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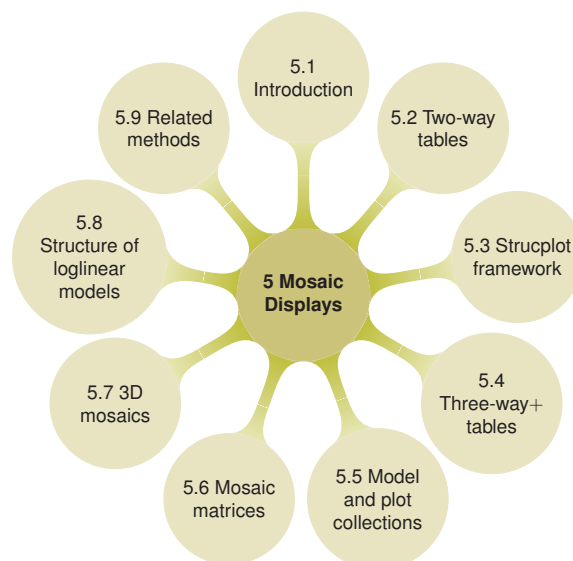
Mosaic Displays for n-Way Tables

Mosaic displays help to visualize the pattern of associations among variables in two-way and larger tables. Extensions of this technique can reveal partial associations, marginal associations, and shed light on the structure of loglinear models themselves.

5.1 Introduction

> Little boxes on the hillside, little boxes made of ticky tacky,
> Little boxes on the hillside, little boxes all the same.
> There's a green one and a pink one, and a blue one and a yellow one,
> And they're all made out of ticky tacky, and they all look just the same.
>
> Words and music by Malvina Reynolds, ©Schroder Music Company 1962, 1990; recorded by Pete Seeger

In Chapter 4, we described a variety of graphical techniques for visualizing the pattern of association in simple contingency tables. These methods are somewhat specialized for particular sizes and shapes of tables: 2×2 tables (fourfold display), $R \times C$ tables (tile plot, sieve diagram), square tables (agreement charts), $R \times 3$ tables (trilinear plots), and so forth.

This chapter describes the ***mosaic display*** and related graphical methods for n-way frequency tables, designed to show various aspects of high-dimensional contingency tables in a hierarchical way. These methods portray the frequencies in an n-way contingency table by a collection of rectangular "tiles" whose size (area) is proportional to the cell frequency. In this respect, the mosaic

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display is similar to the sieve diagram (Section 4.5). However, mosaic plots and related methods described here:

- generalize more readily to *n*-way tables. One can usefully examine 3-way, 4-way, and even larger tables, subject to the limitations of resolution in any graph;

- are intimately connected to loglinear models, generalized linear models, and generalized non-linear models for frequency data;

- provide a method for fitting a series of sequential loglinear models to the various marginal totals of an *n*-way table; and

- can be used to illustrate the relations among variables that are fitted by various loglinear models.

The basic ideas behind these graphical methods are explained for two-way tables in Section 5.2; the ***strