "Lo" "Hi"
..$ Support_Abortion: chr [1:2] "Yes" "No"
```

- (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

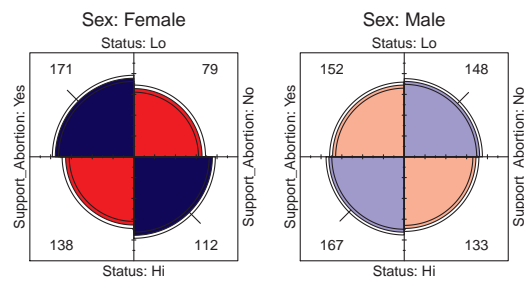
> Abortion2<-aperm(Abortion, c(1,3,2))
> fourfold(Abortion2)
```



- (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  $\chi^2$  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  $3 \times 3$  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  $\chi^2$  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

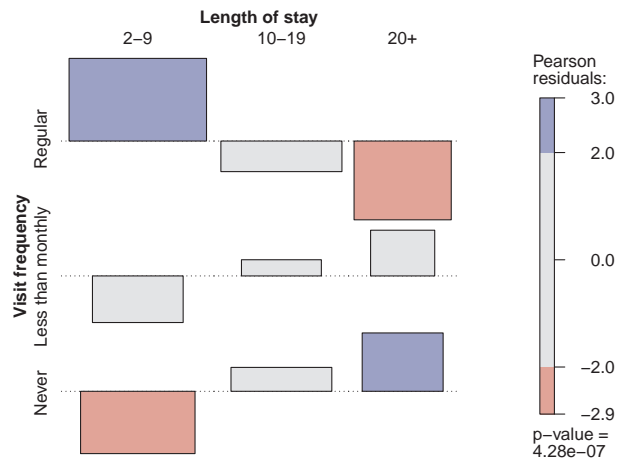
Phi-Coefficient   : NA
Contingency Coeff.: 0.459
Cramer's V       : 0.365
```

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
```

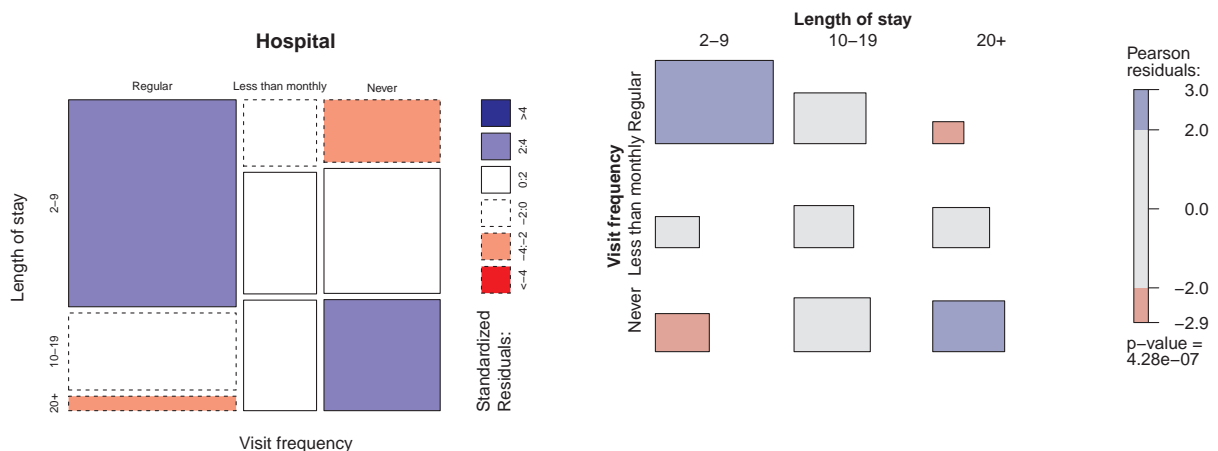
	AltHypothesis	Chisq	Df	Prob
cor	Nonzero correlation	29.1	1	6.74e-08
rmeans	Row mean scores differ	34.4	2	3.40e-08
cmeans	Col mean scores differ	29.6	2	3.72e-07
general	General association	34.9	4	4.86e-07

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, treating both variables as ordinal, has the largest ratio of  $\chi^2/df$ .

#### Exercise 4.5 Continuing with the *Hospital* data:

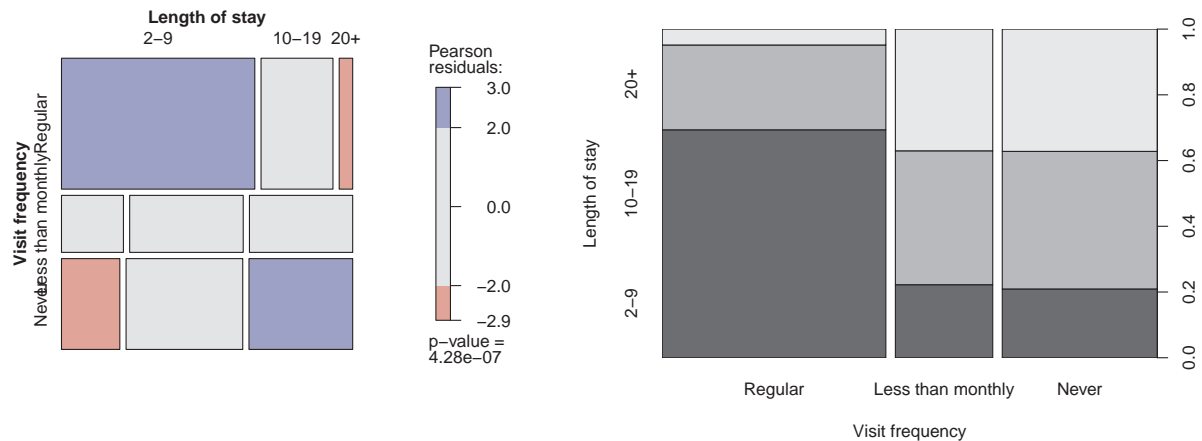
- (a) Try one or more of the following other functions for visualizing two-way contingency tables with this data: `plot()`, `tile()`, `mosaic()`, and `spineplot()`. [For all except `spineplot()`, it is useful to include the argument `shade=TRUE`].  
★

```
> 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  $\kappa$ , both unweighted and weighted.  
 ★ Both unweighted and weighted  $\kappa$  indicate substantial agreement. Fleiss-Cohen weights give greater weight to the "near-misses," so gives a larger value.

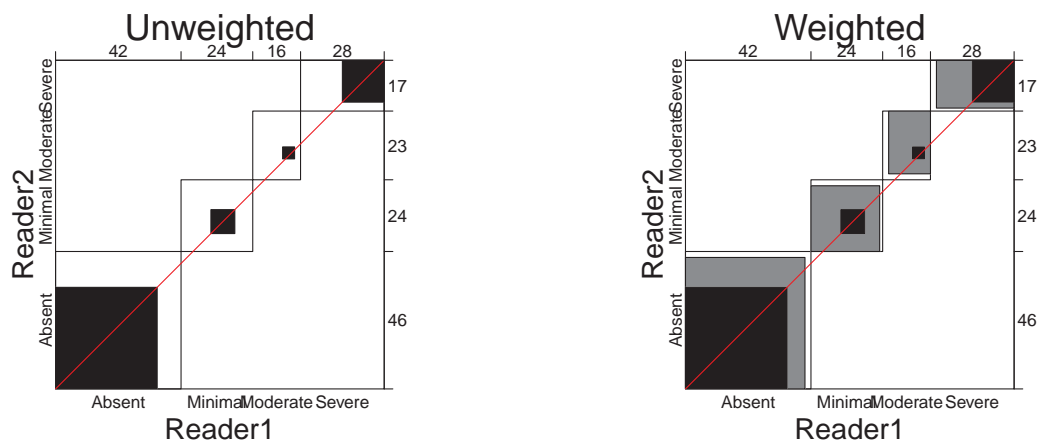
```
> Kappa(Mammograms)
      value      ASE      z Pr(>|z|)
Unweighted 0.371 0.0603   6.15 7.56e-10
Weighted    0.596 0.0492  12.11 8.90e-34

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

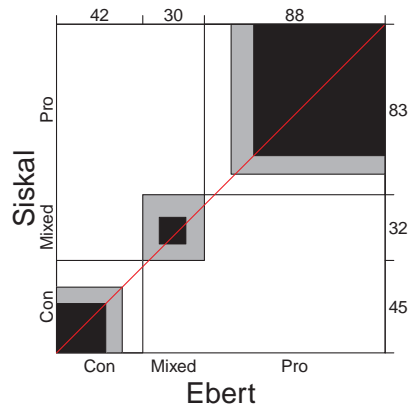
- (a) Assess the strength of agreement between the raters using Cohen's  $\kappa$ , both unweighted and weighted.  
 ★

```
> ratings <- matrix(
+   c(
+     24, 8, 13,
+     8, 13, 11,
+     10, 9, 64
+   ), 3, 3, byrow=TRUE)
> dimnames(ratings) <- list(Siskel=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  $\chi^2$  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,  $E = (T + T^T)/2$ .

★

```
> 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)

```

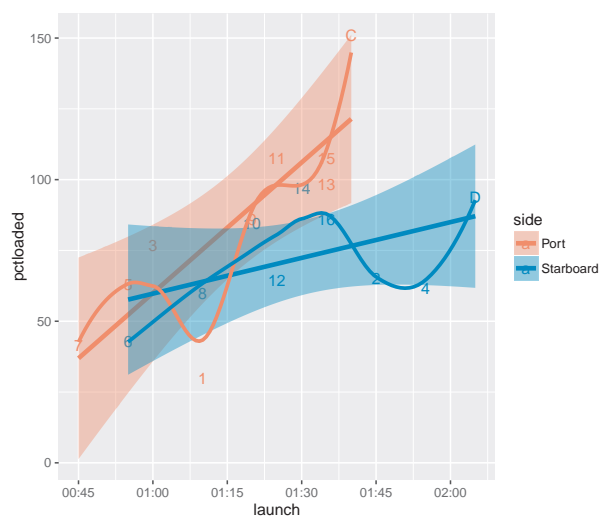
- (b) Produce a plot similar to Figure 4.23, showing the changes over time in this measure.

★ Boats on the port side began loading earlier, but were initially less than half full. Boats launched from the starboard 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  $4 \times 5$  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)

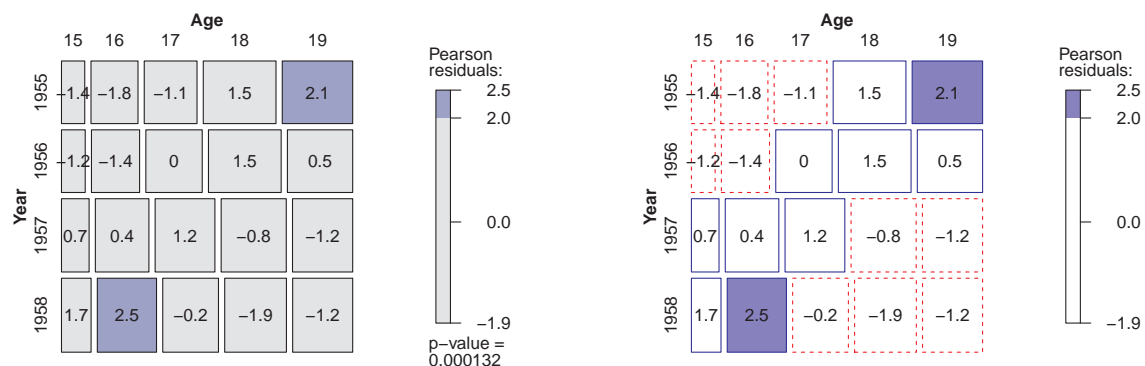
Call:
loglm(formula = ~Year + Age, data = criminal)

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.

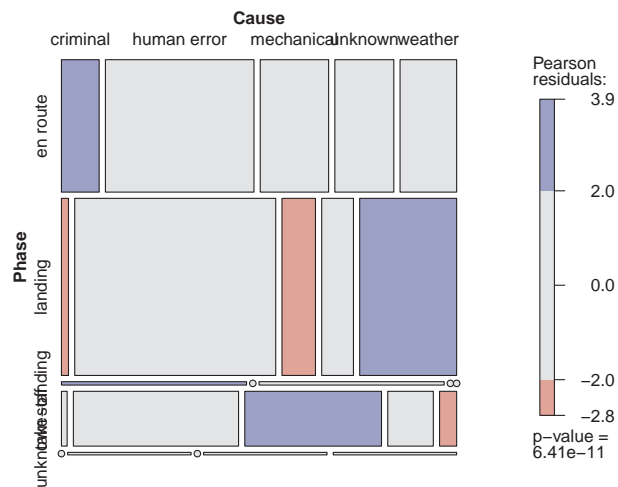
**Exercise 5.2** The data set *AirCrash* in *vcdExtra* gives a database of all crashes of commercial airplanes between 1993–2015, classified by Phase of the flight and Cause of the crash. How can you best show is the nature of the association between these variables in a mosaic plot? Start by making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

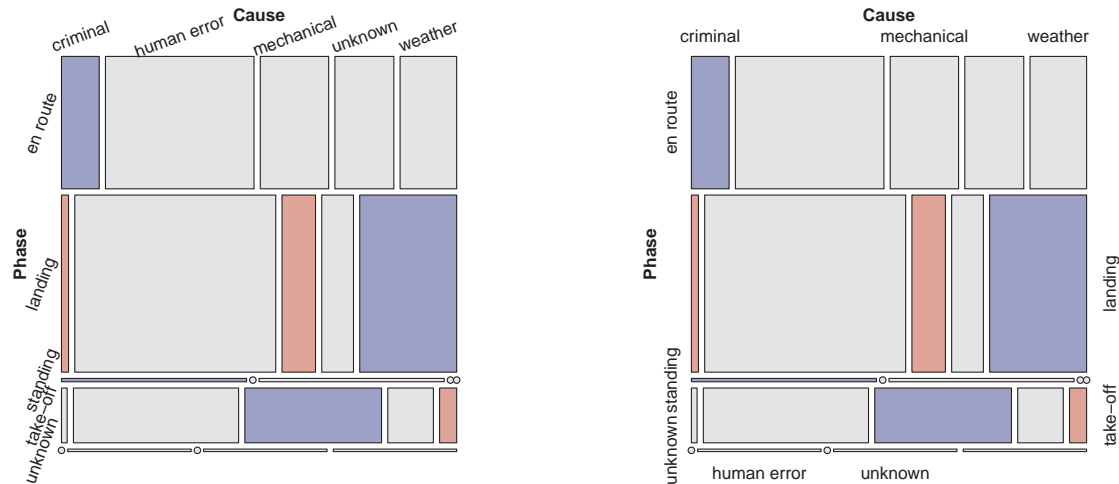


Four cells stand out as having greater than expected frequencies, if Phase and Cause were independent. Both take-off and en-route are positively associated with criminal activities. Crashes in landing are more associated with weather. It is difficult to interpret the unknown cells.

- (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:

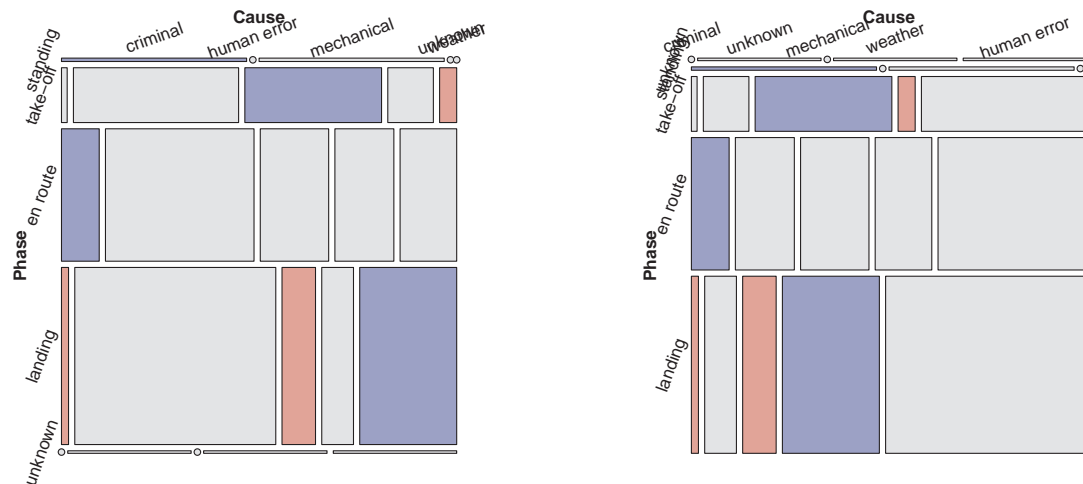
```
> mosaic(aircrash.tab, shade=TRUE, rot_labels=c(20,90,0,70), legend=FALSE)
> mosaic(aircrash.tab, shade=TRUE, alternate_labels=TRUE, legend=FALSE)
```



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



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)
> summary(aircrash.ca, rows=FALSE, columns=FALSE)
```

Principal inertias (eigenvalues):

dim	value	%	cum%	scree plot
1	0.123002	65.6	65.6	*****

```

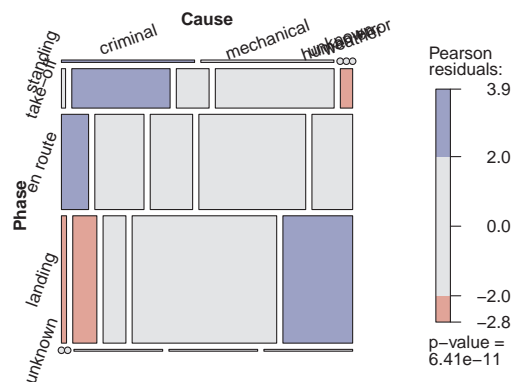
2      0.051548  27.5  93.1  *****
3      0.012340   6.6  99.7    **
4      0.000562   0.3 100.0
-----
Total: 0.187452 100.0

> # 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))

```

Throws	Bats		
	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

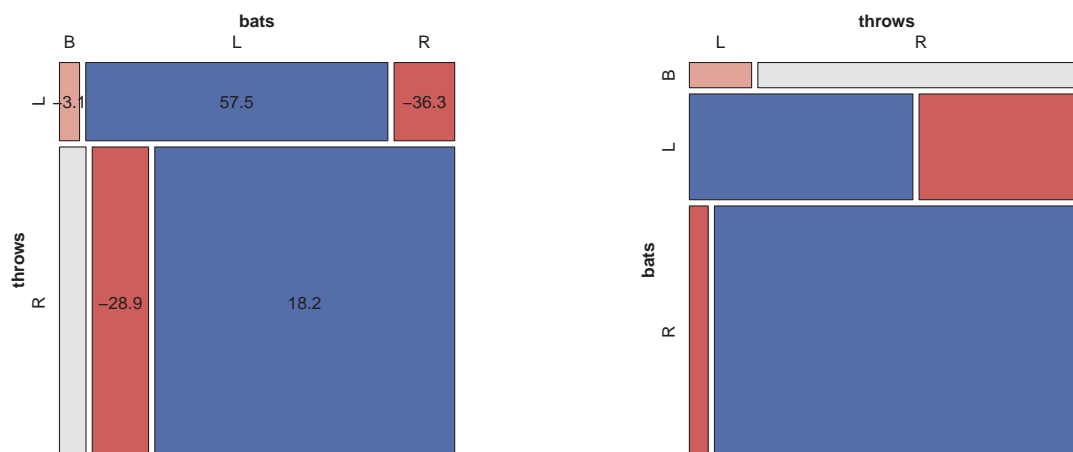
```

- 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.

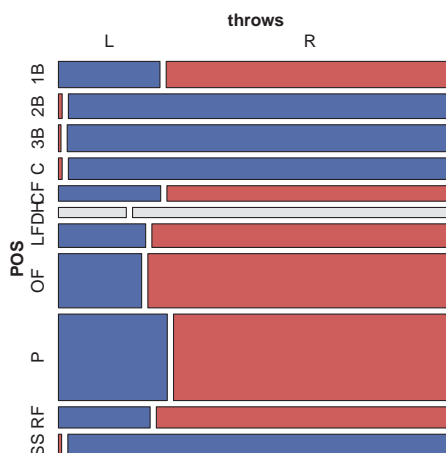
**Exercise 5.4** \* A related analysis concerns differences in throwing handedness among baseball players according to the fielding position they play. The following code calculates such a frequency table.

```
> 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.

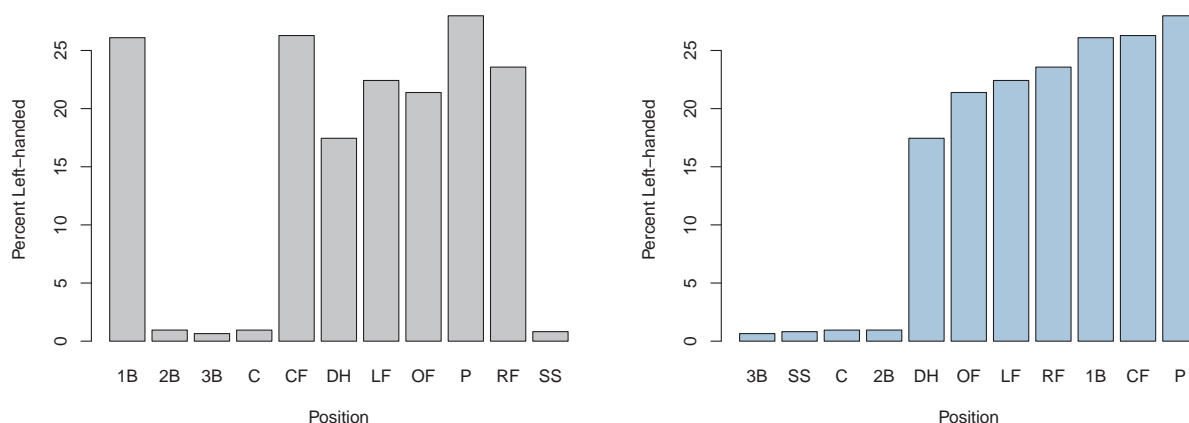
```
> mosaic(throwPOS, shade=TRUE, legend=FALSE)
```



- (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.

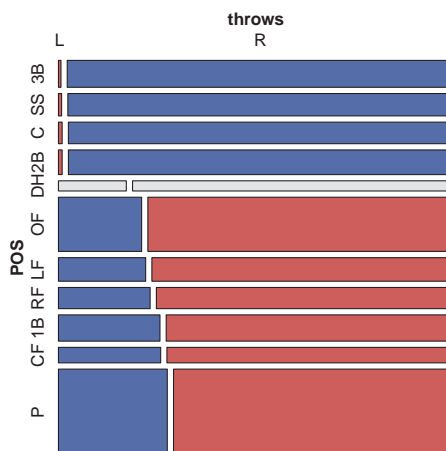
```
> pctLeft <- 100 * throwPOS[,1] / rowSums(throwPOS)
> pctLeft
      1B      2B      3B      C      CF      DH      LF      OF      P      RF      SS
26.100  0.955  0.650  0.952 26.284 17.449 22.419 21.385 27.984 23.571  0.818

> 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 1<sup>st</sup> base have a very small percentage of players who throw left-handed. Given the marginal distributions of handedness and position, outfielders, pitchers and 1<sup>st</sup> 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.

★

- (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.

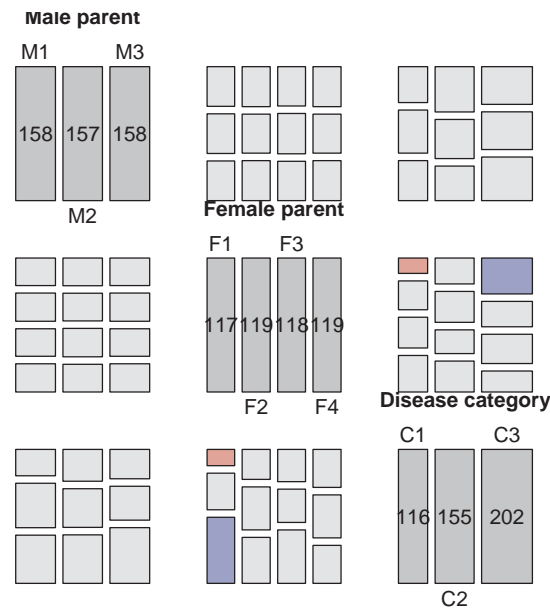
```
> data("jansen.strawberry", package = "agridat")
>
> dat <- jansen.strawberry
> dat <- transform(dat, category = ordered(category,
+                                           levels = c('C1', 'C2', 'C3')))
> levels(dat$male) <- paste0("M", 1:3)
> levels(dat$female) <- paste0("F", 1:4)
>
> jansen.tab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

		Disease category		
Male parent	Female parent	C1	C2	C3
M1	F1	6	13	20
	F2	8	15	17
	F3	13	10	16
	F4	8	21	11
M2	F1	5	13	21
	F2	9	16	14
	F3	16	9	15
	F4	12	13	14
M3	F1	5	10	24
	F2	13	12	15
	F3	3	14	22
	F4	18	9	13

- (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?

★ This was a designed experiment, with male and female parents completely crossed to create 12 populations. Disease categories seem to be associated with female parents, with more serious disease (C3) more prevalent in parent F4.

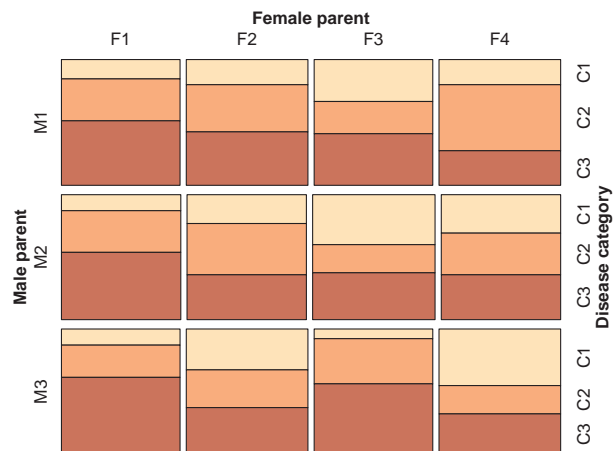
```
> library(vcd)
> pairs(jansen.tab, shade=TRUE)
```



- (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.)

★

```
> cols <- c("moccasin", "lightsalmon1", "indianred")
> mosaic(jansen.tab, highlighting=3, highlighting_fill=cols)
```



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

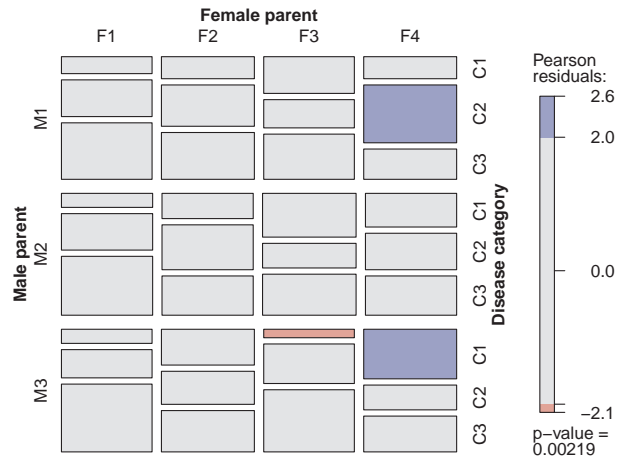
★

```
> # baseline model
> library(MASS)
> loglm(~1*2+3, data=jansen.tab)

Call:
loglm(formula = ~1 * 2 + 3, data = jansen.tab)

Statistics:
              X^2 df    P(> X^2)
Likelihood Ratio 45.63 22 0.0022062
Pearson          45.65 22 0.0021927
```

```
> mosaic(jansen.tab, expected = ~ 1*2+3)
```



**Exercise 5.7** The data set *caith* in MASS (Ripley, 2015) gives another classic  $4 \times 5$  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.

★

```
> Caith <- as.matrix(caith)
> dimnames(Caith)

[[1]]
[1] "blue"    "light"    "medium"   "dark"

[[2]]
[1] "fair"    "red"      "medium"   "dark"     "black"
```

```
> names(dimnames(Caith)) <- c("Eye", "Hair")
```

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

★

```
> (caith.mod <- loglm(~Hair+Eye, data=Caith, fitted=TRUE))

Call:
loglm(formula = ~Hair + Eye, data = Caith, fitted = TRUE)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 1218.3 12      0
Pearson          1240.0 12      0
```

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

★

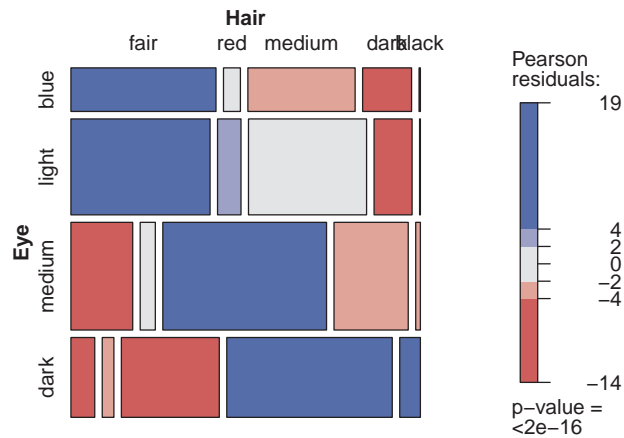
```
> residuals(caith.mod)
```

	Hair				
Eye	fair	red	medium	dark	black
blue	8.63	-0.0193	-2.67	-6.00	-3.94
light	11.60	3.3125	-1.73	-12.19	-6.63
medium	-6.56	-1.0691	7.40	-2.19	-2.20
dark	-16.19	-2.7683	-5.41	16.28	8.46

- (d) Create a mosaic display for this data.

★

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



**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  $\sim \text{Hair} + \text{Eye} \mid \text{Place}$  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,  $\text{Freq} \sim \text{age} + \text{mode} + \text{gender} + \text{result}$  to this data set.

★ You can use `loglm()` directly on the frequency data frame, with `Freq` as the response:

```
> library(MASS)
> loglm(Freq ~ age + mode + gender + result, data = Accident)

Call:
loglm(formula = Freq ~ age + mode + gender + result, data = Accident)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 60320 70      0
Pearson          76865 70      0
```

Or, convert to an array first with `xtabs()`

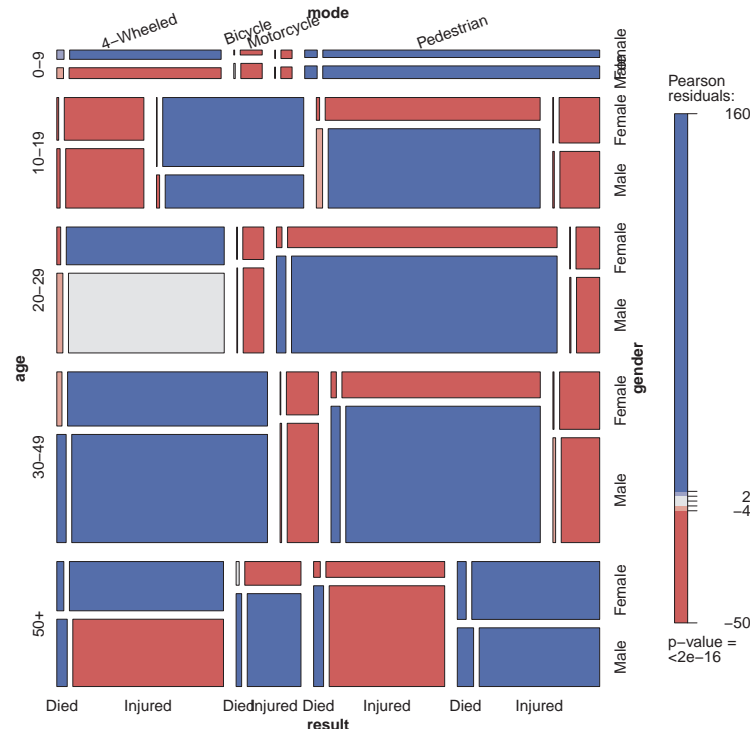
```
> accident.tab <- xtabs(Freq ~ age + mode + gender + result, data = Accident)
> loglm(~ age + mode + gender + result, data = accident.tab)

Call:
loglm(formula = ~age + mode + gender + result, data = accident.tab)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 60320 70      0
Pearson          76865 70      0
```

- (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.*)  
 ★ In this data set, `mode` is arguably an ordered factor, and better results will come from reordering its levels, from Pedestrian to 4-Wheeled vehicle. The order of variables given in `xtabs()` gives a reasonable result. The label overlap can be avoided by rotating the labels for `mode`.

```
> Accident$mode <- ordered(Accident$mode,
+   levels=levels(Accident$mode)[c(4,2,3,1)])
> mosaic(accident.tab, shade=TRUE, rot_labels = c(20, 90, 00, 90))
```



- (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.  
 ★ This fits much better than the mutual independence model, but still has a terrible fit. There still remain important associations between `result` and the other variables

```
> loglm(Freq ~ age * mode * gender + result, data = Accident)
```

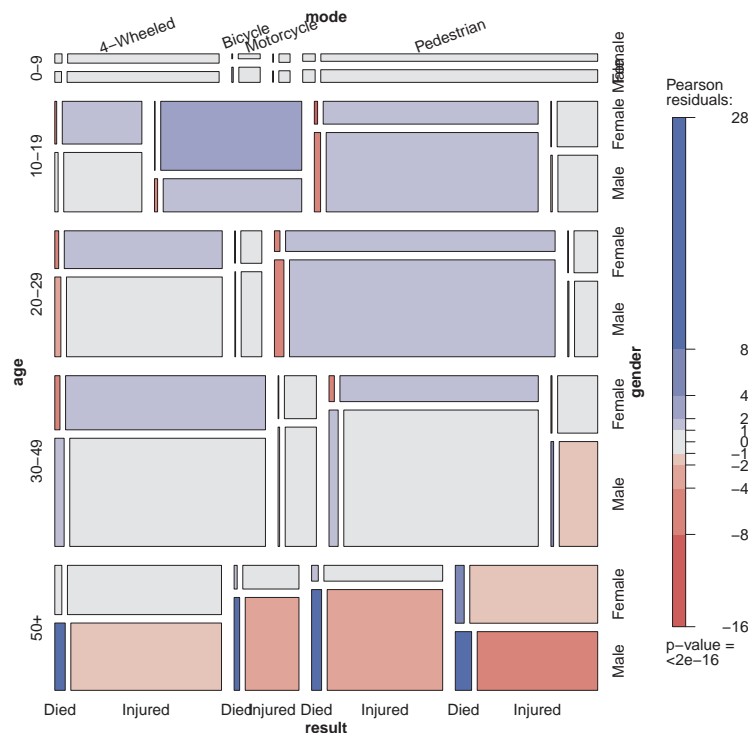
```
Call:
loglm(formula = Freq ~ age * mode * gender + result, data = Accident)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 2217.7 39      0
Pearson          2347.6 39      0
```

- (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?

★ The largest positive residuals appear in the 50+ age group, where males are more likely to have died, regardless of mode. It can also be seen that in the 30–49 age group, more males die in bicycle and motorcycle accidents. Other permutations of the table variables or other displays like doubled-decker plots can highlight other features.

```
> mosaic(accident.tab, expected = ~age * mode * gender + result,
+        shade=TRUE, rot_labels = c(20, 90, 00, 90),
+        gp_args=list(interpolate=c(1,2,4,8)))
```



**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 ...
 $ 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.



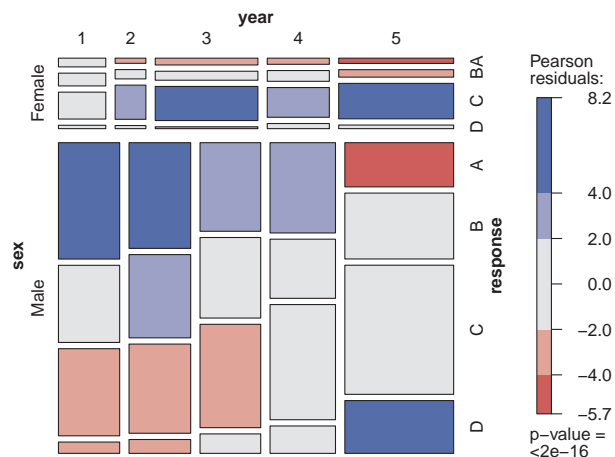
★ The baseline model does not fit well, so response is associated with either year or sex or both. Note that when fitting with `loglm()` (or `glm()`), both `mosaic(mod)` and `plot(mod)` give the corresponding mosaic plot for a model object, `mod`.

```
> library(MASS)
> library(vcdExtra)
> (viet.mod <- loglm(Freq ~ sex * year + response, data=Vietnam))

Call:
loglm(formula = Freq ~ sex * year + response, data = Vietnam)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 361.72 27      0
Pearson          366.36 27      0

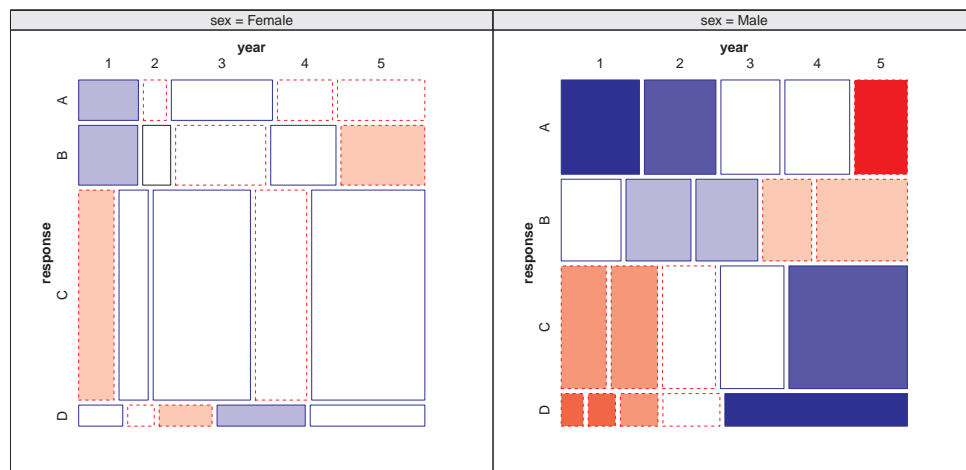
> mosaic(viet.mod)
> # plot(viet.mod) # same
```



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

★ We use `cotabplot()` here, with the formula `~ response + year | sex` to condition on sex. For males, there is a clear association between response and year, with 1<sup>st</sup> year students preferring the more military response A, and later-year students tending toward the more peaceful response D. For females, the association between response and year is weak, and does not show a coherent pattern.

```
> cotabplot(~ response + year | sex, data=vietnam.tab,
+           gp=shading_Friendly, gp_args=list(interpolate=1:4), legend=FALSE)
```



- (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,  $R \perp Y | S$ . Verify that the decomposition of  $G^2$  in Eqn. (5.6) holds for these models.

★ Splitting the data by sex, using `apply()` shows that the association between response and year is strongly significant for males, but not for females.

```
> mods.list <-
+   apply(vietnam.tab, "sex",
+         function(x) loglm(~ response + year, data=x))
> mods.list

$Female
Call:
loglm(formula = ~response + year, data = x)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 13.263 12  0.35022
Pearson          13.294 12  0.34803

$Male
Call:
loglm(formula = ~response + year, data = x)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 203.05 12  0
Pearson          198.50 12  0
```

- (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  $A \perp B \perp C \perp D$ .

★ The basic idea of the notation is that terms in separate []s are said to be independent under a given model. Variables within a [] term are allowed to be associated

- mutual:  $[A] [B] [C] [D] \leftrightarrow A \perp B \perp C \perp D$
- joint:  $[ABC] [D] \leftrightarrow (ABC) \perp D$
- conditional:  $[AD] [BD] [CD] \leftrightarrow (AD) \perp (BD) \perp (CD)$
- markov (order 1):  $[AB] [BC] [CD] \leftrightarrow (AB) \perp (BC) \perp (CD)$
- markov (order 2):  $[ABC] [BCD] \leftrightarrow (ABC) \perp (BCD)$
- saturated: no independence relationship

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

★ The model generating functions, `mutual()`, `joint()`, etc. provide a simple way to specify loglinear models for `loglm()` and `mosaic()`.

```
> loglin2formula(mutual(4, factors=LETTERS[1:4]))
~A + B + C + D
> loglin2formula(joint(4, factors=LETTERS[1:4]))
~A:B:C + D
> loglin2formula(joint(4, factors=LETTERS[1:4], with=1))
~B:C:D + A
> loglin2formula(conditional(4, factors=LETTERS[1:4]))
~A:D + B:D + C:D
> loglin2formula(conditional(4, factors=LETTERS[1:4], with=1))
~B:A + C:A + D:A
> loglin2formula(markov(4, factors=LETTERS[1:4]))
~A:B + B:C + C:D
> loglin2formula(markov(4, factors=LETTERS[1:4], order=2))
~A:B:C + B:C:D
> loglin2formula(saturated(4, factors=LETTERS[1:4]))
~A:B:C:D
```

**Exercise 5.12** The dataset *Titanic* classifies the 2,201 passengers 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.

★

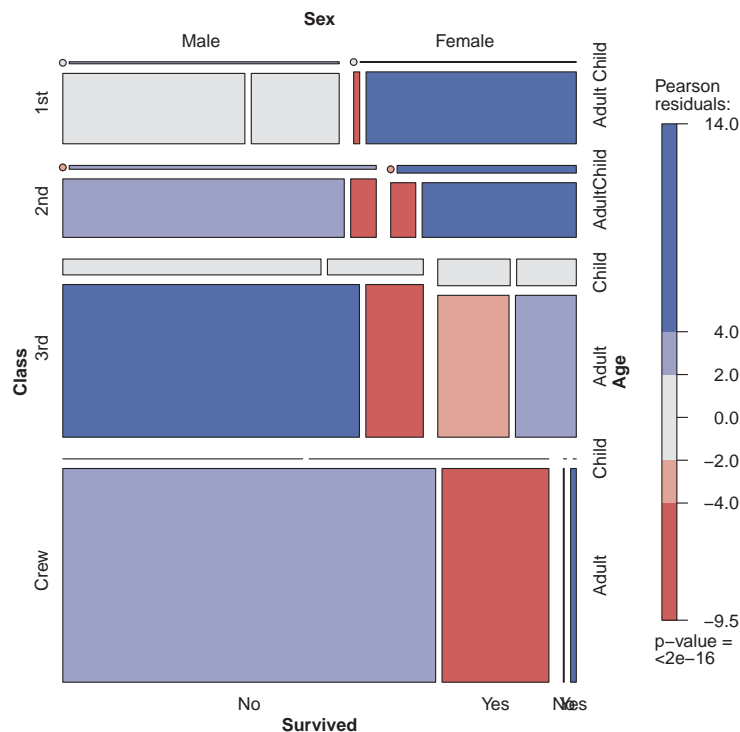
```
> # what is the formula for the joint independence here?
> form1 <- loglin2formula(joint(4, factors=names(dimnames(Titanic))))
> form1
~Class:Sex:Age + Survived

> library(MASS)
> mod1 <- loglm(formula=~Class:Sex:Age + Survived, data=Titanic)
> mod1

Call:
loglm(formula = ~Class:Sex:Age + Survived, data = Titanic)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 671.96 15      0
Pearson          NaN 15      NaN

> mosaic(Titanic, expected=~Class:Sex:Age + Survived, shade=TRUE)
```



- (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. In particular, MCA plots are now simpler, using a new `mcaplot()` function, presently in `vcdExtra`, and lines can be added to MCA plots using `multilines()`. Coordinates for CA/MCA plots can more readily be extracted using `cacoord()`.

**Exercise 6.1** The *JobSat* data in `vcdExtra` gives a  $4 \times 4$  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):

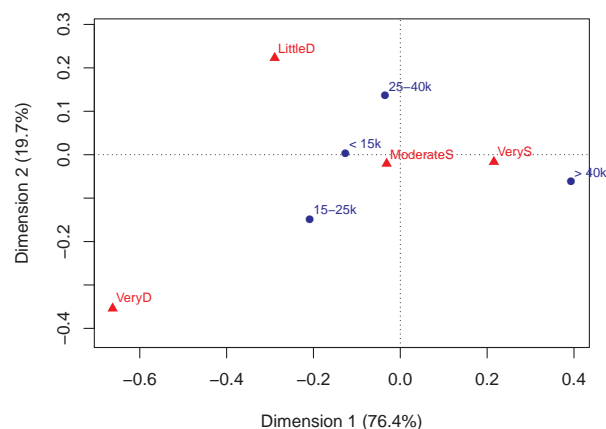
dim	value	%	cum%	scree plot
1	0.047496	76.4	76.4	*****
2	0.012248	19.7	96.1	*****
3	0.002397	3.9	100.0	*

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  $4 \times 5$  table *criminal* from the `logmult` package.

- (a) What percentages of the Pearson  $\chi^2$  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	

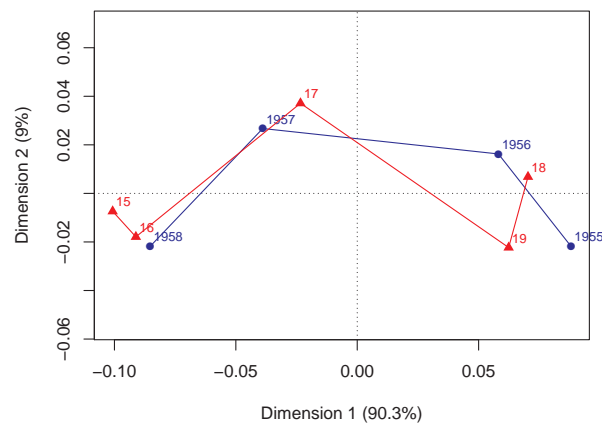
-----

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  $5 \times 5$  table of Phase of the flight and Cause of the crash.

- (a) What percentages of the Pearson  $\chi^2$  for association are explained by the various dimensions?

★ `aircrash.tab` was calculated in Exercise 5.2.

```
> aircrash.tab
Phase      Cause
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):

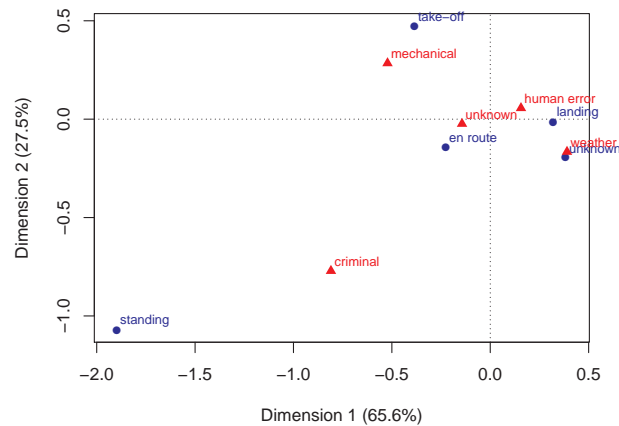
dim  value      %  cum%  scree plot
1    0.123002  65.6  65.6  *****
2    0.051548  27.5  93.1  *****
3    0.012340   6.6  99.7  **
4    0.000562   0.3 100.0

-----
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)
```

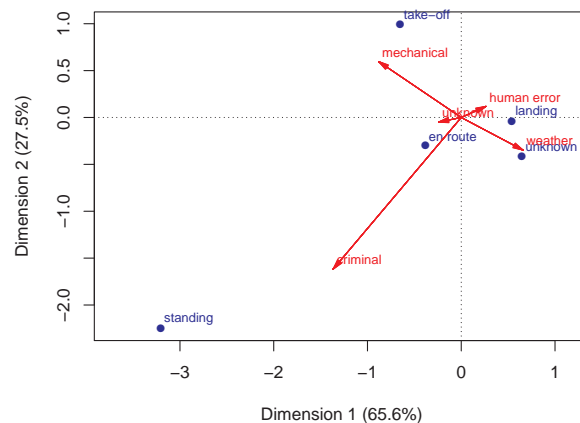


Dimension 1 largely distinguishes standing from landing, where the main causes are human error and weather problems. Dimension 2 largely distinguishes standing from take-off, where mechanical problems are more prevalent.

- (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))
```



**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):
```

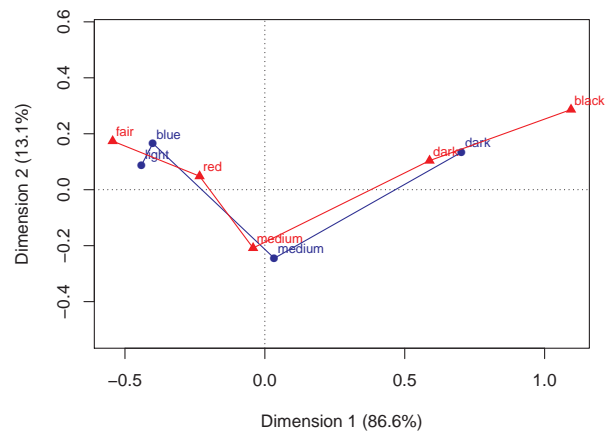
dim	value	%	cum%	scree plot
1	0.199245	86.6	86.6	*****
2	0.030087	13.1	99.6	***
3	0.000859	0.4	100.0	
-----				
Total: 0.230191 100.0				

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)  $6 \times 4$  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
```

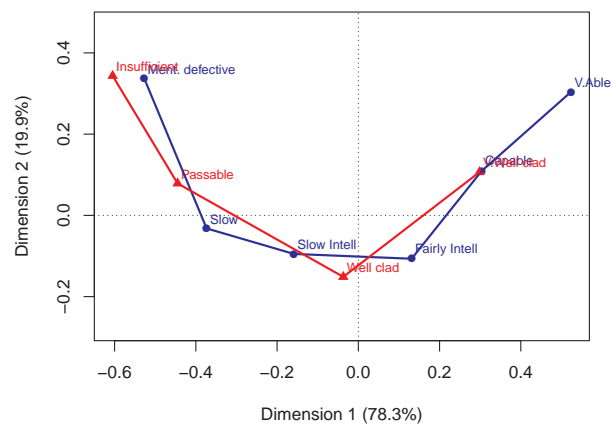
```

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 | FrI |   310    999     88 |  131 601  67 | -107 398 176 |
5 | Cpbl |   217   1000    223 |  304 885 253 |  109 115 129 |
6 | VAb1 |    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.

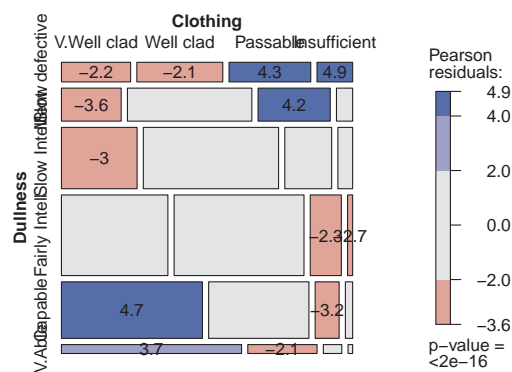
- (b) Make an analogous mosaic plot of this table. Interpret this in relation to the correspondence analysis plot.

★

```

> 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 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 create 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()`.

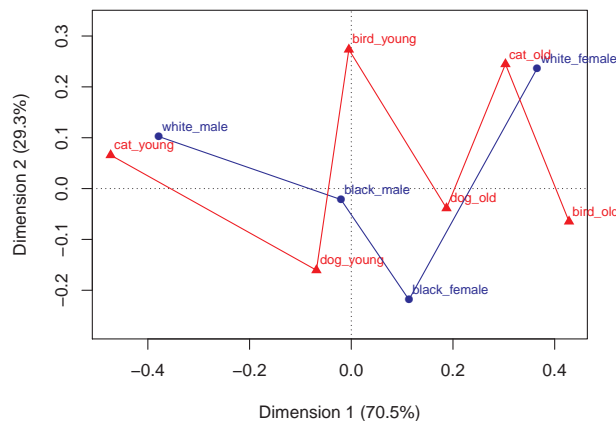
```
> dim <- c(3, 2, 2, 2)
> factors <- expand.grid(Pet=c("dog", "cat", "bird"),
+                        Age=c("young", "old"),
+                        Color=c("black", "white"),
+                        Sex=c("male", "female"))
> means <-
+ with(factors, {
+   20 +
+   ifelse(Pet=="dog", 10, 0) +
+   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"))
> # stack
> as.matrix(ftable(Pet + Age ~ Color + Sex, tab))
```

	Pet_Age					
Color_Sex	dog_young	dog_old	cat_young	cat_old	bird_young	bird_old
black_male	36	30	16	6	16	5
black_female	30	25	8	4	7	5
white_male	22	13	18	3	12	1
white_female	11	18	3	6	11	4

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

★

```
> library(ca)
> pets.ca <- ca(as.matrix(ftable(Pet + Age ~ Color + Sex, tab)))
> plot(pets.ca, lines=TRUE)
```



**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)
> summary(TV3S.ca, rows=FALSE, columns=FALSE)
```

Principal inertias (eigenvalues):

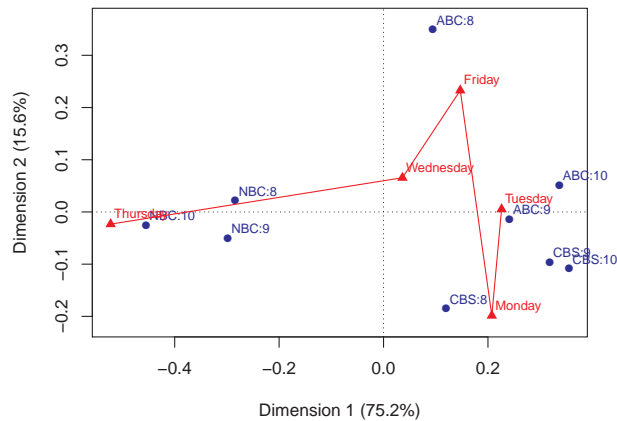
dim	value	%	cum%	scree plot
1	0.089629	75.2	75.2	*****
2	0.018576	15.6	90.8	****
3	0.008992	7.5	98.3	**
4	0.002001	1.7	100.0	

-----  
Total: 0.119198 100.0

- (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))
```

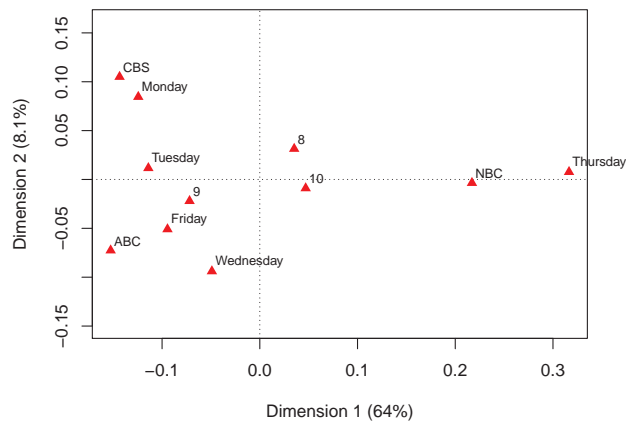


Overall, the plot is somewhat similar to that of Figure 6.4 except for the (arbitrary) reversal of Dimension 1. The category points for NBC cluster near Thursday, while those for ABC and CBS are at the other end of that dimension and Dimension 2 is related to the difference in viewership to those channels.

- (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.

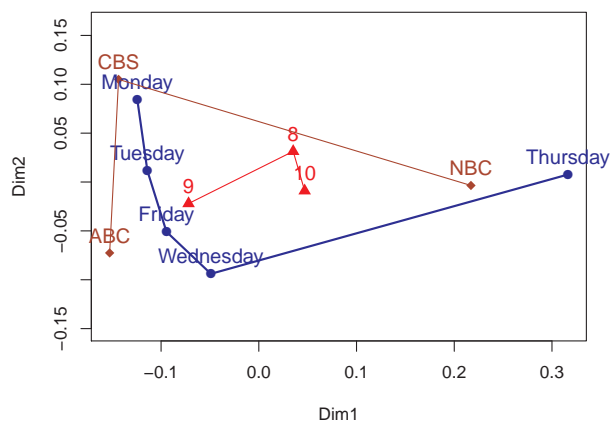
★ The MCA analysis differs in that it includes all pairwise associations of Day, Time and Network rather than just the joint independence model analyzed by the stacking approach.

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



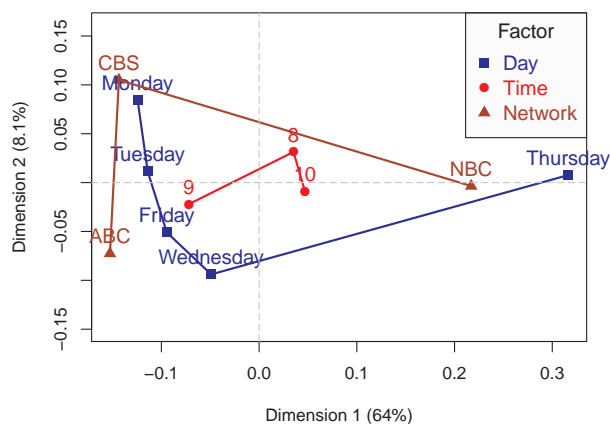
The default plot is somewhat difficult to read because the factor points aren't distinguished by color or shape. A customized plot can be constructed as follows (as illustrated in the text, e.g., for Figure 6.10).

```
> 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$factor))
>
> cols <- c("blue", "red", "brown")
> lwd <- 2
> plot(Dim2 ~ Dim1, type='n', data=coords, asp=1)
> points(coords[,1:2], pch=rep(16:18, nlev), col=rep(cols, nlev), cex=1.2)
> text(coords[,1:2], labels=coords$level, col=rep(cols, nlev), pos=3, cex=1.2, xpd=TRUE)
> multilines(coords[, c("Dim1", "Dim2")], group=coords$factor, col=cols, lwd=lwd)
```



A similar plot can now be produced more simply using:

```
> mcaplot(TV3.mca, legend=TRUE)
```



**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
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

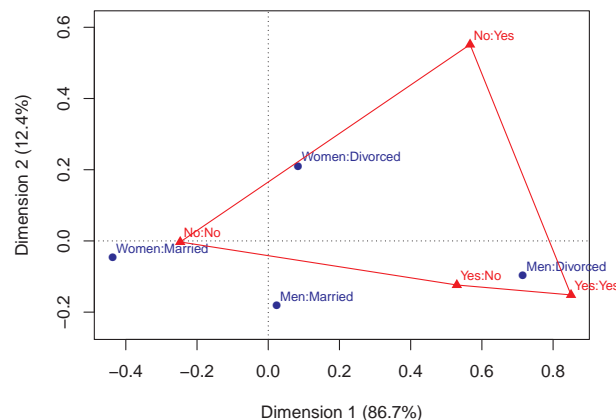
Total: 0.176606 100.0

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 and sex.

★ Two dimensions account for 97.5% of the association between response and the combinations of year and sex.

```
> data(Vietnam, package="vcdExtra")
> vietnam.tab <- xtabs(Freq ~ sex + year + response, data=Vietnam)
> vietnam.stacked <- as.matrix(structable(response ~ sex + year, vietnam.tab), sep=":")
>
> vietnam.ca <- ca(vietnam.stacked)
> summary(vietnam.ca, rows=FALSE, columns=FALSE)

Principal inertias (eigenvalues):
```

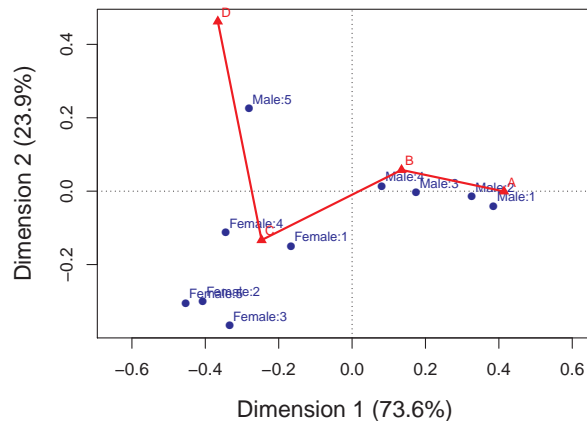
dim	value	%	cum%	scree plot
1	0.085680	73.6	73.6	*****
2	0.027881	23.9	97.5	*****
3	0.002854	2.5	100.0	*

-----  
Total: 0.116415 100.0

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

★

```
> plot(vietnam.ca, cex.lab=1.3, lines=c(FALSE, TRUE), lwd=2)
```



Dimension 1 corresponds to the ordering of the response categories, from the “dove” response D (“Withdraw military forces immediately”) to the “hawk” response A (“Defeat North Vietnam by widespread bombing ...”). Males are ordered progressively from hawk to dove by their years in schools, with a big gap between year 4 and 5 (graduate students). Females cluster around response C (“De-escalate military activity ...”) with no obvious trend over year in school.

- (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.

★ The MCA solution only accounts for 82.3% of the bivariate associations in 2D, and not much better in 3D.

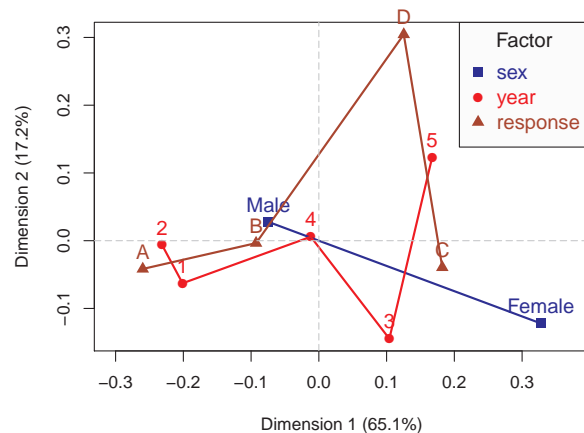
```
> vietnam.mca <- mjca(vietnam.tab)
> summary(vietnam.mca, rows=FALSE, columns=FALSE)

Principal inertias (eigenvalues):
```

dim	value	%	cum%	scree plot
1	0.028219	65.1	65.1	*****
2	0.007445	17.2	82.3	*****
3	0.000380	0.9	83.2	
4	1e-06000	0.0	83.2	

-----  
Total: 0.043317

```
> mcaplot(vietnam.mca, legend=TRUE)
```



The plot of the MCA solution is somewhat difficult to interpret, because neither the response categories nor year are ordered as one would expect. This turns out to be an example where MCA is not that useful, because the association of response and year is different for males and females— i.e., there is a three-way association in this table. MCA, however, only accounts for pairwise associations among the table variables.

**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:

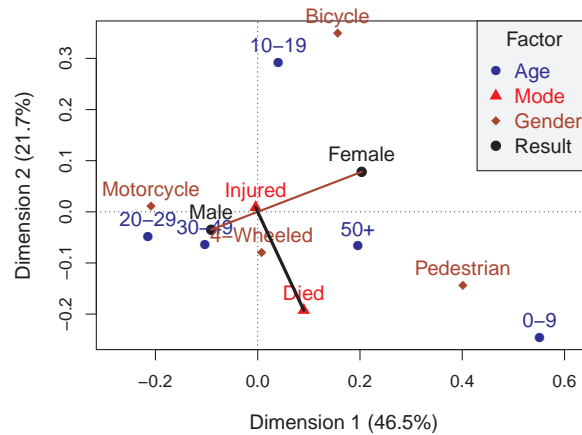
	name	mass	qlt	inr	k=1	cor	ctr	k=2	cor	ctr
1	age:0-9	13	672	107	551	561	152	-246	111	65
2	age:10-19	49	678	91	40	13	3	292	665	354
3	age:20-29	56	784	85	-215	747	102	-48	37	11
4	age:30-49	76	546	75	-103	396	32	-63	149	26
5	age:50+	56	687	85	196	616	84	-67	72	21
6	result:Died	11	515	100	90	92	3	-192	422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



```
> res <- plot(accident.mca, labels=0, pch='.', cex.lab=1.2)
> coords <- data.frame(res$cols, accident.mca$factors)
> 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    0.0000000   0.0  84.5
4    0.0000000   0.0  84.5
5    0.0000000   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 |
```

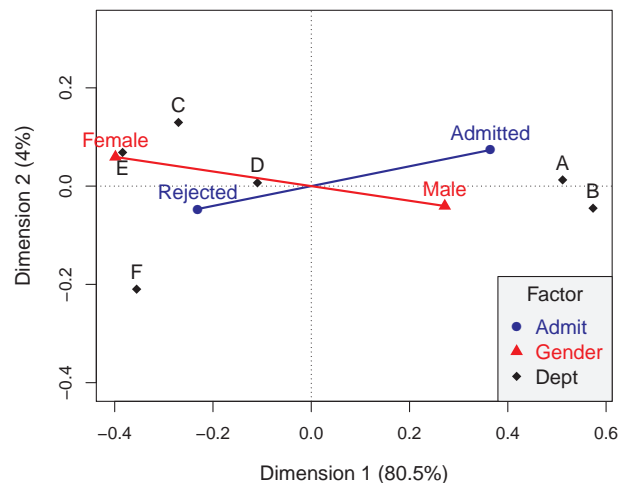


5		Dept:A		69	838	117		512	837	156		13	1	2	
6		Dept:B		43	829	124		573	824	123		-45	5	15	
7		Dept:C		68	731	108		-270	594	43		130	137	199	
8		Dept:D		58	832	106		-110	828	6		7	3	0	
9		Dept:E		43	812	117		-384	787	55		69	25	35	
10		Dept:F		53	737	116		-355	547	58		-210	190	406	

(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** Arbutnot'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 *Arbutnot* 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

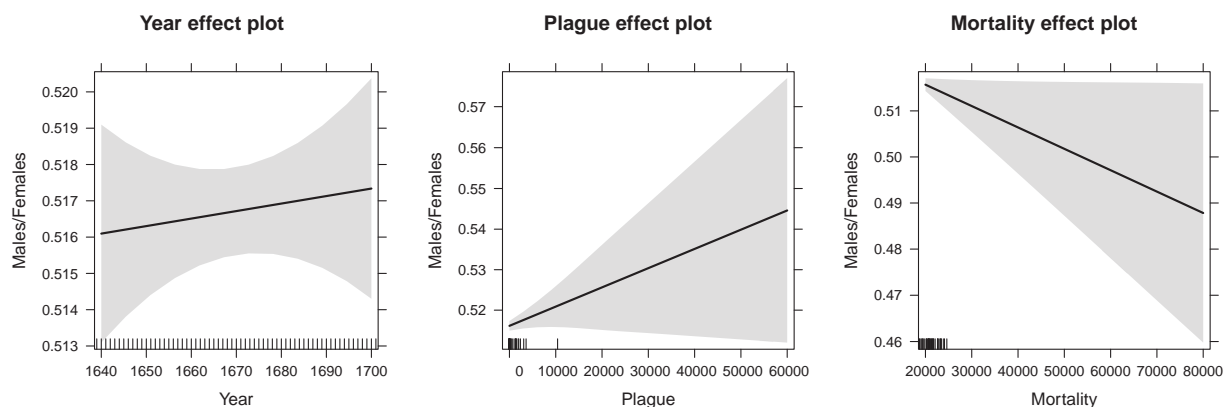
Number of Fisher Scoring iterations: 3

> 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)
```



In the plots for Plague and Mortality, it is apparent that both are extremely skewed. One alternative is to represent these as  $\log(\text{Plague}+1)$  and  $\log(\text{Mortality})$  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)

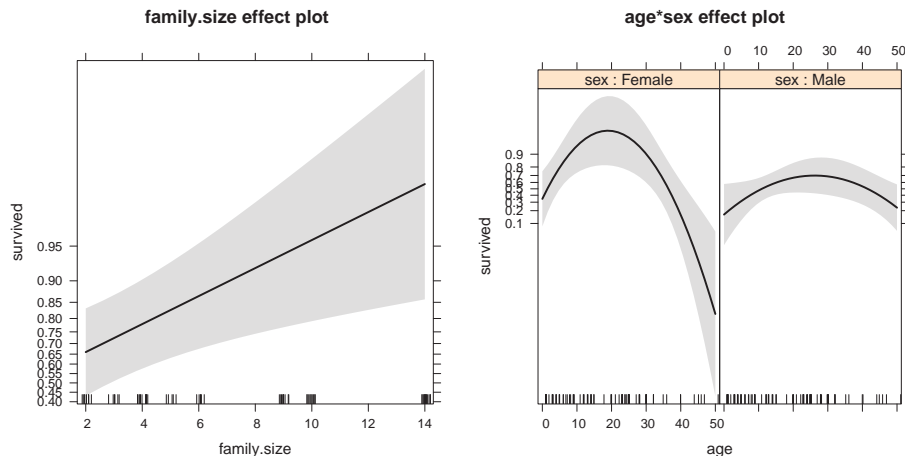
Response: survived
             LR Chisq Df Pr(>Chisq)
poly(age, 2)   14.94  2  0.00057 ***
sex             4.24  1  0.03944 *
family.size    11.54  1  0.00068 ***
poly(age, 2):sex 12.24  2  0.00220 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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.

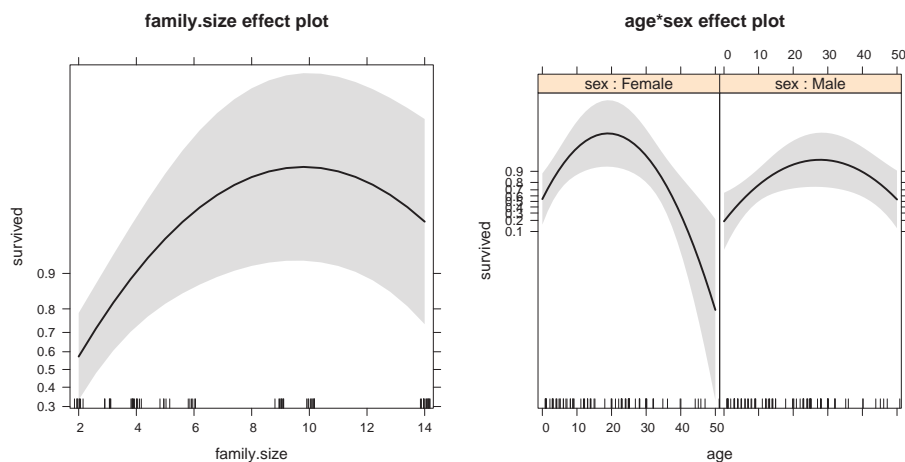
★

```
> 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?

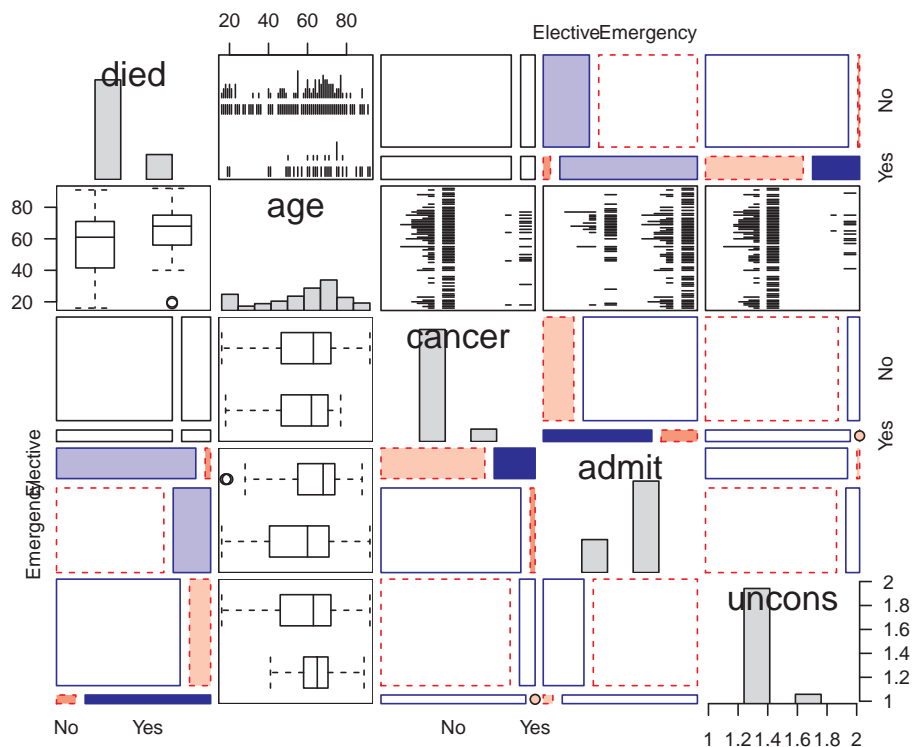
★

**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)))
```

★ First, begin with the `gpairs()` plot:

```
> 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  $3 \times 2^3$  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.)



```
> # reorder levels
> Caesar.df$Infection <- factor(Caesar.df$Infection, levels=c("None", "Type 1", "Type 2"))
> Caesar.df$Risk <- factor(Caesar.df$Risk, levels=c("No", "Yes"))
> Caesar.df$Antibiotics <- factor(Caesar.df$Antibiotics, levels=c("No", "Yes"))
> Caesar.df$Planned <- factor(Caesar.df$Planned, levels=c("No", "Yes"))
> # Logistic regression : None vs (Type 1, Type 2)
> caesar.glm <- glm(Infect ~ Risk + Antibiotics + Planned, weights = Freq,
+                   data=Caesar.df, family=binomial)
> caesar.glm

Call: glm(formula = Infect ~ Risk + Antibiotics + Planned, family = binomial,
  data = Caesar.df, weights = Freq)

Coefficients:
  (Intercept)          RiskYes  AntibioticsYes      PlannedYes
    -0.793         1.827         -3.001         -0.906

Degrees of Freedom: 16 Total (i.e. Null); 13 Residual
Null Deviance: 301
Residual Deviance: 236 AIC: 244
```

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

★ By both the Wald tests from `summary()` and the Type II LR tests from `car::Anova` all three factors have significant effects on the probability of infection.

```
> library(car)
> summary(caesar.glm)

Call:
glm(formula = Infect ~ Risk + Antibiotics + Planned, family = binomial,
  data = Caesar.df, weights = Freq)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-6.747 -0.443  0.000  3.234  5.420

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -0.793     0.478   -1.66   0.097 .
RiskYes        1.827     0.436    4.19  2.8e-05 ***
AntibioticsYes -3.001     0.459   -6.53  6.4e-11 ***
PlannedYes     -0.906     0.408   -2.22   0.026 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 300.85  on 16  degrees of freedom
Residual deviance: 236.36  on 13  degrees of freedom
AIC: 244.4

Number of Fisher Scoring iterations: 6
> Anova(caesar.glm)

Analysis of Deviance Table (Type II tests)

Response: Infect
              LR Chisq Df Pr(>Chisq)
Risk           20.6   1   5.8e-06 ***
Antibiotics    56.5   1   5.7e-14 ***
Planned         5.2   1    0.022 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

★ From the coefficients in the model given above, Risk factors increase the log odds of infection by 1.83; treatment with Antibiotics decreases the log odds by 3.0; a planned C-section decreases the log odds of infection by 0.91.

These effects can perhaps be more easily interpreted in terms of the odds ratios calculated below, that give the multiple of the odds for the Yes group compared to the No group. For example, Risk can be said to multiply the odds by 6.22; Antibiotics multiplies the odds by 0.05, or a decrease of 95%; a planned C-section multiplies the odds of infection by 0.40, a decrease of 60%.

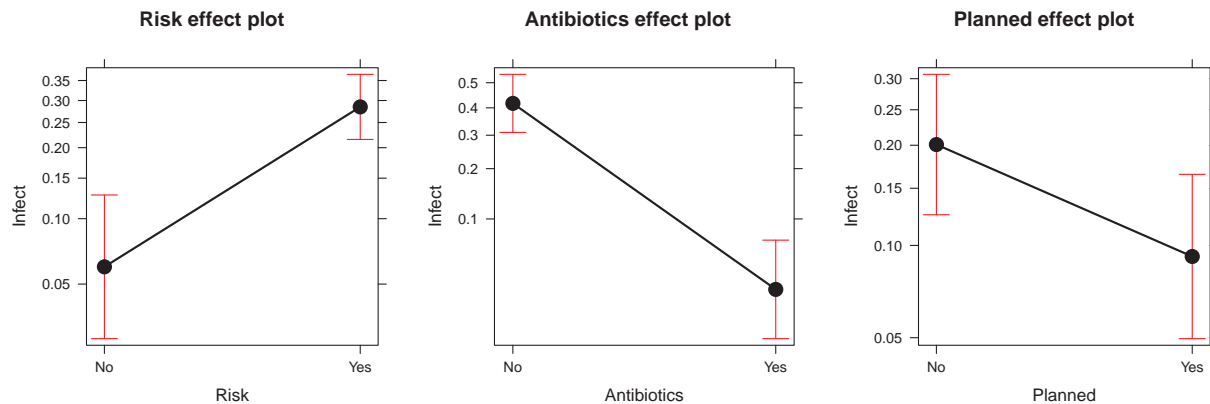
```
> exp(cbind(OddsRatio=coef(caesar.glm),
+           confint(caesar.glm)))
```

	OddsRatio	2.5 %	97.5 %
(Intercept)	0.452263	0.170362	1.13401
RiskYes	6.215158	2.736586	15.35990
AntibioticsYes	0.049734	0.019257	0.11742
PlannedYes	0.403978	0.176257	0.88092

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

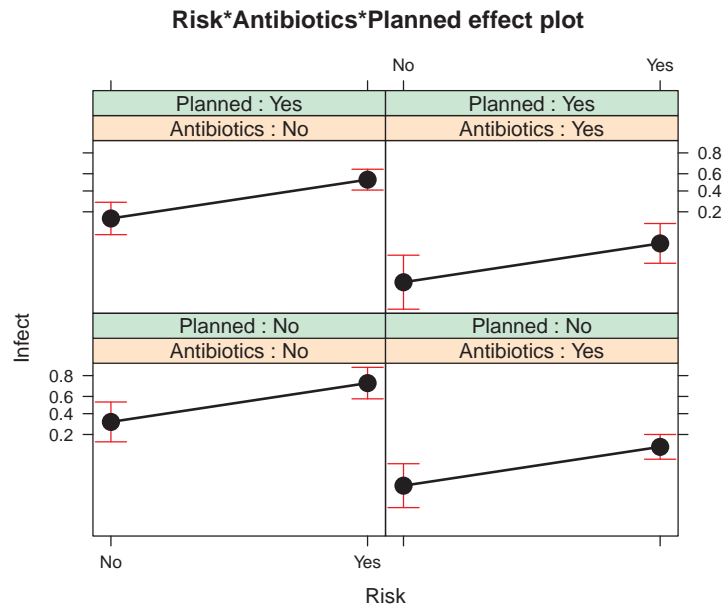
★ Two kinds of effect plots are useful here: `allEffects()`, that gives plots for each of the (main effect) terms in the model, and a full-model plot, showing predicted log odds of infection for all combinations of Risk, Antibiotics and Planned.

```
> library(effects)
> plot(allEffects(caesar.glm), rows=1, cols=3)
```



Full-model plot:

```
> plot(Effect(c("Risk", "Antibiotics", "Planned"), caesar.glm), layout=c(2,2))
```



**Exercise 7.6** The data set *birthwgt* 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, {
+   low <- factor(low)
+   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)
+ })

```

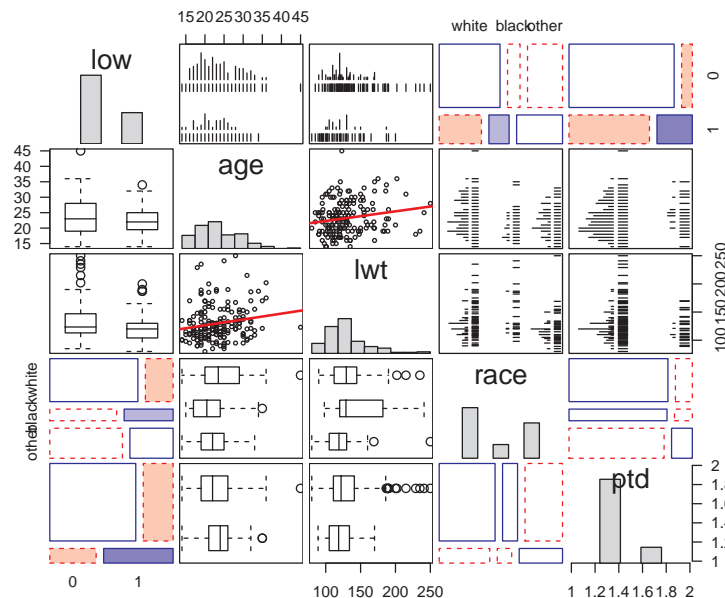
- (a) Make some exploratory plots showing how low birth weight varies with each of the available predictors. In some cases, it will probably be helpful to add some sort of smoothed summary curves or lines.

★ There are a wide variety of plots one could make for this data set. It is not unreasonable to start with a `gpairs()` plot for an overview. The first row and column shows the relations of low birth weight to the predictors. From this we can see that low birth weight (`low==1`) is associated with lower age, lower mother's weight (`lwt`), `race=="black"`, and previous premature labors (`ptd`).

```

> library(gpairs)
> vars <- c("low", "age", "lwt", "race", "ptd")
> gpairs(birthwt[,vars],
+   diag.pars=list(fontsize=16, hist.color="lightgray"),
+   lower.pars = list(scatter="lm"),
+   upper.pars = list(scatter="lm"),
+   mosaic.pars=list(gp=shading_Friendly,
+   gp_args=list(interpolate=1:4)))

```



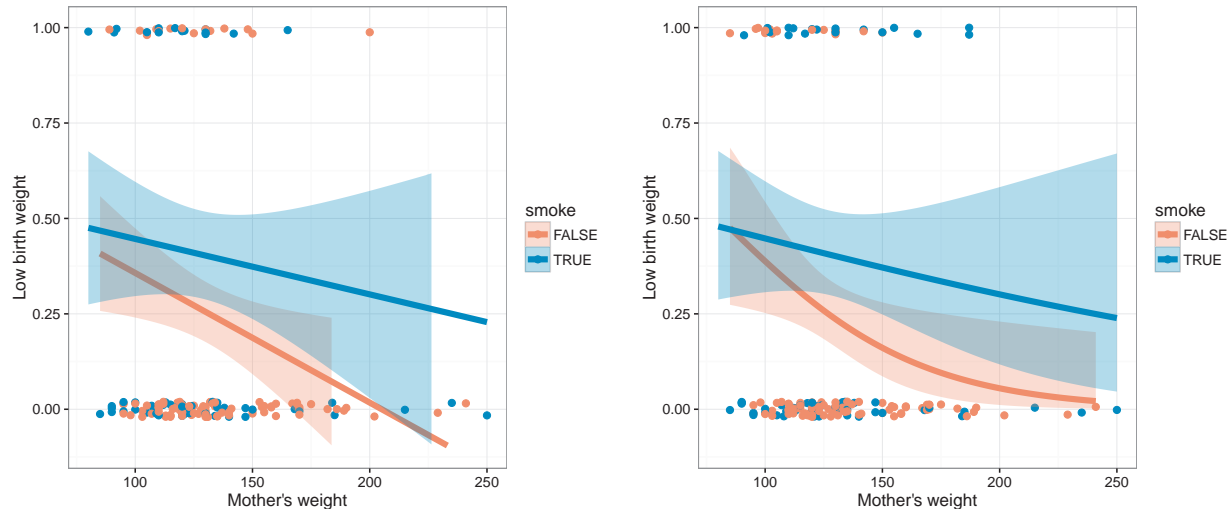
Other plots can explore particular relationships with low birth weight more thoroughly. Here we just show some example plots using `ggplot2` (Wickham and Chang, 2015) for the relationship between `low` and mother's weight (`lwt`) conditioned by smoking status.

```

> library(ggplot2)
> gg <- ggplot(birthwt, aes(x=lwt, y=as.numeric(low)-1, color=smoke)) +
+   geom_point(position=position_jitter(height=0.05, width=0), size=2) +
+   ylim(-.1, 1) + theme_bw() +
+   xlab("Mother's weight") + ylab("Low birth weight")
>
> # use lm smoother
> gg + geom_smooth(method="lm", aes(fill=smoke), alpha=0.3, size=2)
> # use glm smoother
> gg + geom_smooth(method="glm", method.args=list(family = binomial),
+   aes(fill=smoke), alpha=0.3, size=2)

```





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

★ Here, we just start with the main effects model, then eliminate non-significant terms. A more general analysis could use `MASS::stepAIC()`, test for non-linear relations, and the presence of interaction effects.

```
> # quick check on important effects
> bwt.mod0 <- glm(low ~ age + lwt + race + smoke + ptd + ht + ui + ftv,
+                 data=birthwt, family = binomial)
> summary(bwt.mod0)
```

```
Call:
glm(formula = low ~ age + lwt + race + smoke + ptd + ht + ui +
     ftv, family = binomial, data = birthwt)
```

```
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.704  -0.807  -0.501   0.884   2.215
```

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.82302    1.24471   0.66  0.5085
age          -0.03723    0.03870  -0.96  0.3360
lwt          -0.01565    0.00708  -2.21  0.0271 *
raceblack    1.19241    0.53596   2.22  0.0261 *
raceother    0.74068    0.46174   1.60  0.1087
smokeTRUE     0.75553    0.42502   1.78  0.0755 .
ptdTRUE      1.34376    0.48062   2.80  0.0052 **
htTRUE       1.91317    0.72074   2.65  0.0079 **
uiTRUE       0.68020    0.46434   1.46  0.1430
ftv1        -0.43638    0.47939  -0.91  0.3627
ftv2+        0.17901    0.45638   0.39  0.6949
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for binomial family taken to be 1)
```

```
Null deviance: 234.67  on 188  degrees of freedom
Residual deviance: 195.48  on 178  degrees of freedom
AIC: 217.5
```

```
Number of Fisher Scoring iterations: 4
```

```
> car::Anova(bwt.mod0)
```

```
Analysis of Deviance Table (Type II tests)
```

```
Response: low
      LR Chisq Df Pr(>Chisq)
age      0.94  1  0.3318
lwt      5.47  1  0.0193 *
race     5.75  2  0.0564 .
smoke    3.20  1  0.0737 .
ptd     8.11  1  0.0044 **
ht      7.46  1  0.0063 **
```

```

ui          2.11  1    0.1463
ftv         1.36  2    0.5071
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> # remove NS terms
> bwt.mod1 <- update(bwt.mod0, . ~ . - ui - ftv)
> Anova(bwt.mod1)

Analysis of Deviance Table (Type II tests)

Response: low
      LR Chisq Df Pr(>Chisq)
age      1.33  1    0.2487
lwt      5.40  1    0.0201 *
race      6.24  2    0.0441 *
smoke     4.62  1    0.0316 *
ptd      8.73  1    0.0031 **
ht       6.46  1    0.0111 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova(bwt.mod1, bwt.mod0, test="Chisq")

Analysis of Deviance Table

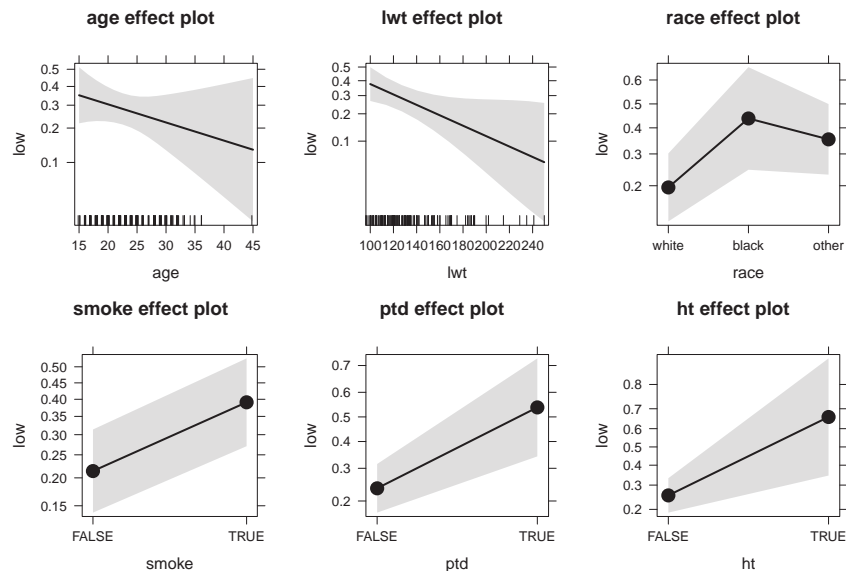
Model 1: low ~ age + lwt + race + smoke + ptd + ht
Model 2: low ~ age + lwt + race + smoke + ptd + ht + ui + ftv
      Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1          181         199
2          178         196   3      3.68    0.3

```

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



```
> plot(allEffects(bwt.mod1), ci.style="bands")
```



**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.

★ For analysis using `glm()` it is useful to consider the ordering of factors for the interpretation of coefficients, contrasts and plots. In the *Accident* data, *mode* is an unordered factor, but it is probably more useful to reorder the levels to make *Pedestrian* the reference level.

```
> levels(Accident$mode) <- c("Pedestrian", "Bicycle", "4-Wheeled", "Motorcycle" )
> acc.mod1 <- glm(result=="Died" ~ age + mode + gender,
+               data=Accident, weight=Freq, family=binomial)
> Anova(acc.mod1)

Analysis of Deviance Table (Type II tests)

Response: result == "Died"
      LR Chisq Df Pr(>Chisq)
age      1179  4  <2e-16 ***
mode      137  3  <2e-16 ***
gender    468  1  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- (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.

★ In the all two-way model, all terms are significant and the addition of these terms is a significant improvement over the main effects model.

```
> acc.mod2 <- update(acc.mod1, . ~ .^2)
> Anova(acc.mod2)

Analysis of Deviance Table (Type II tests)

Response: result == "Died"
      LR Chisq Df Pr(>Chisq)
age      1101  4  < 2e-16 ***
mode      136  3  < 2e-16 ***
gender    419  1  < 2e-16 ***
age:mode   122 12  < 2e-16 ***
age:gender  47  4  1.6e-09 ***
mode:gender  22  3  6.7e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova(acc.mod1, acc.mod2, test="Chisq")

Analysis of Deviance Table

Model 1: result == "Died" ~ age + mode + gender
Model 2: result == "Died" ~ age + mode + gender + age:mode + age:gender +
mode:gender
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1      71      64599
2      52      64384 19      214  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

★ In the three-way model, the term `age:mode:gender` is not significant, and `anova()` shows that it does not improve the two-way model. Using `LRstats()`, the two-way model has the best AIC and BIC.

```
> acc.mod3 <- update(acc.mod1, . ~ .^3)
> Anova(acc.mod3)

Analysis of Deviance Table (Type II tests)

Response: result == "Died"
      LR Chisq Df Pr(>Chisq)
age      1101  4  < 2e-16 ***
mode      136  3  < 2e-16 ***
gender    419  1  < 2e-16 ***
age:mode   122 12  < 2e-16 ***
age:gender  47  4  1.6e-09 ***
mode:gender  22  3  6.7e-05 ***
age:mode:gender 13 12    0.37
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova(acc.mod1, acc.mod2, acc.mod3, test="Chisq")

Analysis of Deviance Table

Model 1: result == "Died" ~ age + mode + gender
Model 2: result == "Died" ~ age + mode + gender + age:mode + age:gender +
```

```

mode:gender
Model 3: result == "Died" ~ age + mode + gender + age:mode + age:gender +
mode:gender + age:mode:gender
Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1      71      64599
2      52      64384 19      214 <2e-16 ***
3      40      64371 12      13  0.37
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

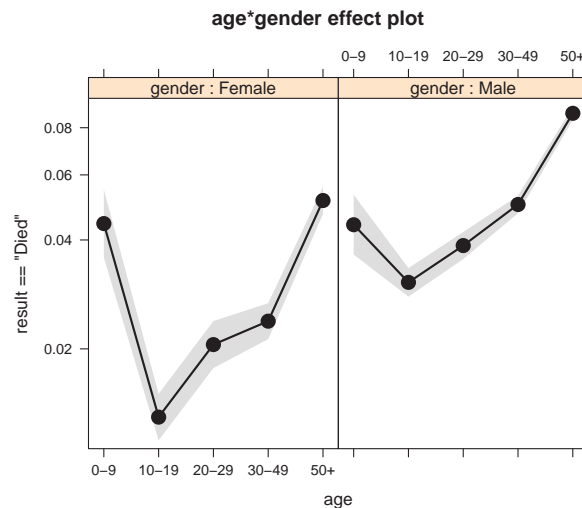
> LRstats(acc.mod1, acc.mod2, acc.mod3)

Likelihood summary table:
      AIC   BIC LR Chisq Df Pr(>Chisq)
acc.mod1 64617 64638 64599 71 <2e-16 ***
acc.mod2 64440 64507 64384 52 <2e-16 ***
acc.mod3 64451 64547 64371 40 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

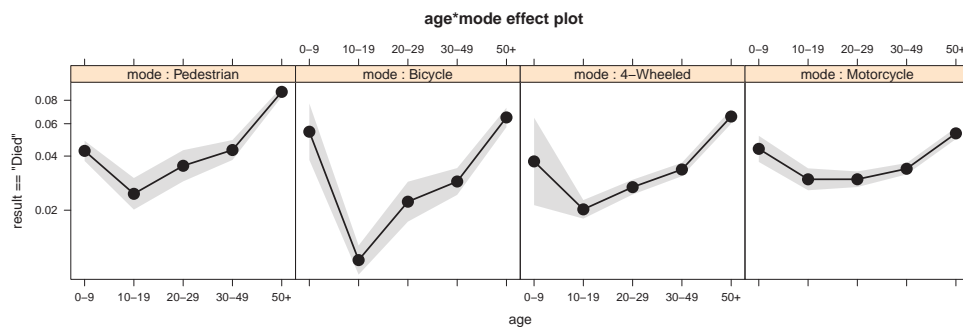
- (d) Interpret the results of the analysis using effect plots for the two-way model, separately for each of the model terms. Describe verbally the nature of the age\*gender effect. Which mode of transportation leads to greatest risk of death?  
★ Controlling for mode, males and females have similar profiles, with the lowest probability of death in the 10–19 group, and highest in the 50+ age group.

```
> plot(Effect(c("age", "gender"), acc.mod2), ci.style="bands")
```

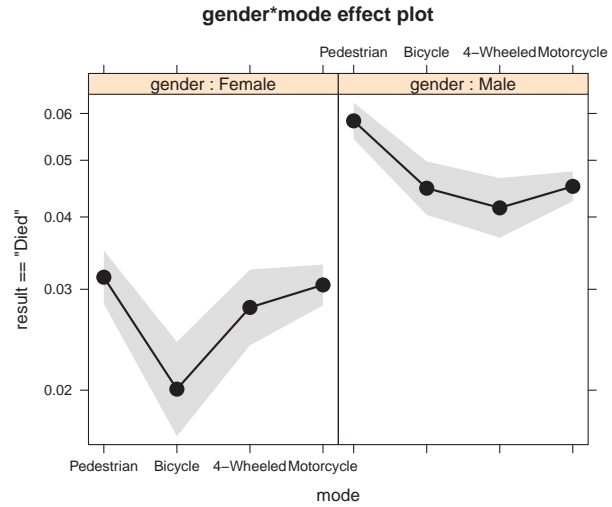


There are roughly similar profiles across age, with bicycle accidents showing the greatest differences among age groups.

```
> plot(Effect(c("age", "mode"), acc.mod2), ci.style="bands", layout=c(4,1))
```

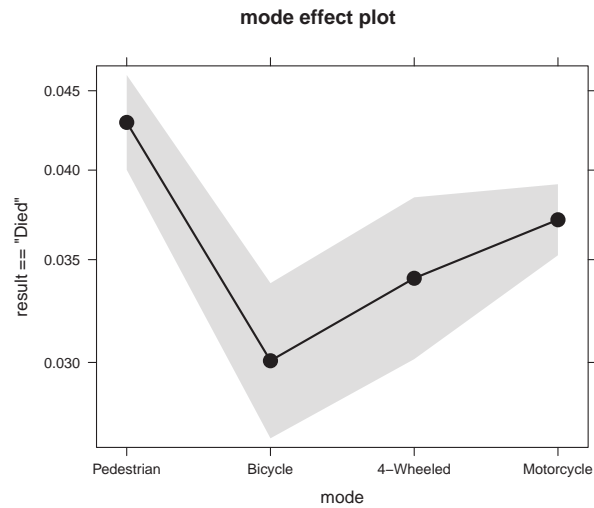


```
> plot(Effect(c("gender", "mode"), acc.mod2), ci.style="bands")
```



Overall, accidents involving motorcycles have the greatest probability of death, controlling for all other factors.

```
> plot(Effect("mode", acc.mod2), ci.style="bands")
```



## 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.

★ We start fitting the proportional odds model using `polr()`:

```
> library(car)
> library(MASS)
> Womenlf$partic <- ordered(Womenlf$partic,
+ levels = c("not.work", "parttime", "fulltime"))
> Wlf.polr <- polr(partic ~ hincome + children + region, data = Womenlf)
> Anova(Wlf.polr)
```

Analysis of Deviance Table (Type II tests)

```
Response: partic
      LR Chisq Df Pr(>Chisq)
hincome      8.5  1  0.0035 **
children    50.3  1  1.3e-12 ***
region       1.9  4  0.7547
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

to see that *region* has no significant effect on the comparison of the different response categories; we will ignore it in the further analysis. Now, we try comparing the proportional and non-proportional odds models by refitting them using `vglm()`:

```
> library(VGAM)
> Wlf.po <- vglm(partic ~ hincome + children, data = Womenlf,
+ family = cumulative(parallel = TRUE))
>
> Wlf.npo <- vglm(partic ~ hincome + children, data = Womenlf,
+ family = cumulative(parallel = FALSE))
> Wlf.ppo <- vglm(partic ~ hincome + children, data = Womenlf,
+ family = cumulative(parallel = FALSE ~ hincome))
```

The warnings indicate that the non-proportional odds model does not converge, leaving the object returned by `vglm()` without log-likelihood, and making impossible the comparison using `lrtest()`:

```
> logLik(Wlf.npo)

[1] NaN

> VGAM::lrtest(Wlf.po, Wlf.npo)

Likelihood ratio test

Model 1: partic ~ hincome + children
Model 2: partic ~ hincome + children
#Df LogLik Df Chisq Pr(>Chisq)
1 522 -221
2 520 -2
```

It is, however, possible to fit a partial proportional odds model, relaxing the assumption for *hincome*:

```
> Wlf.ppo <- vglm(partic ~ hincome + children, data = Womenlf,
+ family = cumulative(parallel = FALSE ~ hincome))
```

The comparison with `lrtest()` now yields:

```
> VGAM::lrtest(Wlf.po, Wlf.ppo)
```

```

Likelihood ratio test

Model 1: partic ~ hincome + children
Model 2: partic ~ hincome + children
#Df LogLik Df Chisq Pr(>Chisq)
1 522 -221
2 521 -219 -1 4.14 0.042 *
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

showing that the partial proportional odds model is preferable to the proportional odds model. The graphical assessment using the method described in Section 8.1.4 provides further insights:

```

> library(rms)
> Wlf.po2 <- lrm(partic ~ hincome + children, data = Womenlf)
> Wlf.po2

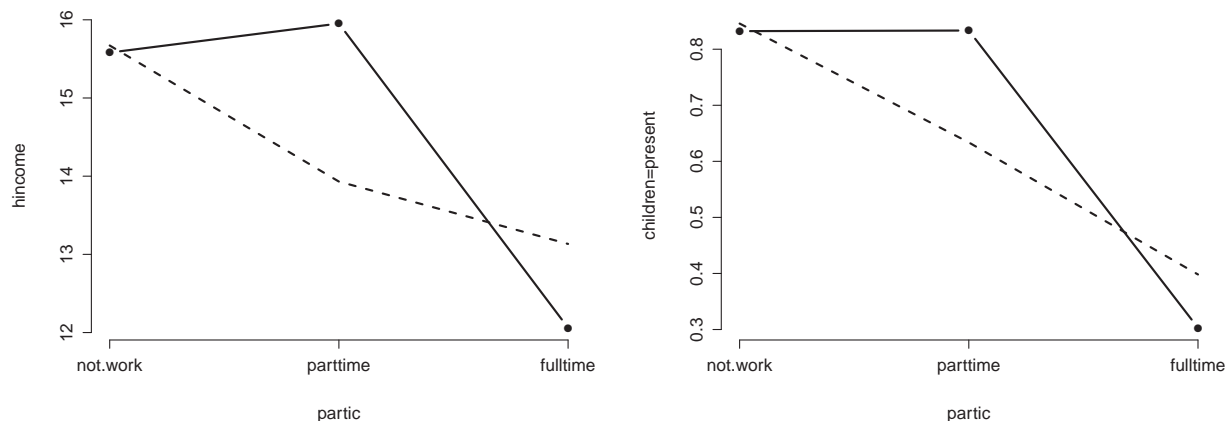
Logistic Regression Model

lrm(formula = partic ~ hincome + children, data = Womenlf)
      Model Likelihood      Discrimination      Rank Discrim.
      Ratio Test      Indexes      Indexes
Obs      263      LR chi2      58.83      R2      0.236      C      0.723
not.work 155      d.f.      2      g      1.083      Dxy      0.446
parttime 42      Pr(> chi2) <0.0001      gr      2.954      gamma      0.461
fulltime 66      gp      0.236      tau-a      0.253
max |deriv| 4e-08      Brier      0.209

      Coef      S.E.      Wald Z      Pr(>|Z|)
y>=parttime      1.8520      0.3863      4.79      <0.0001
y>=fulltime      0.9409      0.3699      2.54      0.0110
hincome      -0.0539      0.0195      -2.77      0.0057
children=present -1.9720      0.2869      -6.87      <0.0001

> plot.xmean.ordinaly(partic ~ hincome + children, data = Womenlf,
+                       lwd=2, pch=16, subn=FALSE)

```



The mean values for `hincome` do indeed not follow the fitted ones under the proportional odds model. Also, the first two categories, `not.work` and `parttime`, are not well distinguished.

**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.

- 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.)

★ All three factors have significant effects on satisfaction in this simple model.

```
> data("housing", package="MASS")
> str(housing)

'data.frame': 72 obs. of  5 variables:
 $ Sat : Ord.factor w/ 3 levels "Low"<"Medium"<...: 1 2 3 1 2 3 1 2 3 1 ...
 $ Infl: Factor w/ 3 levels "Low","Medium",...: 1 1 1 2 2 2 3 3 3 1 ...
 $ Type: Factor w/ 4 levels "Tower","Apartment",...: 1 1 1 1 1 1 1 1 1 2 ...
 $ Cont: Factor w/ 2 levels "Low","High": 1 1 1 1 1 1 1 1 1 1 ...
 $ Freq: int  21 21 28 34 22 36 10 11 36 61 ...

> # proportional odds model
> library(MASS)
> PO.mod <- polr(Sat ~ Infl + Type + Cont, data=housing, weights=Freq)
> car::Anova(PO.mod)

Analysis of Deviance Table (Type II tests)

Response: Sat
      LR Chisq Df Pr(>Chisq)
Infl  108.2   2  < 2e-16 ***
Type   55.9   3  4.4e-12 ***
Cont   14.3   1  0.00016 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Although not asked in the question, it is important to assess whether the proportional odds assumption hold statistically (using VGAM), following the methods described in Section 8.1.3, or graphically (using rms (Harrell, Jr., 2015)), following Section 8.1.4. Here, we illustrate the statistical test using `vglm()`.

```
> library(VGAM)
> # PO model
> PO.vglm <- vglm(Sat ~ Infl + Type + Cont, data=housing,
+               family=cumulative(parallel=TRUE), weights=Freq)
> # NPO model
> NPO.vglm <- vglm(Sat ~ Infl + Type + Cont, data=housing,
+               family=cumulative(parallel=FALSE), weights=Freq)
> # See if PO assumption holds
> VGAM::lrtest(PO.vglm, NPO.vglm)

Likelihood ratio test

Model 1: Sat ~ Infl + Type + Cont
Model 2: Sat ~ Infl + Type + Cont
  #Df LogLik Df Chisq Pr(>Chisq)
1 136 -1740
2 130 -1735 -6  8.57      0.2
```

- (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"`.)
- ★ Forward selection from the main effects model adds the interactions of `Infl:Type` and `Type:Cont`. That is, the effect of type of dwelling on satisfaction varies both with influence and contact with other residents.

```
> house.step <- stepAIC(PO.mod, scope = ~.^2, direction = "forward")

Start: AIC=3495.2
Sat ~ Infl + Type + Cont

      Df  AIC
+ Infl:Type  6 3485
+ Type:Cont  3 3492
<none>      0 3495
+ Infl:Cont  2 3499

Step: AIC=3484.6
Sat ~ Infl + Type + Cont + Infl:Type

      Df  AIC
+ Type:Cont  3 3483
<none>      0 3485
+ Infl:Cont  2 3489

Step: AIC=3482.7
Sat ~ Infl + Type + Cont + Infl:Type + Type:Cont

      Df  AIC
<none>      0 3483
+ Infl:Cont  2 3487
```



The result of `stepAIC()` includes an anova summary of the steps.

```
> house.step$anova
Stepwise Model Path
Analysis of Deviance Table

Initial Model:
Sat ~ Infl + Type + Cont

Final Model:
Sat ~ Infl + Type + Cont + Infl:Type + Type:Cont

      Step Df Deviance Resid. Df Resid. Dev    AIC
1          6    22.509     1673    3479.1 3495.1
2 + Infl:Type 6    22.509     1667    3456.6 3484.6
3 + Type:Cont 3     7.945     1664    3448.7 3482.7

> Anova(house.step)

Analysis of Deviance Table (Type II tests)

Response: Sat
      LR Chisq Df Pr(>Chisq)
Infl    106.5  2  < 2e-16 ***
Type     55.9  3  4.4e-12 ***
Cont     15.1  1    0.0001 ***
Infl:Type 21.8  6    0.0013 **
Type:Cont  7.9  3    0.0472 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The next step, refitting the model chosen by `stepAIC()` is not strictly necessary (because that model was saved as `house.step`), but using the argument `Hess=TRUE` saves computation for some of the plots below.

```
> PO.mod2 <- polr(formula = Sat ~ Infl + Type + Cont + Infl:Type + Type:Cont,
+                 data = housing, Hess=TRUE, weights=Freq)
```

- (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.

★ A first step in plotting is to join the data with the predicted values.

```
> fit.step <- cbind(housing, predict(house.step, type="probs"))
> head(fit.step)

  Sat Infl Type Cont Freq   Low Medium   High
1  Low  Low Tower Low   21 0.30948 0.28988 0.40064
2 Medium Low Tower Low   21 0.30948 0.28988 0.40064
3  High  Low Tower Low   28 0.30948 0.28988 0.40064
4  Low Medium Tower Low   34 0.33933 0.29227 0.36841
5 Medium Medium Tower Low   22 0.33933 0.29227 0.36841
6  High Medium Tower Low   36 0.33933 0.29227 0.36841
```

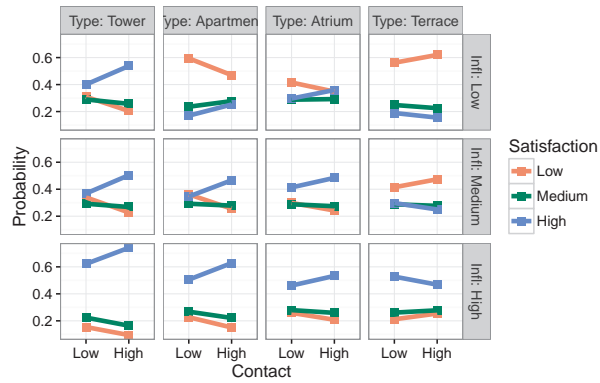
Plotting predicted probabilities with `ggplot2` is quite flexible, but requires that the data in `fit.step` be reshaped to long format.

```
> library(reshape2)
> plotdat <- melt(fit.step,
+               id.vars = c("Sat", "Infl", "Type", "Cont"),
+               measure.vars = c("Low", "Medium", "High"),
+               variable.name = "Satisfaction",
+               value.name = "Probability")
```

Then, we can plot  $y = \text{Probability}$  against one factor as  $x$ , and use `facet_grid()` to show panels for the other factors as rows and columns. This gives what we call a “full-model plot.”

```
> library(ggplot2)
> ggplot(plotdat, aes(x = as.integer(Cont), y = Probability, color = Satisfaction)) +
+   facet_grid(Infl ~ Type, labeller=label_both) +
+   geom_point(size=2.5, shape=15) +
+   geom_line(size=1.5) +
+   xlab("Contact") +
+   ggtitle("Fitted Probabilities from PO Interaction Model for Satisfaction") +
+   scale_x_discrete(breaks=1:2, labels=c("Low", "High")) +
+   theme_bw()
```

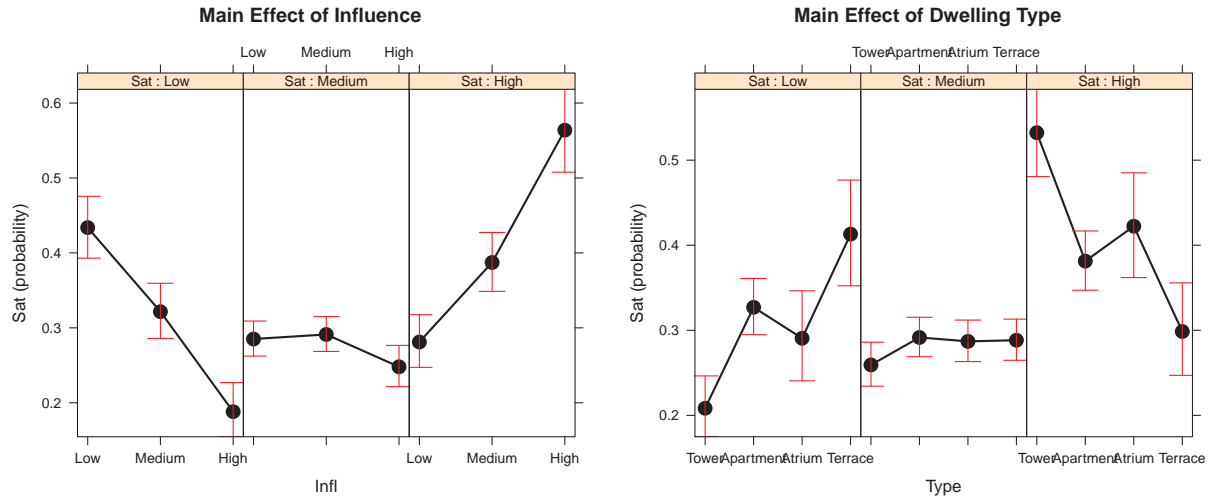
itted Probabilities from PO Interaction Model for Satisfaction



For ease of interpreting the model, effect plots give a more convenient visual summary. The model has 5 terms, and it is useful to plot them all; we only show selected terms here.

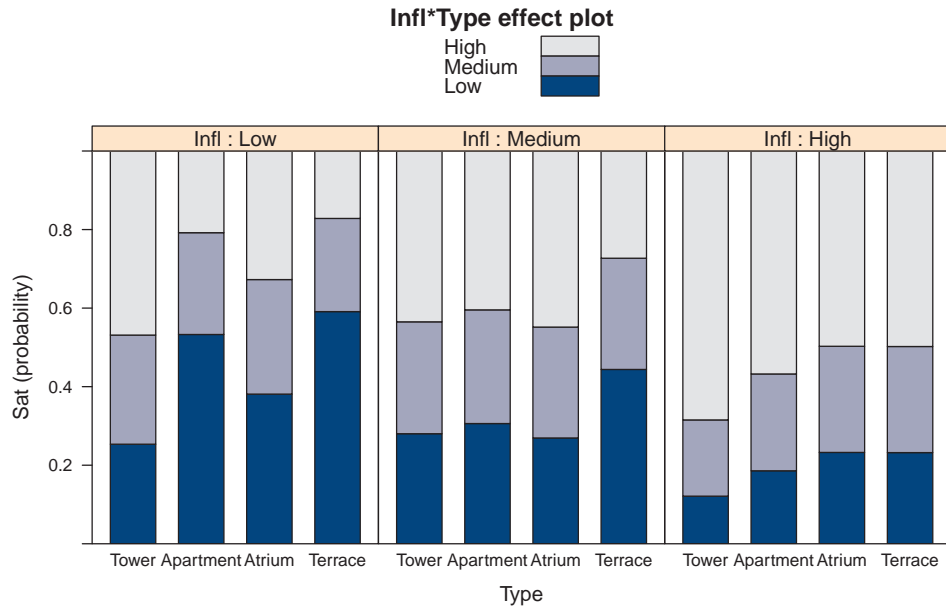
Main effects of influence and type:

```
> plot(Effect("Infl", PO.mod2), main="Main Effect of Influence", layout=c(3,1))
> plot(Effect("Type", PO.mod2), main="Main Effect of Dwelling Type", layout=c(3,1))
```



Interaction of influence and type:

```
> plot(Effect(c("Infl", "Type"), PO.mod2), style="stacked")
```



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

★ As Influence increases, high satisfaction also increases, low satisfaction decreases and medium satisfaction remains relatively constant. Dwelling type also has opposite effects on high and low satisfaction, with Tower dwellers being highest on high satisfaction and Terrace dwellers lowest. Again, medium satisfaction seems to be relatively static across dwelling type. High satisfaction also increases with high contact.

**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,  $\text{Network} \sim \text{Day} + \text{Time}$ , 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.

```
★
> library(nnet)
> tv.model = multinom(Network ~ Day + Time, data = TV.df,
+                      weights = Freq, Hess = TRUE)

# weights:  48 (30 variable)
initial  value 41318.808177
iter   10 value 38935.947713
iter   20 value 38818.222728
iter   30 value 38756.956301
final   value 38752.186202
converged

> car::Anova(tv.model)

Analysis of Deviance Table (Type II tests)

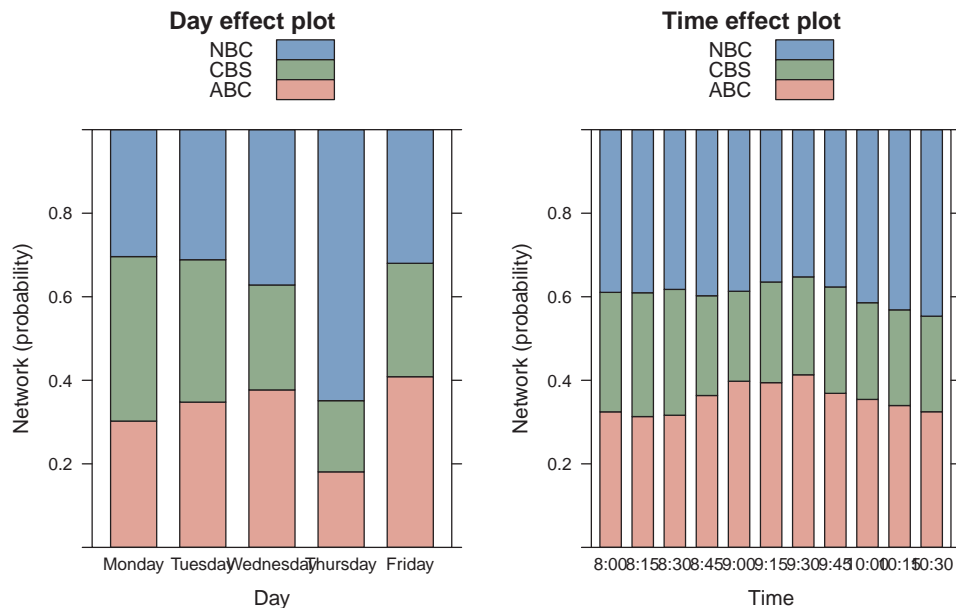
Response: Network
      LR Chisq Df Pr(>Chisq)
Day      3400   8  <2e-16 ***
Time      301  20  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Both *Day* and *Time* are clearly significant when comparing the Networks.

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

★

```
> library(effects)
> plot(allEffects(tv.model), style = "stacked")
```



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

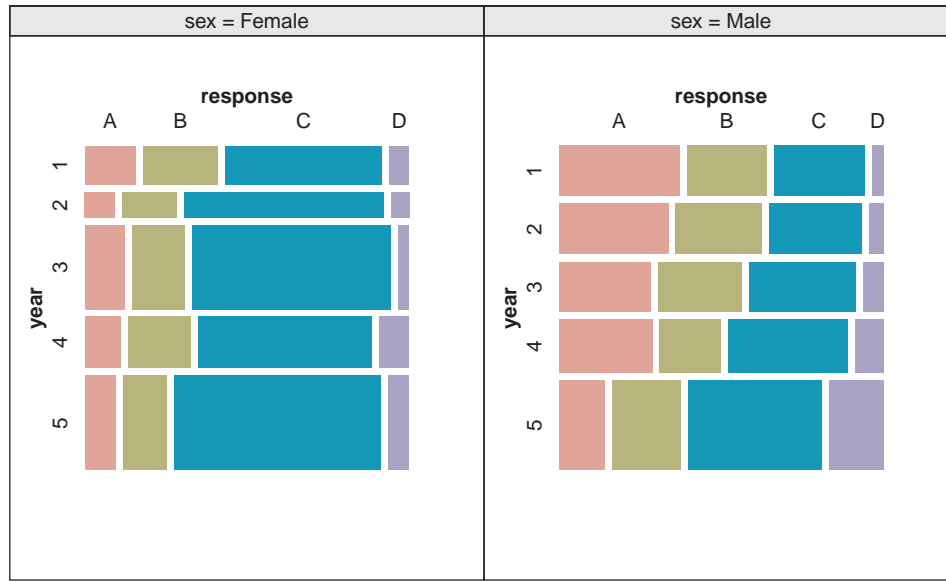
★ The effect plots for Day clearly show a peak for NBC on Thursday, at the expense of the two other networks. ABC has most viewers on Tuesday and Wednesday, whereas CBS is the most popular Network on Monday. These results are consistent with the results from the correspondence analysis. Regarding time, ABC is most viewed from 8:45 to 9:30—after that, the viewing probability decreases in favor of NBC.

**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 variable in relation to year and sex.

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

★ The Vietnam data is pretabulated; for a first explorative view, we transform it into tabular format, and use a conditional mosaicplot (with Marimekko shading) to get ideas on the structure.

```
> library(vcdExtra)
> data(Vietnam)
> Vtn_tab = xtabs(Freq ~ ., data = Vietnam)
> cotabplot(~ year + response | sex, data = Vtn_tab,
+           gp = shading_Marimekko(Vtn_tab[1,,]))
```



Whereas male students have a clear tendency to choose the more peaceful options C and D only with higher study year (the mosaic plot suggests a linear relationship of `year` and `response`), the situation is less clear for female students—there seems to be a general tendency for response C (negotiations), independent from the study year.

The proportional odds model is fitted using `polr()`. Before, we make sure that the response is indeed treated as ordinal:

```
> library(MASS)
> Vietnam$response = ordered(Vietnam$response)
> Vtn_polr = polr(response ~ year * sex, data = Vietnam,
+               weights = Freq, Hess = TRUE)
> summary(Vtn_polr)

Call:
polr(formula = response ~ year * sex, data = Vietnam, weights = Freq,
      Hess = TRUE)

Coefficients:
              Value Std. Error t value
year           0.101     0.0548    1.84
sexMale        -1.437     0.2230   -6.44
year:sexMale     0.233     0.0603    3.87

Intercepts:
              Value Std. Error t value
A|B    -1.353     0.206    -6.574
B|C    -0.254     0.204    -1.244
C|D     2.188     0.210    10.397

Residual Deviance: 7757.06
AIC: 7769.06

> car::Anova(Vtn_polr)

Analysis of Deviance Table (Type II tests)

Response: response
              LR Chisq Df Pr(>Chisq)
year           166.5   1  < 2e-16 ***
sex             58.5   1  2.1e-14 ***
year:sex        15.0   1  0.00011 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Clearly, all terms are significant, including the interaction term with `sex` as expected from the mosaic plots.

- (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.

★ We refit the model using `vglm()`, and compare it to the non-proportional odds model with `lrtest()`:

```
> library(VGAM)
> Vtn_PO = vglm(response ~ year * sex, data = Vietnam,
+               weights = Freq, family = cumulative(parallel = TRUE))
> Vtn_NPO = vglm(response ~ year * sex, data = Vietnam,
+               weights = Freq, family = cumulative(parallel = FALSE))
> VGAM::lrtest(Vtn_NPO, Vtn_PO)

Likelihood ratio test

Model 1: response ~ year * sex
Model 2: response ~ year * sex
  #Df LogLik Df Chisq Pr(>Chisq)
1 108 -3840
2 114 -3879 6 77.6 1.1e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The unconstrained model fits better than the proportional odds model—again as expected, since for women, the proportional odds assumption seems not be reasonable.

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

★

```
> library(nnet)
> library(car)
> Vtn_mtn = multinom(response ~ year * sex, data = Vietnam, weights = Freq)

# weights:  20 (12 variable)
initial value 4362.668354
iter  10 value 3927.047674
final value 3838.854903
converged

> summary(Vtn_mtn)

Call:
multinom(formula = response ~ year * sex, data = Vietnam, weights = Freq)

Coefficients:
      (Intercept)      year  sexMale year:sexMale
B      0.39288 -0.00051719 -0.97197      0.14692
C      1.14525  0.14751329 -1.88983      0.17082
D     -1.31002  0.19089252 -2.00838      0.45507

Std. Errors:
      (Intercept)      year  sexMale year:sexMale
B      0.39149 0.110209 0.41055      0.116272
C      0.33686 0.093731 0.35726      0.099851
D      0.56775 0.150979 0.61640      0.162177

Residual Deviance: 7677.7
AIC: 7701.7

> car::Anova(Vtn_mtn)

Analysis of Deviance Table (Type II tests)

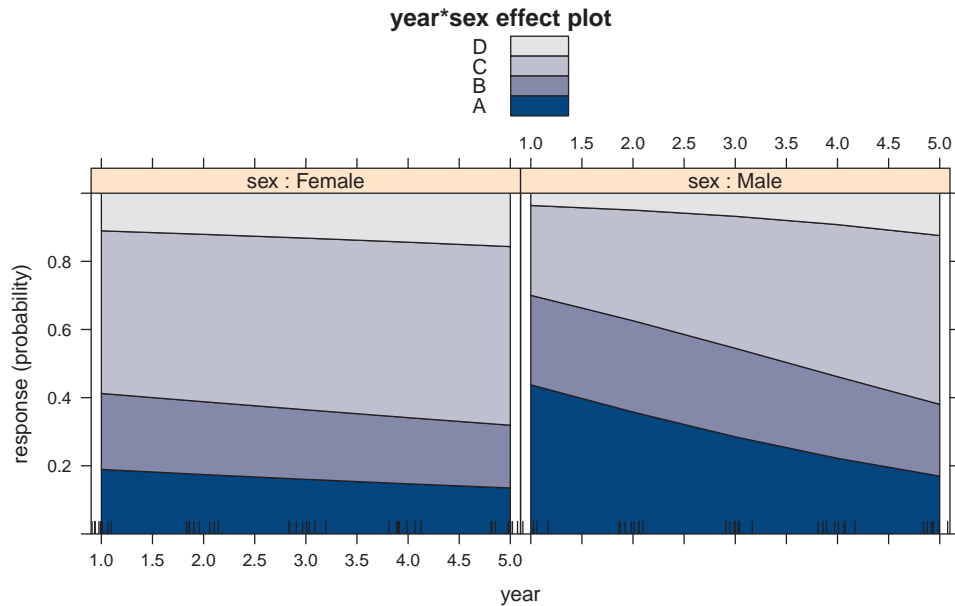
Response: response
      LR Chisq Df Pr(>Chisq)
year      175.9  3 <2e-16 ***
sex       137.6  3 <2e-16 ***
year:sex    7.8  3  0.051 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

All terms are again significant, although weakly so for the interaction term.

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

★

```
> library(effects)
> plot(allEffects(Vtn_polr), style = "stacked")
```



The effect of `year` on `response` under the fitted model differentiates male and female students: Whereas the majority of female students prefer the more peaceful options in general (with a slight increase over the years), a majority of male students are in favor of more violent options as freshmen, but change their opinion dramatically during the studies so that the situation is reversed at the end. The model is consistent with the findings from the exploratory mosaic plot.

- (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.  
 ★ To achieve this, we first construct an artificial variable `yearMale`, with non-zero entries only for male students:

```
> Vietnam = within(Vietnam, yearMale <- year * (sex == "Male"))
> Vtn_mtn2 = multinom(response ~ sex + yearMale, data = Vietnam, weights = Freq)

# weights: 16 (9 variable)
initial value 4362.668354
iter 10 value 3894.170452
final value 3841.568268
converged

> Anova(Vtn_mtn2)
Analysis of Deviance Table (Type II tests)

Response: response
          LR Chisq Df Pr(>Chisq)
sex          243   3  <2e-16 ***
yearMale      178   3  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova(Vtn_mtn, Vtn_mtn2)
Likelihood ratio tests of Multinomial Models

Response: response
  Model Resid. df Resid. Dev  Test      Df LR stat. Pr(Chi)
1 sex + yearMale      111    7683.1  Test      3  5.4267 0.14309
2   year * sex        108    7677.7 1 vs 2      3  5.4267 0.14309
```

The simpler model is not significant worse than the general model with interaction, and should therefore be preferred.

## 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,  $[A][C][M]$ .

★

```
> library(vcdExtra)
> data(DaytonSurvey)
> Dayton.ACM = aggregate(Freq ~ cigarette + alcohol + marijuana,
+                         data = DaytonSurvey, FUN = sum)
> ACM.mutual = loglm(Freq ~ ., data = Dayton.ACM)
> ACM.mutual
```

Call:  
loglm(formula = Freq ~ ., data = Dayton.ACM)

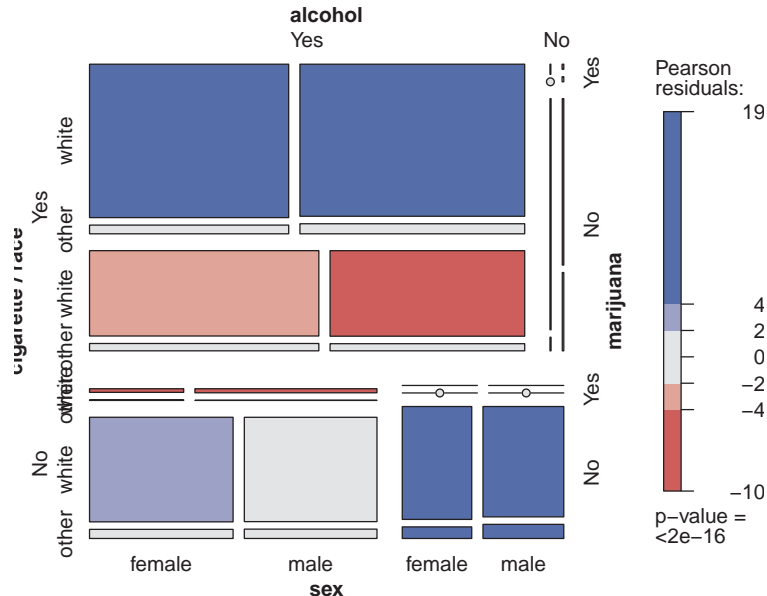
Statistics:

	X <sup>2</sup>	df	P(> X <sup>2</sup> )
Likelihood Ratio	1286.0	4	0
Pearson	1411.4	4	0

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

★ We can start creating a mosaic display for the complete table, using residual-based shading:

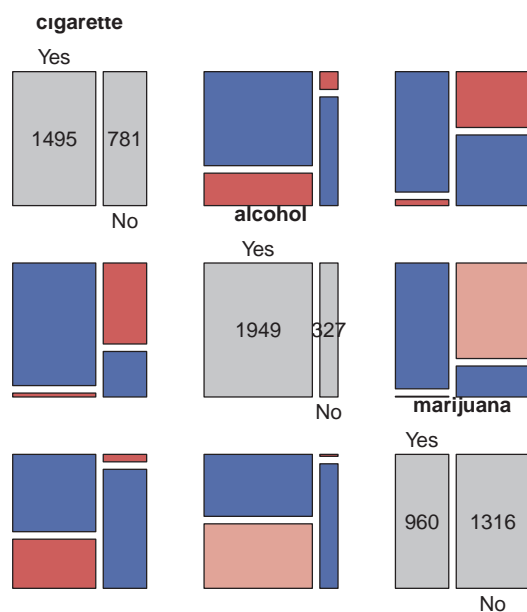
```
> mosaic(Freq ~ ., data = DaytonSurvey, shade = TRUE)
```



By default, the expected values (and residuals) are taken from the mutual independence model. As we can see from the structure and the shading, the model fits badly. Alternatively, we can inspect all pairwise (marginal) associations using `pairs()`. For this, we need to transform the data into contingency table form first:

```
> Dayton.tab = xtabs(Freq ~ ., data = Dayton.ACM)
> pairs(Dayton.tab, type = "pairwise", shade = TRUE)
```



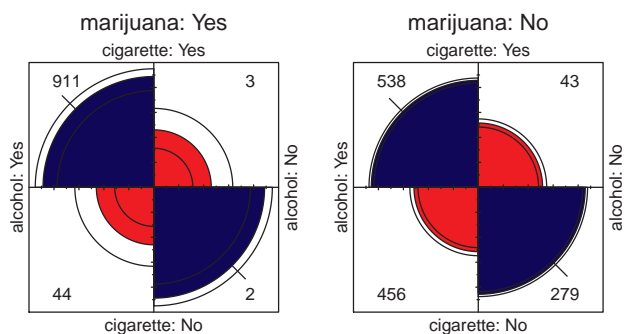


Clearly, the variables are associated mutually. In particular, in the mosaic for `cigarette` and `alcohol`, too many people who drink also smoke (and, conversely, too many people who don't drink also don't smoke) than would be expected under the mutual independence model.

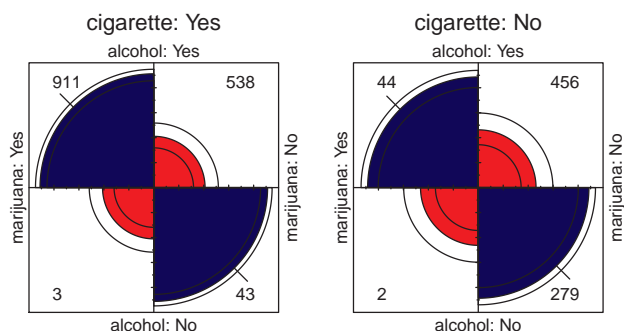
- (c) Use `fourfold()` to produce fourfold plots for each pair of variables, AC, AM, and CM, stratified by the remaining one. Describe these associations verbally.

★ A fourfold plot visualizes the log-odds ratios between two binary variables. To plot all pairwise combinations, given the third, of the Dayton data, we permute the table dimensions:

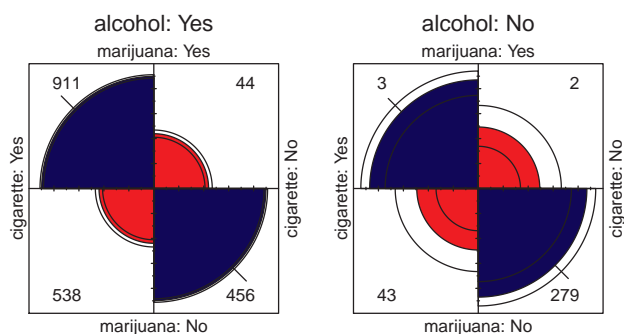
```
> fourfold(aperm(Dayton.tab, c(1, 2, 3)))
```



```
> fourfold(aperm(Dayton.tab, c(2, 3, 1)))
```



```
> fourfold(aperm(Dayton.tab, c(3, 1, 2)))
```



All 6 displays exhibit a positive association between two of the three drugs (more people who drink also smoke than expected under independence, etc.) which illustrates that the hypothesis of mutual independence is not tenable. However, these mutual association patterns are independent from the third, so a reasonable model might be the homogeneous association model (= no three-way association), as investigated in the next exercise.

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

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

★

```
> ACM.joint = loglm(Freq ~ alcohol * cigarette + marijuana, data = Dayton.ACM)
> ACM.joint

Call:
loglm(formula = Freq ~ alcohol * cigarette + marijuana, data = Dayton.ACM)
```

```
Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 843.83 3      0
Pearson          704.91 3      0
```

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

★

```
> ACM.cond = loglm(Freq ~ (alcohol + cigarette) * marijuana, data = Dayton.ACM)
> ACM.cond

Call:
loglm(formula = Freq ~ (alcohol + cigarette) * marijuana, data = Dayton.ACM)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 187.75 2      0
Pearson          177.61 2      0
```

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

★

```
> ACM.hom = loglm(Freq ~ alcohol * cigarette + alcohol * marijuana +
+                 cigarette * marijuana, data = Dayton.ACM)
> ACM.hom

Call:
loglm(formula = Freq ~ alcohol * cigarette + alcohol * marijuana +
       cigarette * marijuana, data = Dayton.ACM)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 0.37399 1 0.54084
Pearson          0.40110 1 0.52652
```

(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?

★

```
> anova(ACM.mutual, ACM.joint, ACM.cond, ACM.hom, test = "Chisq")

LR tests for hierarchical log-linear models

Model 1:
  Freq ~ .
Model 2:
  Freq ~ alcohol * cigarette + marijuana
Model 3:
  Freq ~ (alcohol + cigarette) * marijuana
Model 4:
  Freq ~ alcohol * cigarette + alcohol * marijuana + cigarette * marijuana

      Deviance df Delta(Dev) Delta(df) P(> Delta(Dev))
Model 1  1286.01995 4
Model 2   843.82664 3  442.19331      1      0.00000
Model 3   187.75430 2  656.07234      1      0.00000
Model 4    0.37399 1  187.38032      1      0.00000
Saturated  0.00000 0    0.37399      1      0.54084

> LRstats(ACM.mutual, ACM.joint, ACM.cond, ACM.hom)

Likelihood summary table:
      AIC  BIC LR Chisq Df Pr(>Chisq)
ACM.mutual 1343 1343    1286 4 <2e-16 ***
ACM.joint   903  903     844 3 <2e-16 ***
ACM.cond    249  249     188 2 <2e-16 ***
ACM.hom      63   64       0 1    0.54
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The homogeneous association model is clearly the best model: it is not significantly worse than the saturated model, and has the lowest AIC and BIC values.

**Exercise 9.3** The data set *Caesar* in *vcdExtra* gives a  $3 \times 2^3$  frequency table classifying 251 women who gave birth by Caesarian section by Infection (three levels: none, Type 1, Type2) and Risk, whether Antibiotics

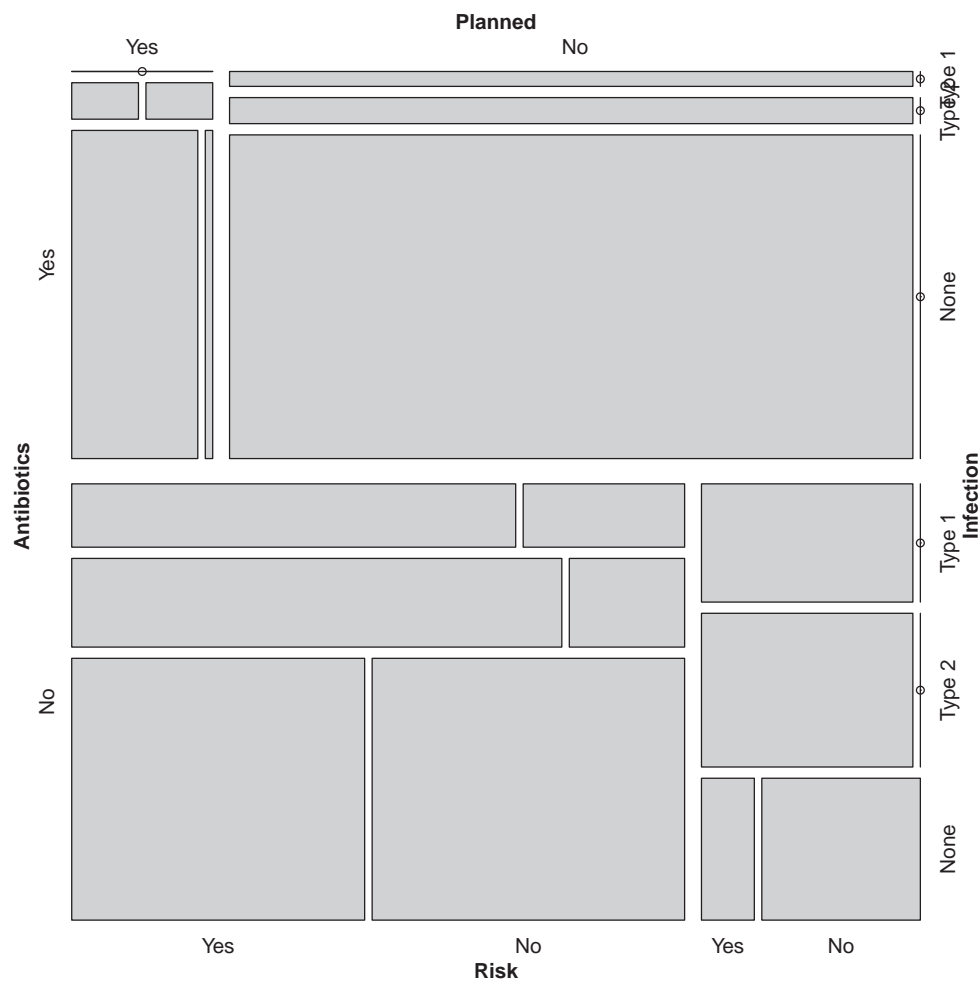
were used, and whether the Caesarian section was Planned or not. Infection is a natural response variable, but the table has quite a few zeros.

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

★

```
> library(vcdExtra)
> data(Caesar)
> mosaic(aperm(Caesar, c(3,4,1,2)))
> structable(aperm(Caesar, c(3,4,1,2)))
```

		Planned		Yes		No	
		Risk		Yes	No	Yes	No
Antibiotics	Infection	Type 1	Type 2	0	0	4	0
				1	1	7	0
				17	1	87	0
	None	Type 1	Type 2	11	4	10	0
				17	4	13	0
				30	32	3	9



Zero cells occur essentially for unplanned sections without risk factors (except for no antibiotics/no infection), and planned sections with risk, antibiotics and Type 1 infection.

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

★

```
> caesar_base = loglm(~ Infection + Planned * Risk * Antibiotics, data = Caesar)
> caesar_base
```

```
Call:
loglm(formula = ~Infection + Planned * Risk * Antibiotics, data = Caesar)
```

```

Statistics:
              X^2 df    P(> X^2)
Likelihood Ratio 85.11 14 3.1566e-12
Pearson          NaN 14      NaN

```

The NaN value for the Pearson Chi-Squared statistics is suspicious. It stems from the fact that some of the expected values (unplanned sections without risk factors and with antibiotics) are 0, yielding NaN values for the corresponding Pearson residuals.

- (c) For the purpose of this exercise, 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.

★

```

> Caesar1 = Caesar + 0.5
> caesar_sampling = loglm(~ Infection + Planned * Risk * Antibiotics, data = Caesar1)
> caesar_sampling

```

```

Call:
loglm(formula = ~Infection + Planned * Risk * Antibiotics, data = Caesar1)

```

```

Statistics:
              X^2 df    P(> X^2)
Likelihood Ratio 77.865 14 7.0291e-11
Pearson          77.814 14 7.1805e-11

```

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

★

```

> caesar_main = loglm(~ Infection * (Risk + Antibiotics + Planned) +
+ (Risk * Antibiotics * Planned), data = Caesar1)
> caesar_main

```

```

Call:
loglm(formula = ~Infection * (Risk + Antibiotics + Planned) +
      (Risk * Antibiotics * Planned), data = Caesar1)

```

```

Statistics:
              X^2 df    P(> X^2)
Likelihood Ratio 25.539  8 1.2592e-03
Pearson          73.682  8 9.0539e-13

```

```

> anova(caesar_sampling, caesar_main, test = "Chisq")

```

LR tests for hierarchical log-linear models

```

Model 1:
~Infection + Planned * Risk * Antibiotics

```

```

Model 2:
~Infection * (Risk + Antibiotics + Planned) + (Risk * Antibiotics * Planned)

```

	Deviance	df	Delta(Dev)	Delta(df)	P(> Delta(Dev))
Model 1	77.865	14			
Model 2	25.539	8	52.326	6	0.00000
Saturated	0.000	0	25.539	8	0.00126

The model fits better than the base model, but nevertheless shows a lack of fit.

**Exercise 9.4** The *Detergent* in *vcdExtra* gives a  $2^3 \times 3$  table classifying a sample of 1,008 consumers according to (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.

★ We can start with an exploratory pairs plot, showing all pairwise associations:

```

> library(vcdExtra)
> pairs(Detergent, type = "pairwise")

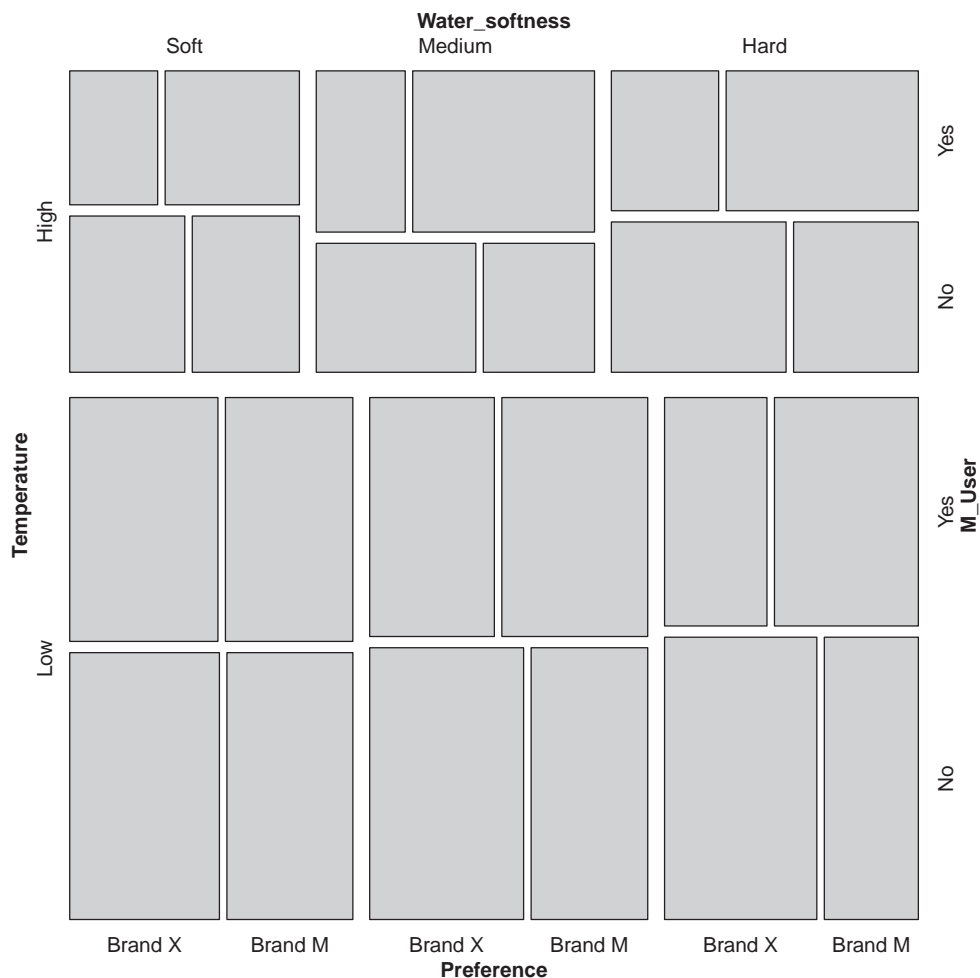
```





This shows, for each combination of `M_User` and `Preference`, the relationship of `temperature` and `Water_softness`. Since the tiles do not align in all four cases, we might again suspect some association between these two variables. Another approach in case of a response variable is to put it *last* in the mosaic, showing conditional (in)dependence structures:

```
> mosaic(~ Temperature + Water_softness + M_User + Preference, data
+ = Detergent)
```



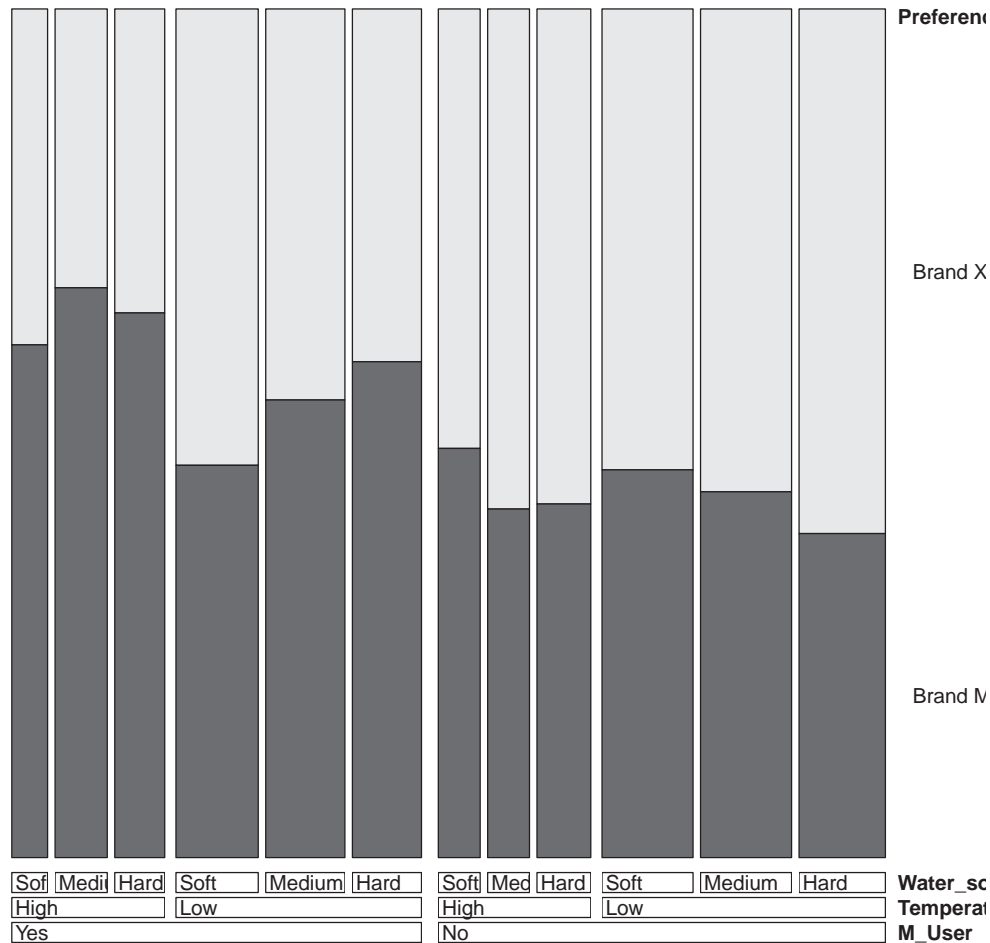
Looking at the mosaic “outside-in”, we first notice the association between `Temperature` and `Water_softness`. Next, we inspect the relationship between `M_User` and `Preference`, *given* all combinations of the other two variables. They seem associated in all cases, except for low temperature and soft water. So finally, both mosaics lead to the same conclusion.

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

★

```
> doubleddecker(Preference ~ M_User + Temperature + Water_softness, data = Detergent)
```





This shows an influence from `M_User` on preference, since all bars are higher for Yes than for No, and some additional influence of Temperature since the structure is different for High and Low (at least for respondents who previously used M).

- (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.

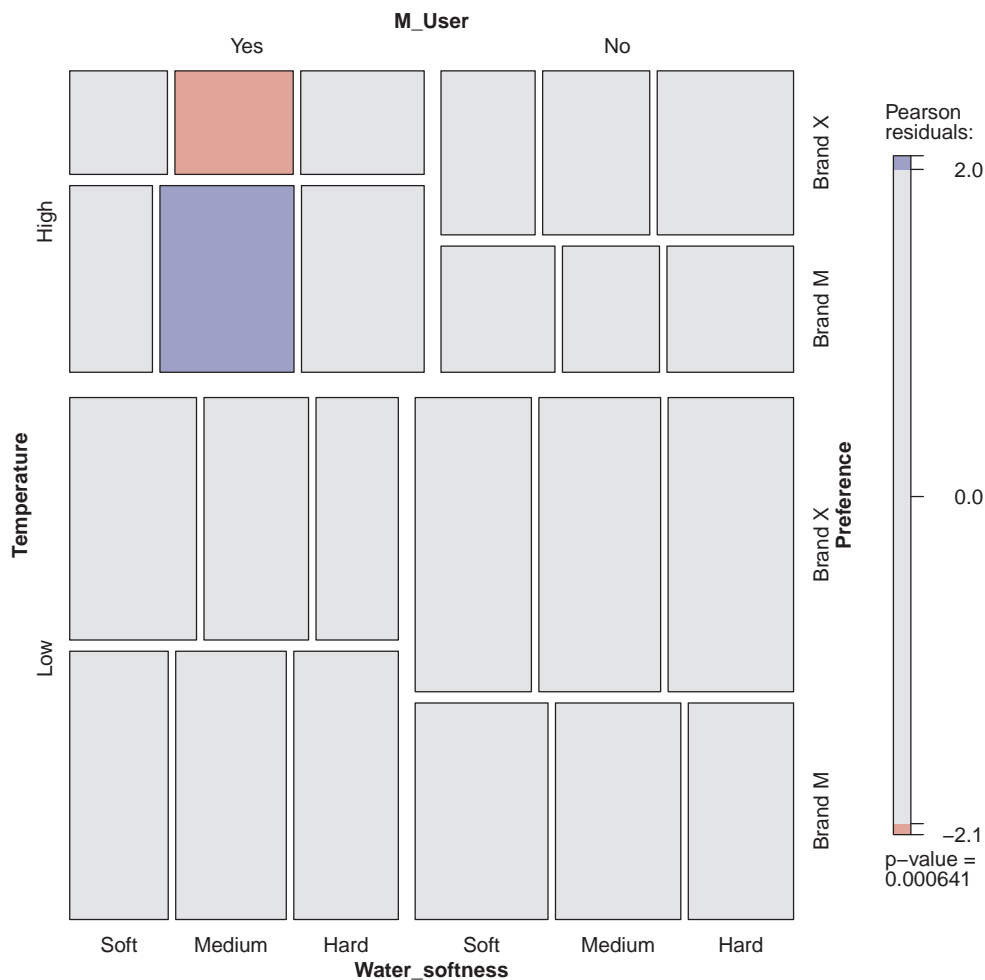
★

```
> detergent_base = loglm(~ Preference + Temperature * M_User *
+ Water_softness, data = Detergent)
> detergent_base

Call:
loglm(formula = ~Preference + Temperature * M_User * Water_softness,
      data = Detergent)

Statistics:
              X^2 df    P(> X^2)
Likelihood Ratio 32.826 11 0.00056150
Pearson          32.469 11 0.00064103

> mosaic(detergent_base)
```



The shaded tiles indicate too many M-Users using M for high temperatures and medium water softness than would be expected under the base model. A model that takes into account the findings from the exploratory analysis would be:

```
> detergent_model2 = loglm(~ Preference * M_User + Temperature *
+                           Water_softness, data = Detergent)
> detergent_model2

Call:
loglm(formula = ~Preference * M_User + Temperature * Water_softness,
      data = Detergent)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 16.248 15  0.36576
Pearson          16.727 15  0.33547
```

Although a mosaic plot with residual-based shading would still show a colored tile for this model, it is not significantly worse than the saturated 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)
```

★ Fit the independence, quasi-independence, symmetry, and quasi-symmetry models for the data `men`. These require the `gnm` (Turner and Firth, 2014) package. It is convenient to use `update()` to add terms to a model.

```
> library(gnm)
> indep <- glm(Freq ~ right + left, data = men, family=poisson)
> quasi <- update(indep, . ~ . + Diag(right, left))
> symm <- glm(Freq ~ Symm(right, left),
+             data = men, family = poisson)
> qsymm <- update(symm, . ~ right + left + .)
```

Nested models can be compared using `anova()` and all models can be compared using `LRstats()`. Note that unlike the data for women, the symmetry model is preferred over quasi-symmetry by AIC and BIC.

```
> anova(indep, quasi, qsymm, test="Chisq")

Analysis of Deviance Table

Model 1: Freq ~ right + left
Model 2: Freq ~ right + left + Diag(right, left)
Model 3: Freq ~ right + left + Symm(right, left)
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1         9      2781
2         5         81  4      2701  <2e-16 ***
3         3          1  2         79  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> # test of marginal homogeneity
> anova(symm, qsymm, test="Chisq")

Analysis of Deviance Table

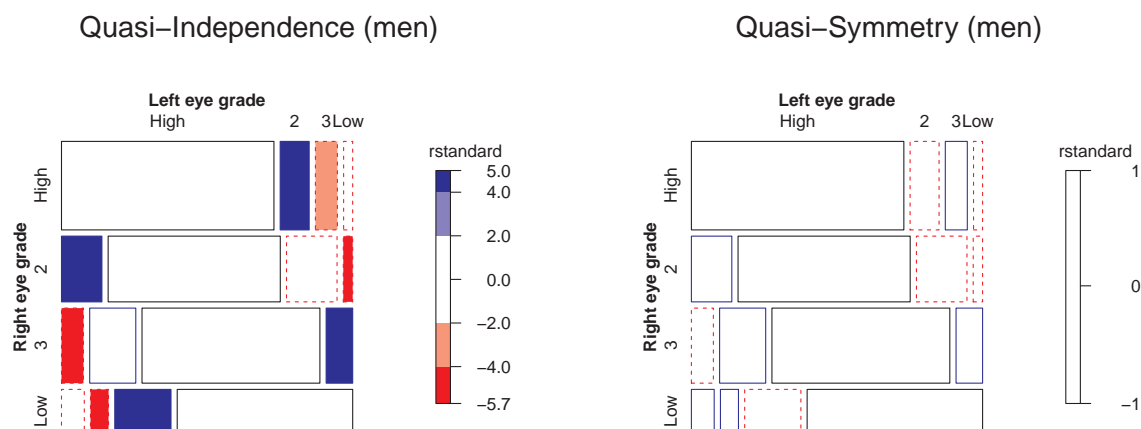
Model 1: Freq ~ Symm(right, left)
Model 2: Freq ~ right + left + Symm(right, left)
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1         6         4.77
2         3         1.09  3         3.68    0.3

> # model summaries, with AIC and BIC
> models <- glmlist(indep, quasi, symm, qsymm)
> vcdExtra::LRstats(models)

Likelihood summary table:
      AIC   BIC LR Chisq Df Pr(>Chisq)
indep 2901 2906      2781  9  < 2e-16 ***
quasi  208  217      81  5  6.6e-16 ***
symm   131  138       5  6    0.57
qsymm  133  143       1  3    0.78
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

As in the text, it is useful to display some of these using mosaic displays like Figure 10.8.

```
> labs <- c("High", "2", "3", "Low")
> largs <- list(set_varnames = c(right="Right eye grade", left="Left eye grade"),
+               set_labels=list(right=labs, left=labs))
> mosaic(quasi, ~right + left, residuals_type="rstandard", gp=shading_Friendly,
+         labeling_args=largs,
+         main="Quasi-Independence (men)" )
> mosaic(qsymm, ~right + left, residuals_type="rstandard", gp=shading_Friendly,
+         labeling_args=largs,
+         main="Quasi-Symmetry (men)" )
```



**Exercise 10.2** Table 10.1 gives a  $4 \times 4$  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()`.  
 ★ First, enter the data into a matrix and assign row and column labels (`dimnames()`).

```
> birthcontrol <- matrix(c(
+ 81, 68, 60, 38,
+ 24, 26, 29, 14,
+ 18, 41, 74, 42,
+ 36, 57, 161, 157), 4, 4, byrow=TRUE)
>
> dimnames(birthcontrol) <-
+   list("presex" = c("WRONG", "Wrong", "wrong", "OK"),
+        "birthcontrol" = c("DISAGREE", "disagree", "agree", "AGREE"))
> birthcontrol
```

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

`loglm()` can handle the data in matrix form.

```
> loglm(~presex + birthcontrol, data=birthcontrol)
Call:
loglm(formula = ~presex + birthcontrol, data = birthcontrol)

Statistics:
              X^2 df P(> X^2)
Likelihood Ratio 127.65  9      0
Pearson          128.68  9      0
```

`glm()` requires that the data be converted to a data frame, but is much more capable in the results it gives.

```

> birthcontrol.df <- as.data.frame(as.table(birthcontrol))
> birth.indep <- glm(Freq ~ presex + birthcontrol,
+                   data = birthcontrol.df, family = poisson)
> summary(birth.indep)

Call:
glm(formula = Freq ~ presex + birthcontrol, family = poisson,
    data = birthcontrol.df)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4.547  -2.582   0.067   1.652   5.258

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)      3.7474    0.0962  38.95 < 2e-16 ***
presexWrong     -0.9768    0.1217  -8.03  9.8e-16 ***
presexwrong     -0.3446    0.0988  -3.49  0.00049 ***
presexOK         0.5092    0.0805   6.32  2.5e-10 ***
birthcontroldisagree 0.1886    0.1072   1.76  0.07861 .
birthcontrolagree  0.7118    0.0968   7.35  2.0e-13 ***
birthcontrolAGREE  0.4565    0.1014   4.50  6.7e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 431.08  on 15  degrees of freedom
Residual deviance: 127.65  on  9  degrees of freedom
AIC: 232.3

Number of Fisher Scoring iterations: 5
> anova(birth.indep)

Analysis of Deviance Table

Model: poisson, link: log

Response: Freq

Terms added sequentially (first to last)

      Df Deviance Resid. Df Resid. Dev
NULL              15          431
presex             3       236.3
birthcontrol       3        67.1

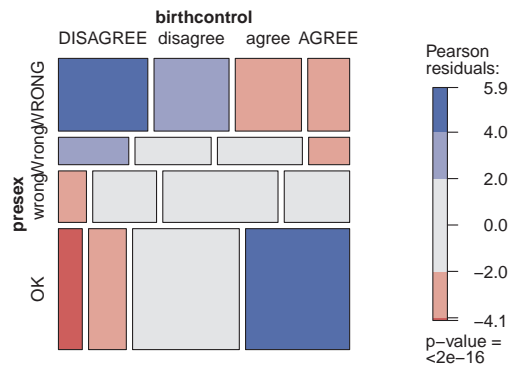
```

- (b) Make a mosaic display showing departure from independence and describe verbally the pattern of association.  
 ★ Those who believe that premarital sex is wrong disagree that birth control should be made available to teenagers, in relation to the strength of their opinion about premarital sex. Only those who believe that premarital sex is OK support birth control for teenagers.

```

> mosaic(birthcontrol, shade=TRUE)

```



- (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.

★ The  $L \times L$  model fits appreciably better than the independence model, for a “cost” of only one extra parameter in the model.

```
> library(gnm)
> linlin <- gnm(Freq ~ presex + birthcontrol +
+               as.numeric(presex) * as.numeric(birthcontrol),
+               data=birthcontrol.df, family=poisson)
> anova(birth.indep, linlin, test="Chisq")

Analysis of Deviance Table

Model 1: Freq ~ presex + birthcontrol
Model 2: Freq ~ presex + birthcontrol + as.numeric(presex) + as.numeric(birthcontrol) +
  as.numeric(presex):as.numeric(birthcontrol)
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1           9      127.7
2           8       11.5  1      116    <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- (d) Fit the RC(1) model with `gnm()`, and test the difference of this against the model of uniform association.

★ The  $L \times L$  model and the RC(1) model both fit well, but the former, with only one parameter for association, is deemed best by AIC and BIC.

```
> RC <- gnm(Freq ~ presex + birthcontrol + Mult(presex, birthcontrol),
+           data=birthcontrol.df, family=poisson, verbose=FALSE)
> anova(linlin, RC, test="Chisq")

Analysis of Deviance Table

Model 1: Freq ~ presex + birthcontrol + as.numeric(presex) + as.numeric(birthcontrol) +
  as.numeric(presex):as.numeric(birthcontrol)
Model 2: Freq ~ presex + birthcontrol + Mult(presex, birthcontrol)
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1           8       11.53
2           4        7.14  4      4.39    0.36

> # compare all models
> LRstats(birth.indep, linlin, RC)

Likelihood summary table:
      AIC BIC LR Chisq Df Pr(>Chisq)
birth.indep 232 238 127.7  9    <2e-16 ***
linlin      118 124  11.5  8     0.17
RC          122 131   7.1  4     0.13
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- (e) Write a brief summary of these results, including plots useful for explaining the relationships in this data set.

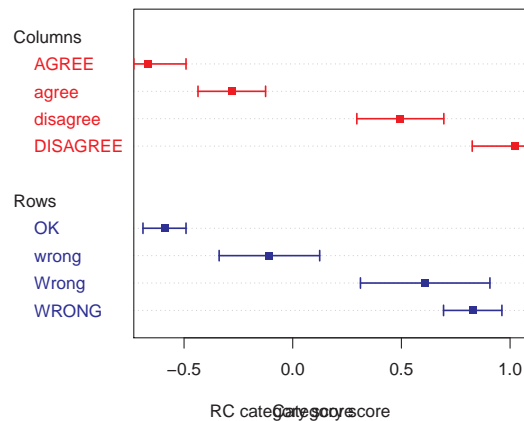
★ Essentially, the association of attitudes toward premarital sex and birth control is that of two ordinal variables: the more one disagrees with premarital sex, the less one is likely to support birth control

for teenagers. The uniform association model, `linlin`, is the most parsimonious, assuming that the categories of `presex` and `birthcontrol` are equally spaced. From the coefficient for the  $L \times L$ , one can say that each step toward viewing premarital sex as OK multiplies the odds of agreement with birth control by 1.33, an increase of 33%.

```
> # odds ratio interpretation
> exp(coef(linlin)[10])
as.numeric(presex):as.numeric(birthcontrol)
1.3309
```

The `logmult` package also fits the RC(1) model and provides a useful plot of the category scores together with confidence intervals via its `plot()` method. From this it can be seen that there is little reason to question that the category scores are equally spaced, except possibly for the WRONG and Wrong categories of `presex`.

```
> library(logmult)
> rcl <- rc(birthcontrol, verbose=FALSE, weighting="marginal", se="jackknife")
Computing jackknife standard errors...
> plot(rcl, pch=15, conf=.95)
> title(xlab="RC category score")
```



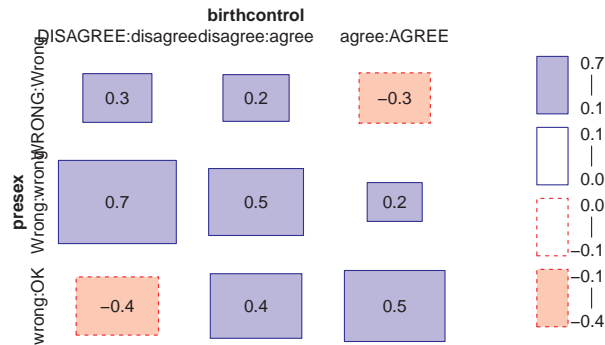
**Exercise 10.3** For the data on attitudes toward birth control in Table 10.1,

- (a) Calculate and plot the observed local log odds ratios.  
 ★ The (log) odds ratios give the log odds of a 1-step change in attitude toward birth control for a 1-step change in the attitude toward premarital sex. Note that the mean of these values is similar to the common log odds ratio fit by the model of uniform association.

```
> (LOR <- loddsratio(birthcontrol))
log odds ratios for presex and birthcontrol
      birthcontrol
presex  DISAGREE:disagree disagree:agree agree:AGREE
WRONG:Wrong      0.25498      0.23436     -0.27148
Wrong:wrong      0.74316      0.48129      0.16184
wrong:OK        -0.36367      0.44786      0.54124
> exp(mean(as.matrix(LOR)))
[1] 1.2811
```

A simple plot of these is a `tile()` plot, showing how the odds ratios change systematically in each row, decreasing in the first two rows, but increasing in the last row. This is similar to the `corrplot()` shown in Figure 10.2 in the text.

```
> tile(LOR)
```



(b) Also fit the R, C, and R+C models.

★

```
> Rscore <- as.numeric(birthcontrol.df$presex)
> Cscore <- as.numeric(birthcontrol.df$birthcontrol)
>
> # row effects model (mental)
> roweff <- glm(Freq ~ presex + birthcontrol +
+               presex:Cscore,
+               family = poisson, data = birthcontrol.df)
>
> coleff <- glm(Freq ~ presex + birthcontrol +
+               Rscore:birthcontrol,
+               family = poisson, data = birthcontrol.df)
>
> RplusC <- glm(Freq ~ presex + birthcontrol +
+               Rscore:birthcontrol + presex:Cscore,
+               family = poisson, data = birthcontrol.df)
>
> LRstats(birth.indep, roweff, coleff, RplusC, linlin)
```

```
Likelihood summary table:
      AIC BIC LR Chisq Df Pr(>Chisq)
birth.indep 232 238 127.7 9 <2e-16 ***
roweff      120 128 9.5 6 0.15
coleff      120 128 9.1 6 0.17
RplusC      122 131 6.9 4 0.14
linlin      118 124 11.5 8 0.17
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(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.

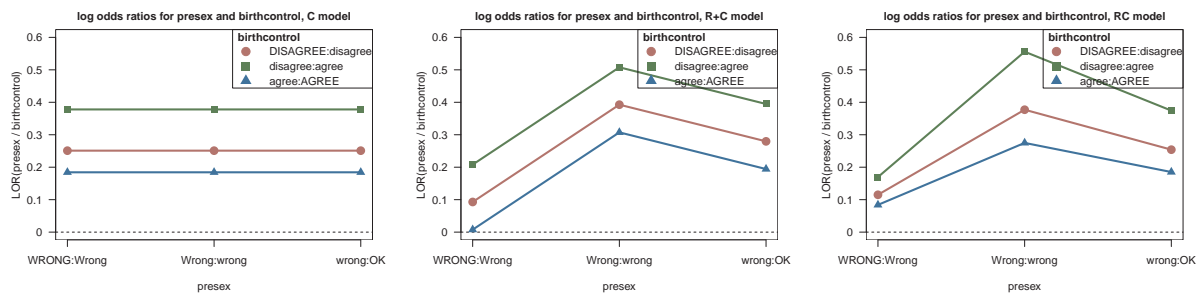
★ Here is a simple function to extract the fitted values from a given model, calculate the log odds ratios, and plot them.

```
> plot_LOR_fit <- function(model, data, ...) {
+   dim <- dim(data)
+   fit <- matrix(fitted(model), nrow=dim[1], ncol=dim[2], dimnames=dimnames(data))
+   plot(LOR <- loddsratio(fit), ...)
+   invisible(LOR)
+ }
```

Using this, we plot the C, R+C, and RC(1) models below in the style shown in Figure 10.4 in the text. These plots show quite clearly how these models differ in the structure of their fitted log odds ratios.

```
> plot_LOR_fit(coleff, birthcontrol, confidence=FALSE, ylim=c(0, .6),
+   main="log odds ratios for presex and birthcontrol, C model")
>
> plot_LOR_fit(RplusC, birthcontrol, confidence=FALSE, ylim=c(0, .6),
+   main="log odds ratios for presex and birthcontrol, R+C model")
>
> plot_LOR_fit(RC, birthcontrol, confidence=FALSE, ylim=c(0, .6),
+   main="log odds ratios for presex and birthcontrol, RC 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 illustrated in Example 10.4. Summarize these statistical tests in a table.

★ Only the RC2 model fits here.

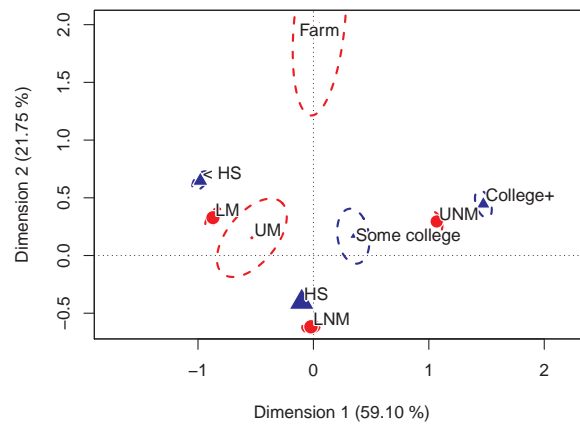
```
> Women.df <- as.data.frame(as.table(Women.tab))
> indep <- glm(Freq ~ Education + Occupation,
+             data = Women.df, family = poisson)
> library(logmult)
> RC1 <- rc(Women.tab, verbose=FALSE, weighting="marginal", se="jackknife")
Computing jackknife standard errors...
> RC2 <- rc(Women.tab, verbose=FALSE, weighting="marginal", se="jackknife", nd=2)
Computing jackknife standard errors...
> LRstats(indep, RC1, RC2)

Likelihood summary table:
      AIC  BIC  LR Chisq Df Pr(>Chisq)
indep 1506 1514    1373  12   <2e-16 ***
RC1    269  283    125   6   <2e-16 ***
RC2    153  171     1   2    0.74
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

★ Dimension 1 most clearly corresponds to Education, ordered from low (< HS) to high (College). Dimension 2 largely reflects the Occupation categories, with `Farm` being most different from the others.

```
> plot(RC2, conf=0.68, cex=1.5)
```



- (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).

★ Given that the RC(1) model does not fit very well here, there is little chance that a simpler model using integer scores would be adequate.

## 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.

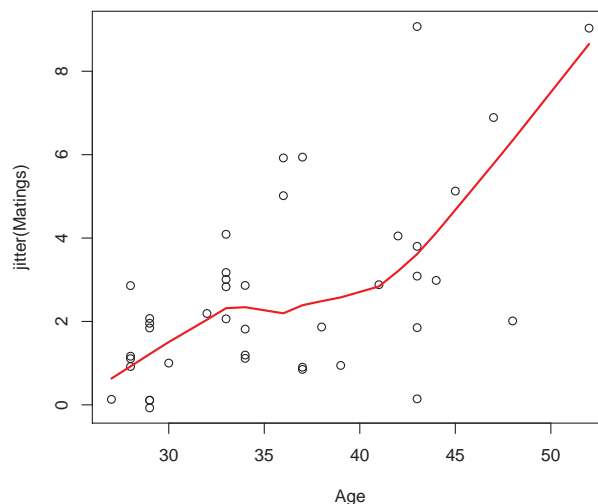
```
> data("case2201", package="Sleuth2")
> elephants <- case2201
> str(elephants)

'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.

★ The simplest plot just jitters the number of matings, and draws a smoothed lowess curve.

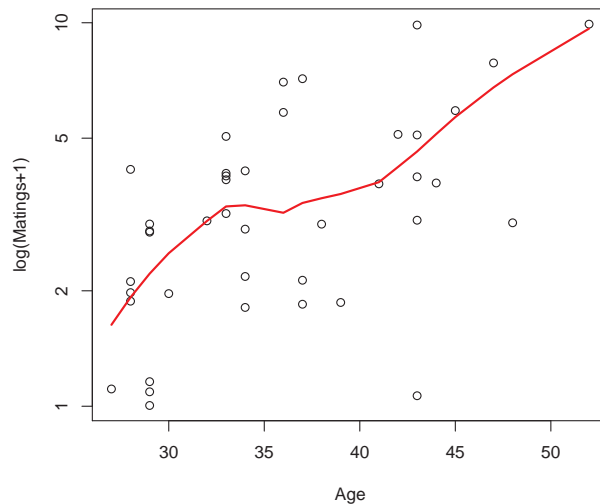
```
> with(elephants, {
+   plot(jitter(Matings) ~ Age)
+   lines(lowess(Age, Matings), lwd=2, col="red")}
+ )
```



- (b) Repeat (a) above, but now plotting  $\log(\text{Matings}+1)$  against *Age* to approximate a Poisson regression with a log link and avoid problems with the zero counts.

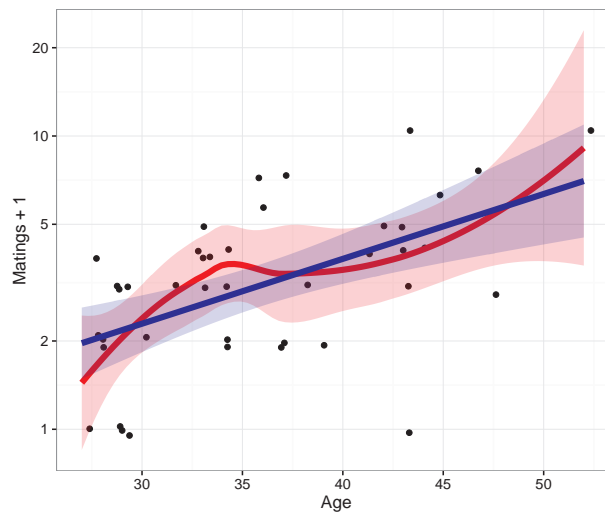
★ As noted in the text, you can use `log="y"`, but then the Y variable should be used as *Y+1* to avoid problems with 0 counts.

```
> with(elephants, {
+   plot(jitter(Matings+1) ~ Age, log="y", ylab="log(Matings+1)")
+   lines(lowess(Age, Matings+1), lwd=2, col="red")}
+ )
```



ggplot2 makes it easy to make a similar plot, and to also overlay the fit of a linear model. This also shows error bands for the loess and linear fits.

```
> library(ggplot2)
> ggplot(elephants, aes(x=Age, y=Matings+1)) +
+   geom_jitter() +
+   geom_smooth(method="loess", color="red", size=2, fill="red", alpha=0.2) +
+   geom_smooth(method="lm", color="blue", size=2, fill="blue", alpha=0.2) +
+   scale_y_log10(breaks=c(1,2,5,10, 20)) +
+   theme_bw()
```



- (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.)

★ `Age-27` shifts the value of intercept to the minimum value in the data. In a model formula, use `I(Age-27)`. The coefficient for `Age` then relates to increments in  $\log(\text{Matings})$ ; exponentiating the coefficient give the multiple of Matings for a unit change in Age.

```
> elephants.mod1 <- glm(Matings ~ I(Age-27), data=elephants, family=poisson)
> coef(elephants.mod1)

(Intercept) I(Age - 27)
0.272698    0.068693

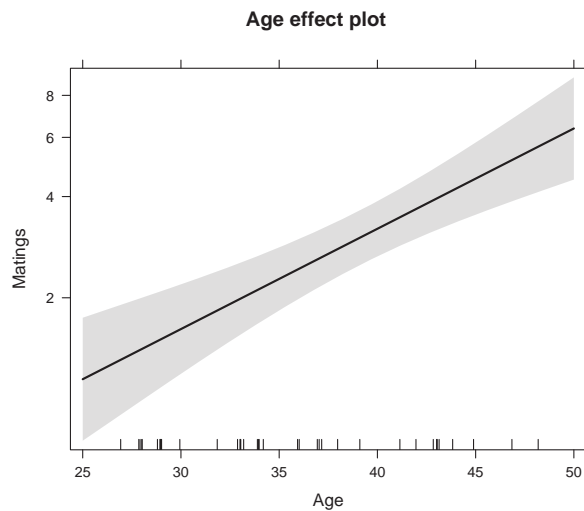
> exp(coef(elephants.mod1))

(Intercept) I(Age - 27)
1.3135      1.0711
```

Thus, at Age 27, these elephants have a predicted 1.31 matings. For each additional year, matings

are expected to be multiplied by 1.07, an increase of 7%. Perhaps the best way to visualize the model predictions are through an effect plot.

```
> plot(Effect("Age", elephants.mod1,
+         xlevels=list(Age=seq(25, 50, 5))))
```



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

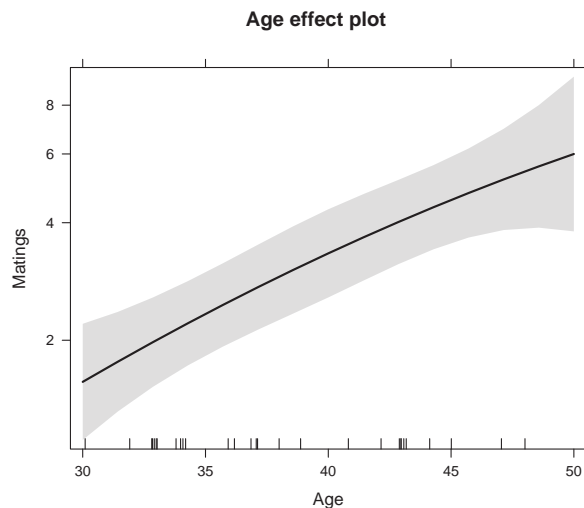
★ There is little evidence for nonlinearity, as evidenced by a test of the quadratic model in Age, or by a plot of the predicted values under this model.

```
> elephants.mod1q <- glm(Matings ~ poly(Age, 2), data=elephants, family=poisson)
> anova(elephants.mod1, elephants.mod1q, test="Chisq")
```

Analysis of Deviance Table

```
Model 1: Matings ~ I(Age - 27)
Model 2: Matings ~ poly(Age, 2)
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1         39      51.0   1    0.185    0.67
2         38      50.8
```

```
> plot(allEffects(elephants.mod1q))
```



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

★ The simple way to assess overdispersion is via `dispersiontest()`, which is not significant here. A more careful answer would fit and compare the overdispersed models suggested.

```
> dispersiontest(elephants.mod1)

Overdispersion test

data:  elephants.mod1
z = 0.496, p-value = 0.31
alternative hypothesis: true dispersion is greater than 1
sample estimates:
dispersion
      1.108
```

**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?

★ For such a factorial design, a useful first step is to examine the sample sizes in the cells of this 4-way classification. The table below shows that the design is very unbalanced, and that there are no slow learners (SL) in age F3.

```
> quine.tab <- xtabs(~ Lrn + Age + Sex + Eth, data=quine)
> ftable(Age + Sex ~ Lrn + Eth, data=quine.tab)
```

Lrn	Eth	Age F0		F1		F2		F3	
		Sex F	M	F	M	F	M	F	M
AL	A	4	5	5	2	1	7	9	7
	N	4	6	6	2	1	7	10	7
SL	A	1	3	10	3	8	4	0	0
	N	1	3	11	7	9	3	0	0

Age here corresponds to “Form”, or grade in school, arguably an ordered factor, so we make it so. The Poisson model `Anova()` shows that all terms are significant. `summary()` shows that the effects of Age have significant linear, quadratic and cubic trends.

```
> data("quine", package="MASS")
> quine$Age <- ordered(quine$Age)
> quine.mod1 <- glm(Days ~ ., data=quine, family=poisson)
> Anova(quine.mod1)
```

Analysis of Deviance Table (Type II tests)

Response: Days

	LR	Chisq	Df	Pr(>Chisq)
Eth	166.8	1	< 2e-16	***
Sex	14.4	1	0.00015	***
Age	168.3	3	< 2e-16	***
Lrn	45.8	1	1.3e-11	***

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
> summary(quine.mod1)
```

Call:  
glm(formula = Days ~ ., family = poisson, data = quine)

Deviance Residuals:

Min	1Q	Median	3Q	Max
-6.81	-3.06	-1.12	1.82	9.91

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	2.8033	0.0434	64.55	< 2e-16 ***
EthN	-0.5336	0.0419	-12.74	< 2e-16 ***
SexM	0.1616	0.0425	3.80	0.00015 ***
Age.L	0.4192	0.0471	8.90	< 2e-16 ***
Age.Q	0.2519	0.0497	5.06	4.1e-07 ***
Age.C	-0.3013	0.0410	-7.34	2.1e-13 ***
LrnSL	0.3489	0.0520	6.70	2.0e-11 ***

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

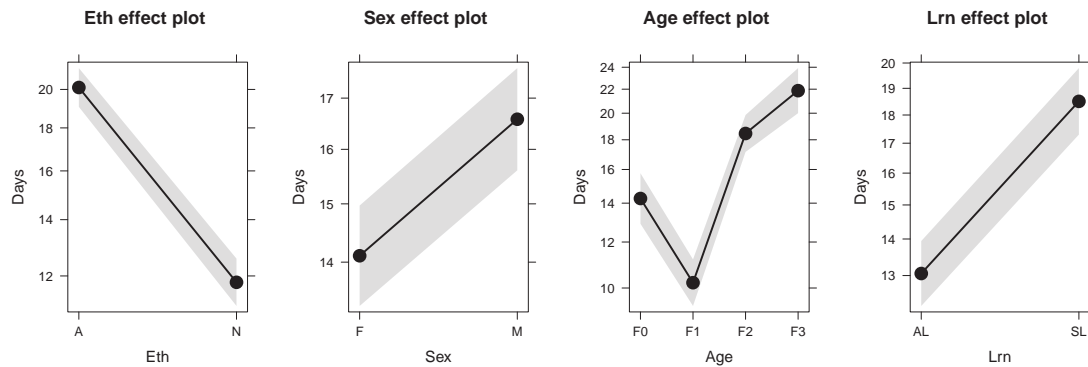
Null deviance: 2073.5 on 145 degrees of freedom

```
Residual deviance: 1696.7 on 139 degrees of freedom
AIC: 2299
```

```
Number of Fisher Scoring iterations: 5
```

Although not asked in the question, a careful analysis will try to understand the fitted model, e.g., via an effect plot.

```
> plot(allEffects(quine.mod1), rows=1, cols=4, ci.style='bands')
```



- (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).

★ `dispersiontest()` reveals very substantial overdispersion, with variance approximately  $\hat{\phi} = 13.2$  times the mean under this model.

```
> library(AER)
> dispersiontest(quine.mod1)

Overdispersion test

data: quine.mod1
z = 5.47, p-value = 2.3e-08
alternative hypothesis: true dispersion is greater than 1
sample estimates:
dispersion
12.53

> quine.mod1q <- glm(Days ~ ., data=quine, family=quasipoisson)
```

- (c) Carry out the same significance tests and explain why the results differ from those for the Poisson model.
- ★ The `Anova()` tests for the quasi-Poisson model `quine.mod1q` show that only ethnicity and age have significant effects, learner status nearly so. Relative to the standard Poisson model, the coefficients are the same, but the standard errors have been adjusted by a factor of  $\hat{\phi}^{-1/2} = 0.28$

```
> Anova(quine.mod1q)

Analysis of Deviance Table (Type II tests)

Response: Days
  LR  Chisq Df Pr(>Chisq)
Eth  12.67  1  0.00037 ***
Sex   1.09  1  0.29560
Age  12.78  3  0.00513 **
Lrn   3.48  1  0.06218 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> coeftest(quine.mod1q)

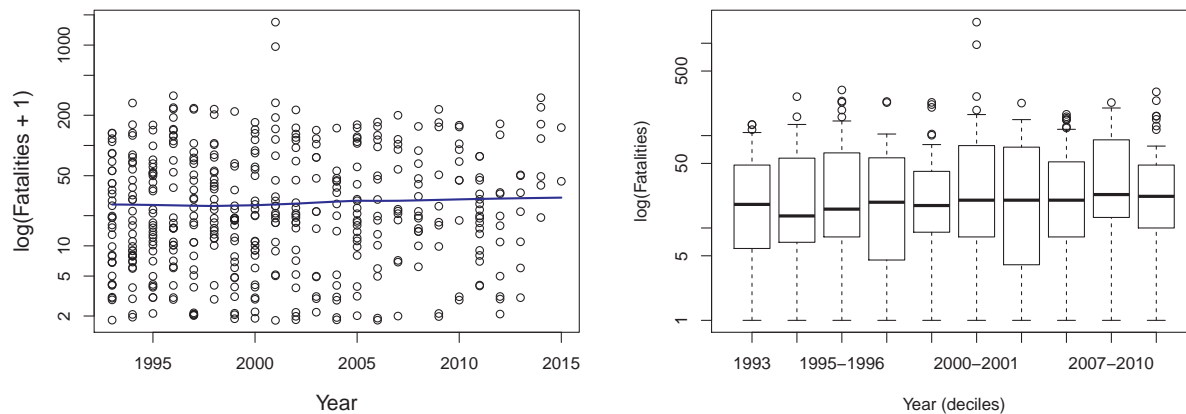
z test of coefficients:

            Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.803      0.158    17.79 < 2e-16 ***
EthN         -0.534      0.152    -3.51 0.00045 ***
SexM          0.162      0.154     1.05 0.29510
Age.L         0.419      0.171     2.45 0.01418 *
Age.Q         0.252      0.181     1.40 0.16288
Age.C        -0.301      0.149    -2.02 0.04297 *
LrnSL         0.349      0.189     1.85 0.06463 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

**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.
- ★ Both *Phase* and *Cause* are unordered factors, whose levels are ordered lexically. For graphics and analysis it is useful to reorder *Phase* in temporal order. Plots of the total number fatalities over Year, in either jittered scatterplot or boxplot form show no overall trend. (Other plots, not shown here, indicate that the number of crashes has decreased over time.) As in the text, we plot these on a log scale.

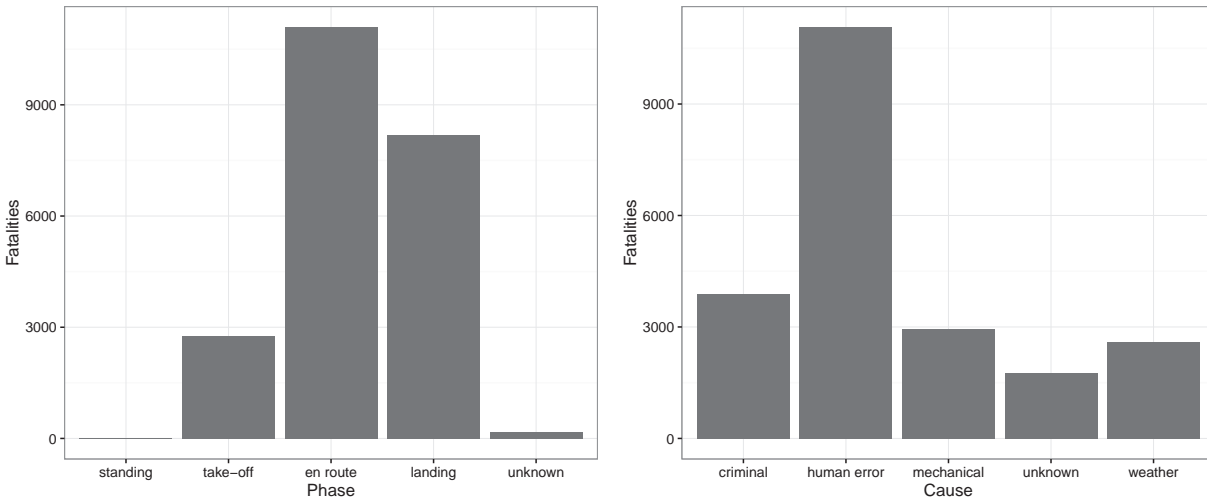
```
> AirCrash$Phase <- factor(AirCrash$Phase,
+                           levels=c("standing", "take-off", "en route", "landing", "unknown"))
> with(AirCrash, {
+   plot(jitter(Fatalities+1) ~ Year, log="y",
+        ylab = "log(Fatalities + 1)", cex.lab=1.25)
+   lines(lowess(Year, Fatalities+1), col="blue", lwd=2)
+ })
> plot(Fatalities ~ cutfac(Year), data=AirCrash, log="y",
+      ylab = "log(Fatalities)", xlab="Year (deciles)")
```



Plots of fatalities against the factors can be done in a variety of forms. Here we use *ggplot2* for bar charts. Note the use of `geom_bar(aes(weight=Fatalities))`, so that the height of each bar is proportional to the number of fatalities; otherwise, it would just show the number of crashes.

```
> ggplot(AirCrash, aes(Phase)) + geom_bar(aes(weight=Fatalities)) +
+   ylab("Fatalities") + theme_bw()
> ggplot(AirCrash, aes(Cause)) + geom_bar(aes(weight=Fatalities)) +
+   ylab("Fatalities") + theme_bw()
```





- (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?

★

```
> crash.mod1 <- glm(Fatalities ~ Phase + Cause + Year,
+                   data=AirCrash, family=poisson)
> Anova(crash.mod1)
```

Analysis of Deviance Table (Type II tests)

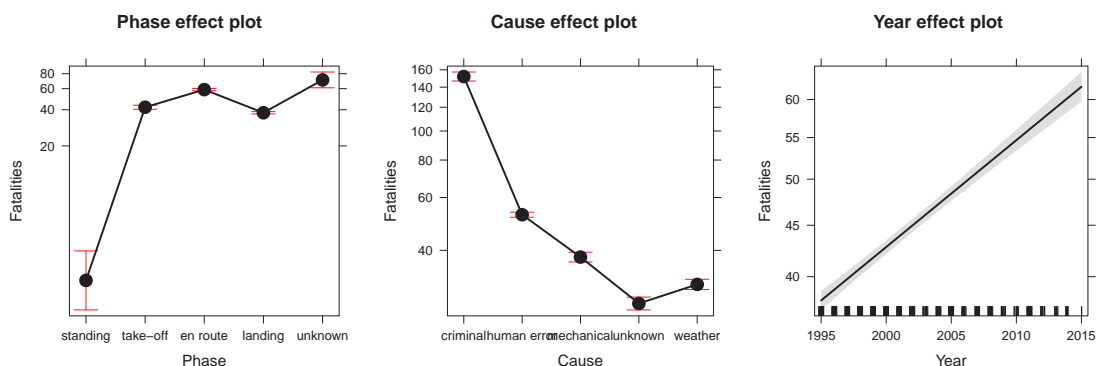
Response: Fatalities

	LR	Chisq	Df	Pr(>Chisq)
Phase	1586	4		<2e-16 ***
Cause	5004	4		<2e-16 ***
Year	436	1		<2e-16 ***

---  
 Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

From the marginal plots for part (a), it appears that most fatalities occur en route or on landing, and the primary cause is human error. However, an effects plot for the main effects model, where other factors are controlled in a given panel, tells a different story: Unknown phase rises to the top, and the greatest cause is criminal activity. The plot for *Year* is slightly misleading, because the range is relatively small compared to the other panels. This can be avoided by setting `ylim=log(c(1,180))` in the plot.

```
> plot(allEffects(crash.mod1), rows=1, cols=3)
```



- (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.

★ A careful analysis would investigate the tradeoff between goodness-of-fit and parsimony in the choice of degrees of freedom. Here we just illustrate the use of `ns(Year, 3)`, allowing 3 df for the *Year* effect. This fits significantly better than the linear model in *Year*.

```
> library(splines)
> crash.mod2 <- glm(Fatalities ~ Phase + Cause + ns(Year,3),
+                   data=AirCrash, family=poisson)
```

```
> anova(crash.mod1, crash.mod2, test="Chisq")

Analysis of Deviance Table

Model 1: Fatalities ~ Phase + Cause + Year
Model 2: Fatalities ~ Phase + Cause + ns(Year, 3)
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1         429      30833
2         427      30724  2      109    <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- (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.

★ We don't show a complete analysis here. `add1()` just looks at each of the two-way interaction terms and reports that adding each one, separately, would decrease the deviance and AIC, resulting in a better-fitting model. `stepAIC()` eventually includes all three two-way terms.

```
> add1(crash.mod2, scope=~.^2, test="Chisq")

Single term additions

Model:
Fatalities ~ Phase + Cause + ns(Year, 3)
      Df Deviance   AIC   LRT Pr(>Chi)
<none>          30724 32862
Phase:Cause     11   29959 32119   765    <2e-16 ***
Phase:ns(Year, 3) 11   30395 32554   329    <2e-16 ***
Cause:ns(Year, 3) 12   28626 30788  2098    <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> # refit the stepAIC final model
> crash.modAIC <- update(crash.mod2, .~. + Phase:Cause + Phase:ns(Year, 3) + Cause:ns(Year, 3))
> Anova(crash.modAIC)

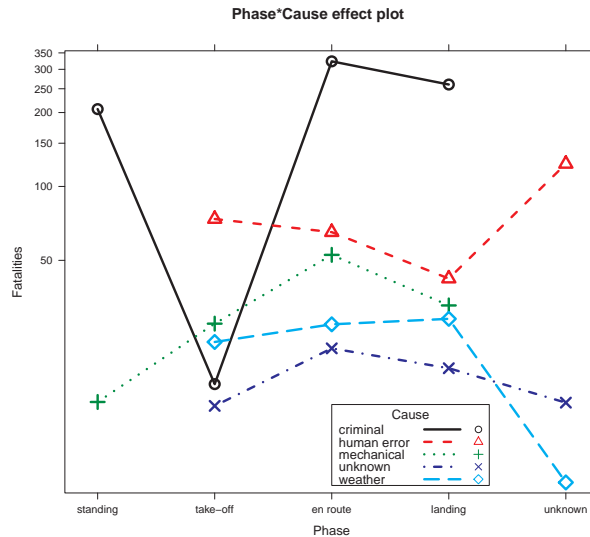
Analysis of Deviance Table (Type II tests)

Response: Fatalities
      LR Chisq Df Pr(>Chisq)
Phase      703  4    <2e-16 ***
Cause     4654  4    <2e-16 ***
ns(Year, 3)  480  3    <2e-16 ***
Phase:Cause  426  8    <2e-16 ***
Phase:ns(Year, 3) 194  8    <2e-16 ***
Cause:ns(Year, 3) 2049 12    <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

★ The number of fatalities in air crashes depends in a complex way on the combinations of Phase, Cause and Year. We illustrate this below with an effect plot for the interaction of Phase and Cause, the interpretation of which just entails trying to describe the patterns in the plot.

```
> plot(Effect(c("Phase", "Cause"), crash.modAIC),
+       multiline=TRUE, lwd=3, key.args=list(x=0.5, y=0.2))
```



**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)
```

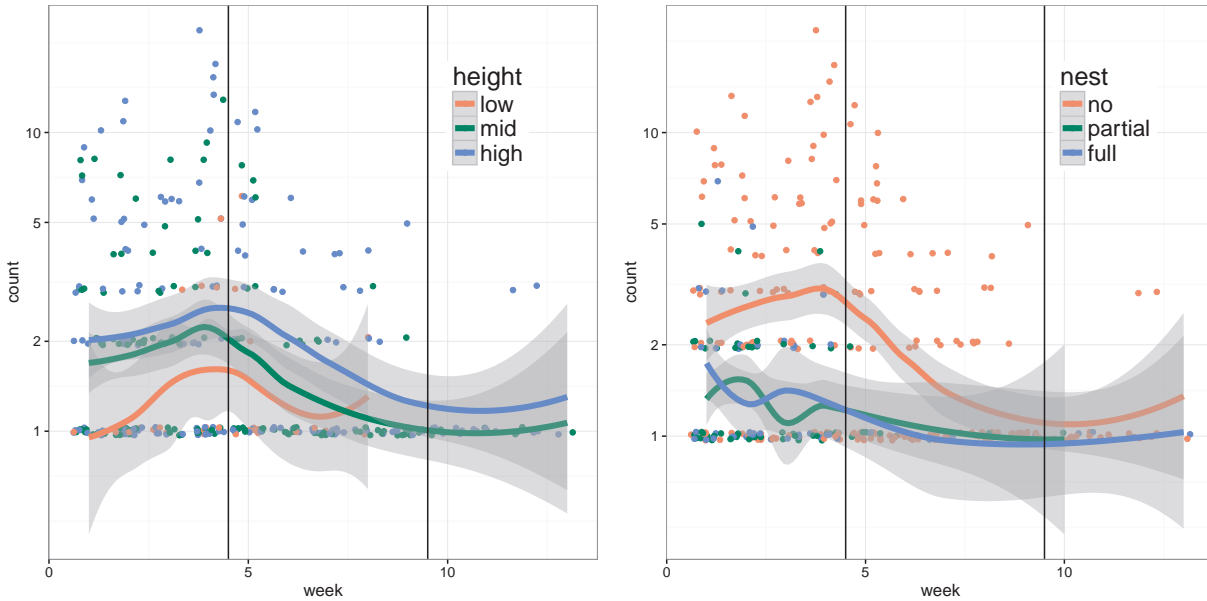
	category	week	station	nest	height	density	tree_health	count
4	Pre	1	C1	partial	high	few	healthy	2
34	Pre	1	B1	no	high	few	dead	1
143	Pre	3	B2	no	mid	few	dead	1
155	Incubation	4	C2	no	mid	few	dead	13
160	Incubation	4	C2	partial	high	few	healthy	1
175	Incubation	4	C4	partial	high	few	dead	3
240	Incubation	6	C2	no	mid	moderate	dead	1
250	Incubation	6	C4	no	high	few	dead	1
314	Incubation	9	B2	no	mid	few	healthy	2
340	<NA>	12	B1	no	high	few	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.

★ Here we use *ggplot2* to plot `count` against `week`, stratified by `height` and `nest`. The plot for `height` shows that counts of advertising birds increase with height in the tree and rise over week at the end of the pre-breeding portion of the season.

```
> my_theme <- theme_bw() +
+   theme(legend.position = c(0.8, 0.8),
+         legend.title = element_text(size=18),
+         legend.text = element_text(size=16))
>
> ggplot(Cormorants, aes(week, count, color=height)) +
+   geom_jitter() +
+   stat_smooth(method="loess", size=2) +
+   scale_y_log10(breaks=c(1,2,5,10)) +
+   geom_vline(xintercept=c(4.5, 9.5)) +
+   my_theme
>
> ggplot(Cormorants, aes(week, count, color=nest)) +
+   geom_jitter() +
+   stat_smooth(method="loess", size=2) +
```

```
+ scale_y_log10(breaks=c(1,2,5,10)) +
+ geom_vline(xintercept=c(4.5, 9.5)) +
+ my_theme
```



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

★ All terms except `tree_health` show significant main effects.

```
> fit1 <- glm(count ~ week + station + nest + height + density + tree_health, data=Cormorants,
+ family = poisson)
> library(car)
> Anova(fit1)

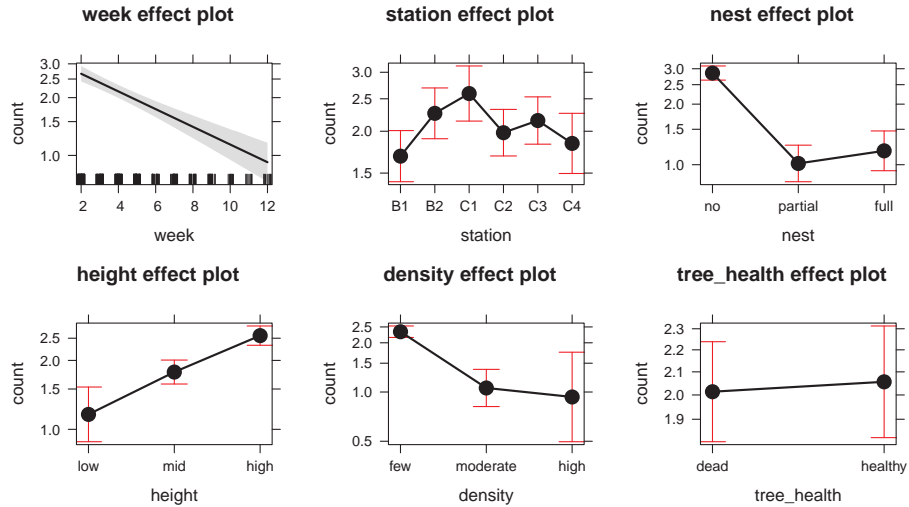
Analysis of Deviance Table (Type II tests)

Response: count
      LR Chisq Df Pr(>Chisq)
week      62.8  1  2.3e-15 ***
station   14.1  5   0.015 *
nest     137.8  2  < 2e-16 ***
height    48.0  2  3.8e-11 ***
density   47.3  2  5.5e-11 ***
tree_health  0.1  1   0.792
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(c) Interpret this model using an effects plot.

★ According to the linear model, counts (a) decrease over weeks in the seasons; (b) are greatest with no nests; (c) increase with height in the tree and (d) are greatest when the density is low.

```
> library(effects)
> plot(allEffects(fit1))
```



- (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.

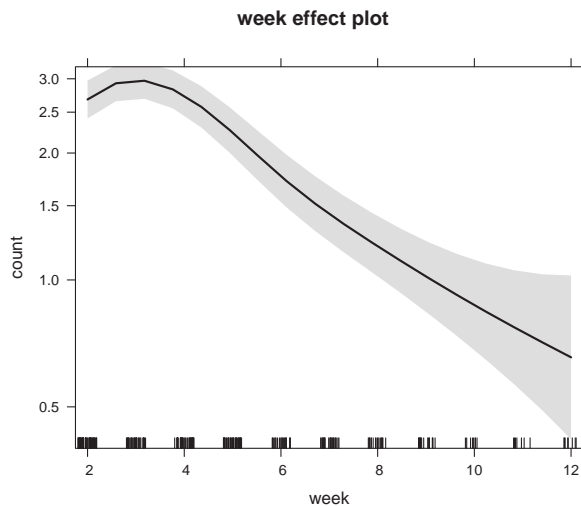
★ Here we drop `tree_health` and use a natural spline with 3 degrees of freedom for `week` to allow a moderate departure from linearity, roughly comparable to a cubic term `poly(week, 3)` in complexity. The effect plot for `week` shows a pronounced rise over the early weeks, followed by a steady decline over the rest of the season.

```
> library(splines)
> fit2 <- glm(count ~ ns(week, 3) + station + nest + height + density, data=Cormorants,
+             family = poisson)
> Anova(fit2)
```

Analysis of Deviance Table (Type II tests)

```
Response: count
          LR Chisq Df Pr(>Chisq)
ns(week, 3)   98.8  3  < 2e-16 ***
station       17.5  5   0.0036 **
nest         129.3  2  < 2e-16 ***
height        59.2  2   1.4e-13 ***
density       48.7  2   2.6e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> plot(Effect("week", fit2))
```



A more thorough analysis would investigate whether there are important interactions among the model terms. The model below checks whether there are interactions of `week` with any of the other factors.

The conclusion is no.

```
> fit3 <- update(fit2, . ~ . + week * (station + nest + height + density))
> Anova(fit3)

Analysis of Deviance Table (Type II tests)

Response: count
      LR Chisq Df Pr(>Chisq)
ns(week, 3)    34.3  2  3.6e-08 ***
station        16.7  5   0.0051 **
nest          129.9  2  < 2e-16 ***
height         59.1  2  1.5e-13 ***
density        48.4  2  3.0e-11 ***
week              0
station:week     1.2  5   0.9449
nest:week        0.0  2   0.9771
height:week      2.7  2   0.2647
density:week     3.5  2   0.1742
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- (e) Test this model for overdispersion, using either a quasipoisson family or `dispersiontest()` in AER.  
 ★ Using `dispersiontest()` on the `fit1` and `fit2` models shows significant overdispersion for the former, but not for the latter. This illustrates that the test for overdispersion assumes that the model is correctly specified.

```
> require(AER)
> dispersiontest(fit1)

Overdispersion test

data:  fit1
z = 1.79, p-value = 0.036
alternative hypothesis: true dispersion is greater than 1
sample estimates:
dispersion
 1.3713

> dispersiontest(fit2)

Overdispersion test

data:  fit2
z = 1.19, p-value = 0.12
alternative hypothesis: true dispersion is greater than 1
sample estimates:
dispersion
 1.1782
```

**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.

★ We illustrate this only for fitting the negative binomial model to the `intensity` variable, the count of parasites. The four areas A1–A4 are ordered from East to West, so the easiest way to do this test of linearity is to create a numeric equivalent.

```
> data("CodParasites", package = "countreg")
>
> ## omit NAs in response
> CodParasites <- subset(CodParasites, !is.na(intensity))
>
> # make a numeric variable from area
> CodParasites$areaEW <- as.numeric(CodParasites$area)
```

Then, we fit negative binomial models with `area` as a factor, and `areaEW` as a numeric variable.

```
> library(MASS)
> cp_nb <- glm.nb(intensity ~ length + area * year, data = CodParasites)
> cp_nb_lin <- glm.nb(intensity ~ length + areaEW * year, data = CodParasites)
> Anova(cp_nb_lin)

Analysis of Deviance Table (Type II tests)

Response: intensity
```

```

length      LR Chisq Df Pr(>Chisq)
areaEW      44.1    1   3.2e-11 ***
year        25.2    2   3.3e-06 ***
areaEW:year  17.2    2   0.00019 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova(cp_nb_lin, cp_nb, test="Chisq")

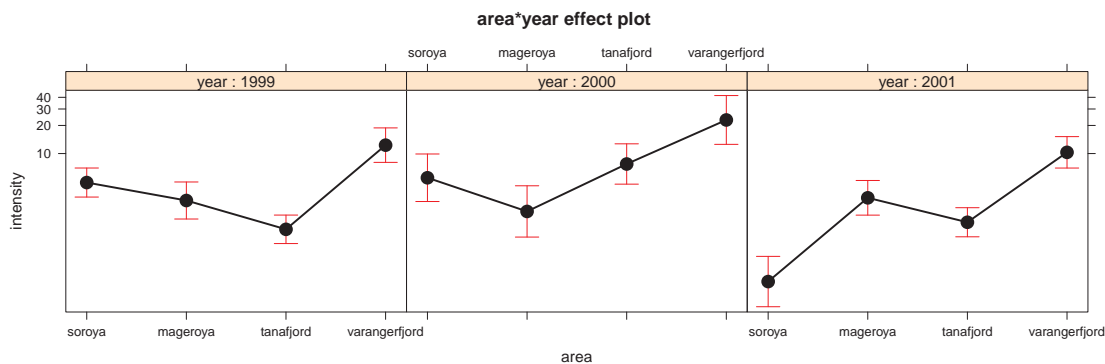
Likelihood ratio tests of Negative Binomial Models

Response: intensity
      Model      theta Resid. df    2 x log-lik.    Test      df LR stat.
1 length + areaEW * year 0.19085    1184      -5088.5
2 length + area * year 0.21531    1178      -5002.7 1 vs 2      6    85.852
  Pr(Chi)
1
2 2.2204e-16

```

The model with area as a factor is significantly better than the model with only a linear effect. Nonetheless, an effect plot shows that the intensity of parasites is greatest in the most eastern area, Varangerfjord (A4) in all three years, lending some credence to the “Russian hypothesis.”

```
> plot(Effect(c("area", "year"), cp_nb), layout=c(3,1))
```



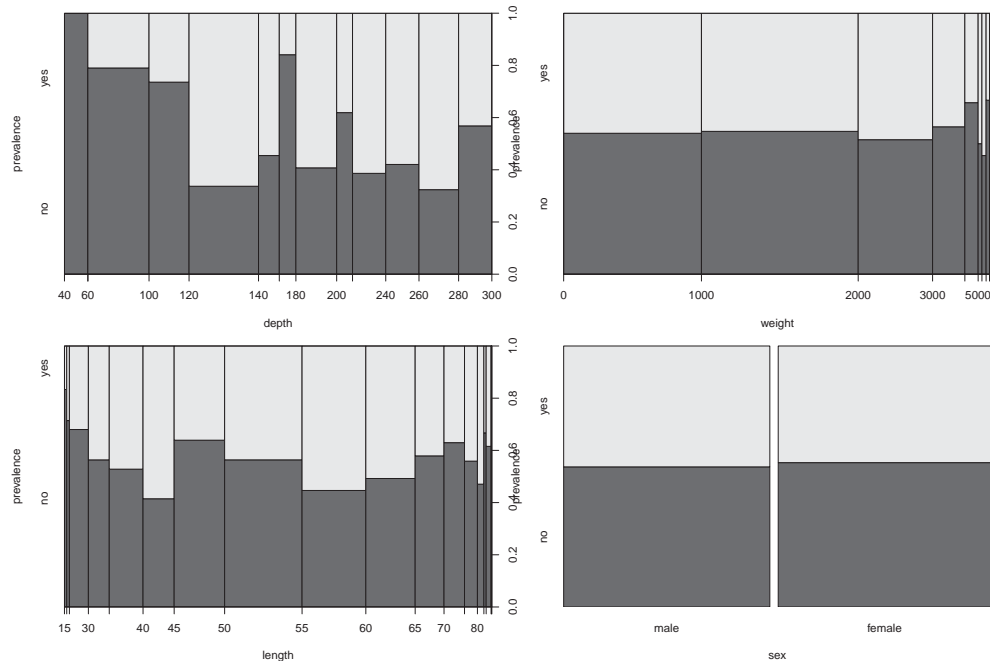
**Exercise 11.6** In Example 11.10, we ignored other potential predictors in the *CodParasites* data: depth, weight, length, sex, stage, and age. Use some of the graphical methods shown in this case study to assess whether any of these are related to prevalence and intensity.

★ Prevalence, a factor corresponding to  $\text{intensity} > 0$ , can be studied by simple plots, that are essentially spineplots. In these plots prevalence seems to vary with depth and length, but not with weight and sex.

```

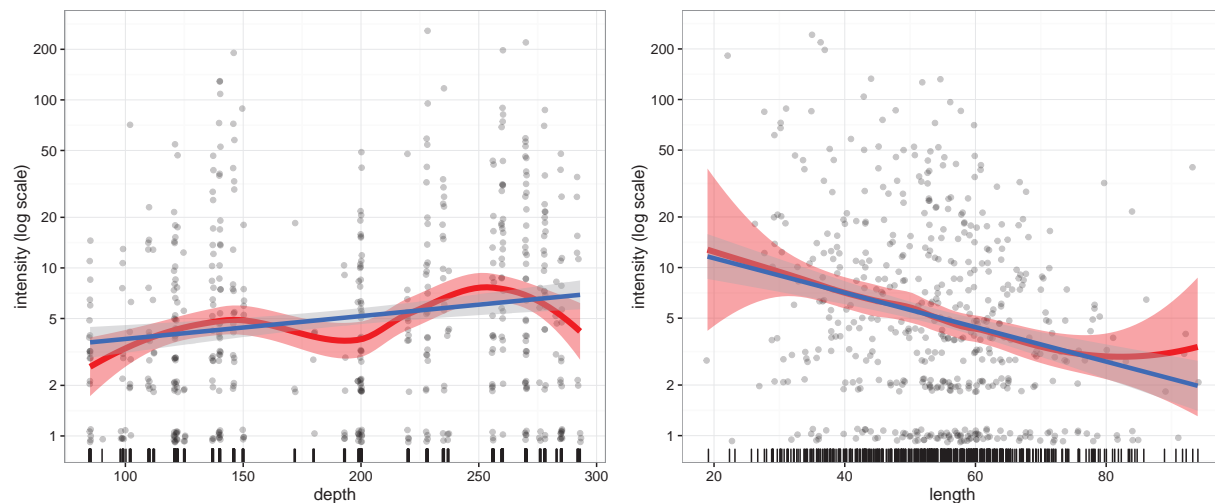
> CodParasites <- subset(CodParasites, sex !=0)
> CodParasites$ssex <- factor(CodParasites$ssex, labels=c("male", "female"))
>
> op <- par(mfrow = c(2, 2), mar=c(4,4,1,1)+.1)
> plot(prevalence ~ depth, data = CodParasites)
> plot(prevalence ~ weight, data = CodParasites)
> plot(prevalence ~ length, data = CodParasites)
> plot(prevalence ~ sex, data = CodParasites)
> par(op)

```



For intensity, the most informative plots use ggplot2, in the style of Figure 11.20. That is, plot jittered points, use a log scale for intensity, and overlay smoothed and linear fits. Intensity increases slightly with depth and decreases with the length of the fish.

```
> CPpos <- subset(CodParasites, intensity>0 & !is.na(length))
> ggplot(CPpos, aes(x=depth, y=intensity)) +
+   geom_jitter(position=position_jitter(height=.1), alpha=0.25) +
+   geom_rug(position='jitter', sides='b') +
+   scale_y_log10(breaks=c(1,2,5,10,20,50,100, 200)) +
+   stat_smooth(method="loess", color="red", fill="red", size=2) +
+   stat_smooth(method="lm", size=1.5) + theme_bw() +
+   labs(y='intensity (log scale)')
>
> ggplot(CPpos, aes(x=length, y=intensity)) +
+   geom_jitter(position=position_jitter(height=.1), alpha=0.25) +
+   geom_rug(position='jitter', sides='b') +
+   scale_y_log10(breaks=c(1,2,5,10,20,50,100, 200)) +
+   stat_smooth(method="loess", color="red", fill="red", size=2) +
+   stat_smooth(method="lm", size=1.5) + theme_bw() +
+   labs(y='intensity (log scale)')
```



**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.

★ Here we fit the hurdle and zero-inflated models, both poisson and negative-binomial, using all predictors. By AIC, model `phd.znb` is best, but by BIC, the regular negative-binomial fares best.

```
> library(MASS)
> library(countreg)
> data("PhdPubs", package="vcdExtra")
>
> phd.nbin <- glm.nb(articles ~ ., data=PhdPubs)
> # hurdle and zero-inflated
> phd.hp <- hurdle(articles ~ ., data=PhdPubs, dist = "poisson")
> phd.hnb <- hurdle(articles ~ ., data=PhdPubs, dist = "negbin")
> phd.zp <- zeroinfl(articles ~ ., data=PhdPubs, dist = "poisson")
> phd.znb <- zeroinfl(articles ~ ., data=PhdPubs, dist = "negbin")
>
> LRstats(phd.nbin, phd.hp, phd.hnb, phd.zp, phd.znb, sortBy="BIC")
```

Likelihood summary table:

	AIC	BIC	LR	Chisq	Df	Pr(>Chisq)
phd.hp	3235	3292		3211	903	<2e-16 ***
phd.zp	3234	3291		3210	903	<2e-16 ***
phd.hnb	3131	3194		3105	902	<2e-16 ***
phd.znb	3126	3188		3100	902	<2e-16 ***
phd.nbin	3135	3169		3121	909	<2e-16 ***

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Examine the zero-inflated negative-binomial model:

```
> summary(phd.znb)
```

Call:  
zeroinfl(formula = articles ~ ., data = PhdPubs, dist = "negbin")

Pearson residuals:

	Min	1Q	Median	3Q	Max
	-1.281	-0.760	-0.286	0.444	6.507

Count model coefficients (negbin with log link):

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	0.3655	0.1399	2.61	0.0090 **
female	-0.1946	0.0758	-2.57	0.0102 *
married	0.1015	0.0843	1.20	0.2288
kid5	-0.1516	0.0542	-2.80	0.0052 **
phdprestige	0.0156	0.0345	0.45	0.6510
mentor	0.0244	0.0035	6.97	3.1e-12 ***
Log(theta)	0.9766	0.1354	7.21	5.4e-13 ***

Zero-inflation model coefficients (binomial with logit link):

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-0.2943	1.2827	-0.23	0.8185
female	0.6580	0.8557	0.77	0.4419
married	-1.4741	0.9176	-1.61	0.1082
kid5	0.6241	0.4410	1.42	0.1570
phdprestige	-0.0113	0.2888	-0.04	0.9689
mentor	-0.8765	0.3152	-2.78	0.0054 **

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Theta = 2.655  
Number of iterations in BFGS optimization: 42  
Log-likelihood: -1.55e+03 on 13 Df

This suggests a simpler model in which `mentor` is the only variable affecting the zero counts. This model is preferable to the full model by both AIC and BIC.

```
> phd.znb1 <- zeroinfl(articles ~ .| mentor, data=PhdPubs, dist = "negbin")
> LRstats(phd.znb, phd.znb1)
```

Likelihood summary table:

	AIC	BIC	LR	Chisq	Df	Pr(>Chisq)
phd.znb	3126	3188		3100	902	<2e-16 ***
phd.znb1	3124	3168		3106	906	<2e-16 ***

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

- (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.

★ As described in the text, effect plots for analogs of hurdle and zero-inflated models can only be made by fitting and graphing separately the models for the zero and positive counts. We use a logistic regression for the zero counts.

```
> phd.zero <- glm(articles==0 ~., data=PhdPubs, family = binomial)
> Anova(phd.zero)

Analysis of Deviance Table (Type II tests)

Response: articles == 0
             LR Chisq Df Pr(>Chisq)
female         2.5    1   0.115
married        3.3    1   0.069 .
kid5           6.6    1   0.010 *
phdprestige    0.3    1   0.572
mentor        51.2    1   8.4e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

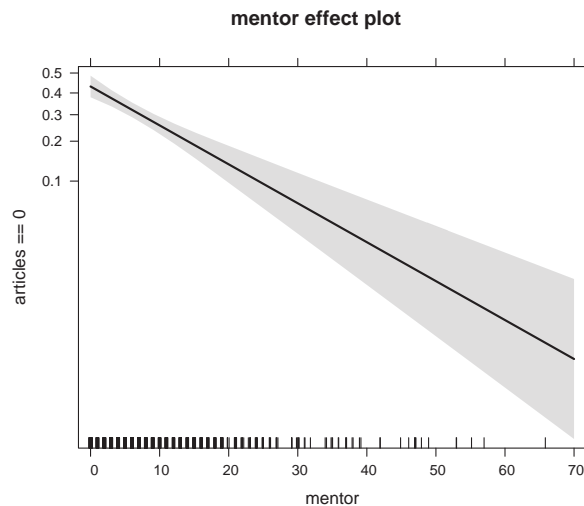
> phd.nzero <- glm.nb(articles ~ ., data=PhdPubs, subset = articles > 0)
> Anova(phd.nzero)

Analysis of Deviance Table (Type II tests)

Response: articles
             LR Chisq Df Pr(>Chisq)
female         7.2    1   0.0071 **
married         1.1    1   0.3043
kid5           5.0    1   0.0256 *
phdprestige     0.0    1   0.8953
mentor        35.8    1   2.2e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

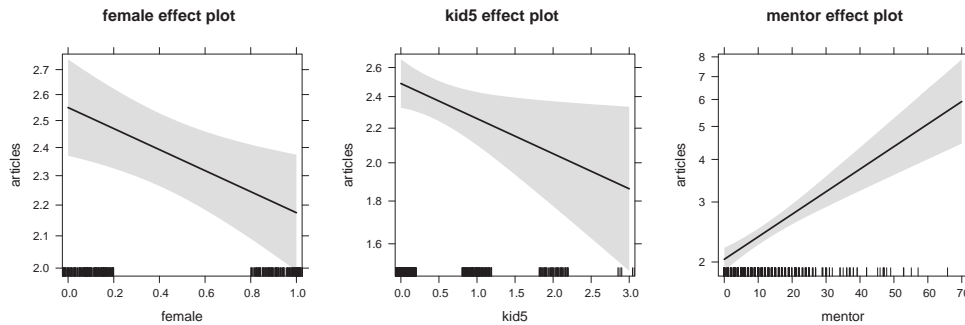
The effect of `mentor` is dramatic: as the number of publications by the mentor increases, the probability that a student will publish zero articles declines markedly.

```
> plot(Effect("mentor", phd.zero))
```



For the positive count model, we plot only the significant effects of `female`, `kids5`, and `mentor`. All have clear interpretations: the number of articles published is lower for females, decreases with the number of young children, and increases with the number of articles published by the mentor.

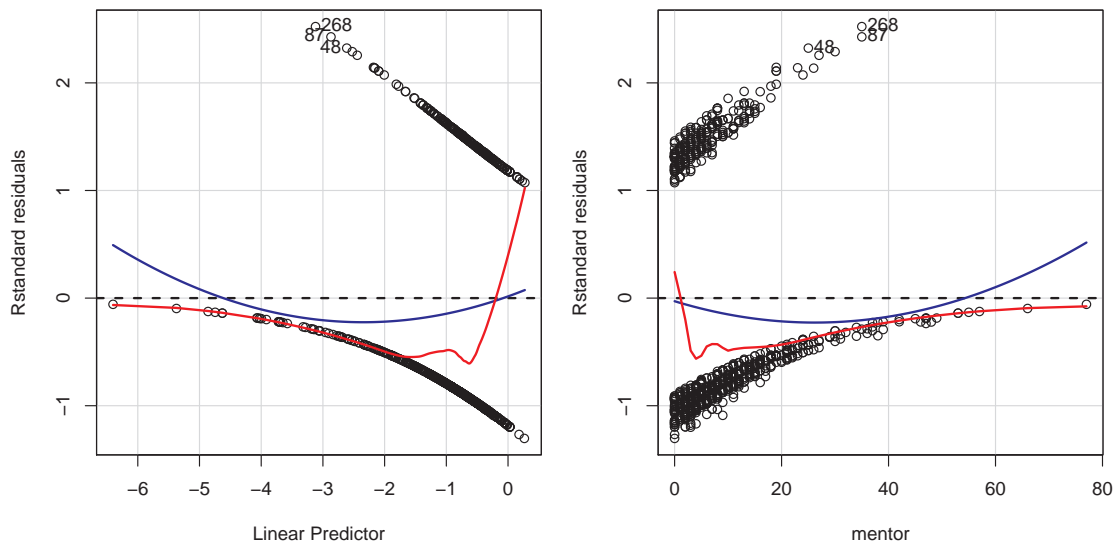
```
> plot(allEffects(phd.nzero)[c(1,3,5)], rows=1, cols=3)
```



- (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.

★ Unfortunately, the best graphic methods, from the car package are unavailable for hurdle and zero-inflated models. A suitable alternative is to use diagnostic plots for separate models for the zero (`phd.zero`) and positive counts (`phd.nzero`). Plots for the zero count component are not particularly remarkable for a logistic regression model.

```
> op <- par(mfrow=c(1,2), mar=c(4,4,1,1)+.1)
> residualPlot(phd.zero, type="rstandard",
+             quadratic=TRUE, col.smooth="red", col.quad="blue", id.n=3)
>
> residualPlot(phd.zero, "mentor", type="rstandard",
+             quadratic=TRUE, col.smooth="red", col.quad="blue", id.n=3)
> par(op)
```

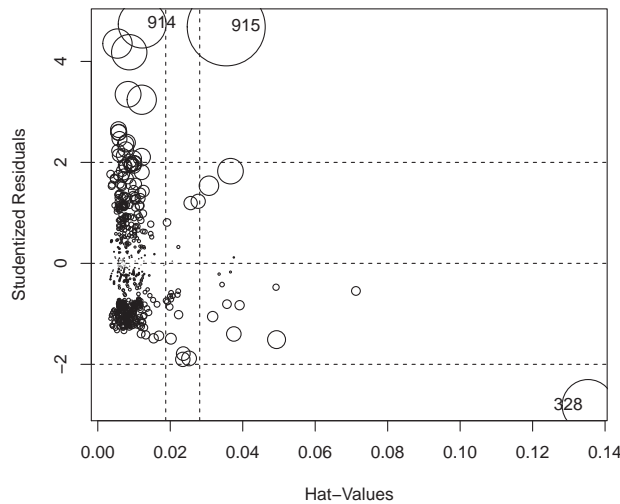


Similar plots for the positive count model (`phd.n zero`) would be done similarly, and are not particularly remarkable, except that they nominate some large positive residuals as unusual.

An influence plot suggests that three cases should be given further scrutiny.

```
> influencePlot(phd.nzero)

  StudRes      Hat      CookD
328 -2.8149 0.135304 0.099324
914  4.7390 0.012247 0.084424
915  4.6849 0.035444 0.224707
```



**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

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

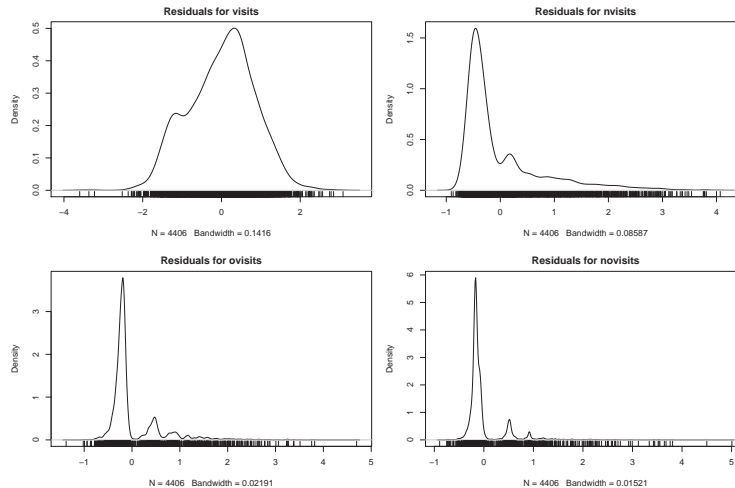
★ This just copies the code from the text to fit the model and calculate the residuals:

```
> data("NMES1988", package="AER")
> nmes2 <- NMES1988[, c(1:4, 6:8, 13, 15, 18)]
>
> clog <- function(x) log(x+1)
> nmes.mlm <- lm(clog(cbind(visits, nvisits, ovisits, novisits)) ~ ., data=nmes2)
> resid<- 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?

★ There are a variety of ways to produce density plots in R, but the simplest for this question is just to use `density()` with default settings. The residuals for `visits` are reasonably symmetric. All the others are quite positively skewed.

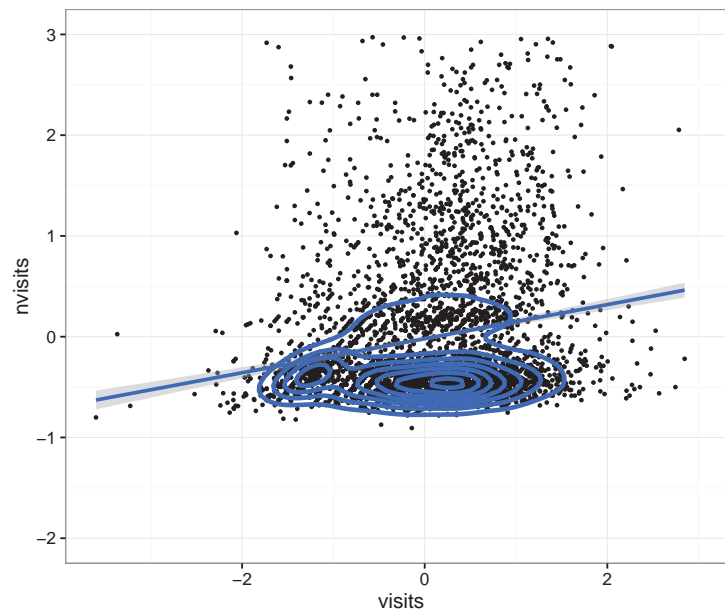
```
> op <- par(mfrow=c(2,2), mar=c(5,4,2,1)+0.1)
> plot(density(resids[,1]), main = "Residuals for visits")
> rug(resids[,1])
>
> plot(density(resids[,2]), main = "Residuals for nvisits")
> rug(resids[,2])
>
> plot(density(resids[,3]), main = "Residuals for ovisits")
> rug(resids[,3])
>
> plot(density(resids[,4]), main = "Residuals for novisits")
> rug(resids[,4])
> par(op)
```



(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) and some smoothed curve. What do you conclude?

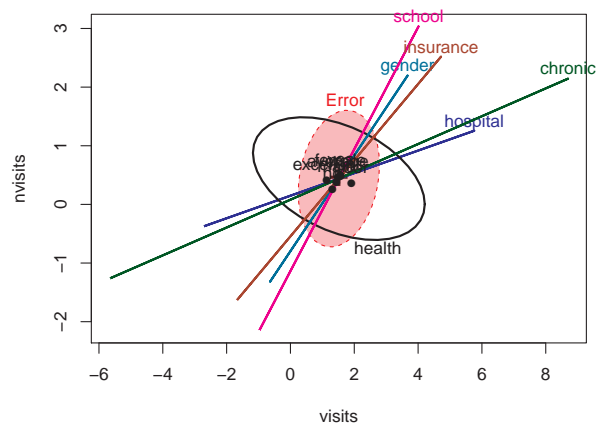
★ Here is just one example for the first two variables, visits, and nvisits. The bivariate distribution is very far from bivariate normal, largely because nvisits is so positively skewed. All other pairs of the residuals would be worse.

```
> ggplot(as.data.frame(resids), aes(x=visits, y=nvisits)) +
+   geom_point(size=0.6) + ylim(c(-2, 3)) +
+   stat_smooth(method="lm") +
+   geom_density2d(size=1.25) + theme_bw()
```



The overall conclusion is that, while Figure 11.40 in the text gives a useful overall summary of the relationship among the multivariate responses, it should only be considered as a rough approximation. For comparison, the plot above corresponds to the error ellipse in the (2,1) panel of Figure 11.40, shown in red in the plot below.

```
> library(heplots)
> heplot(nmes.mlm, variables=1:2, fill=c(TRUE, FALSE))
```



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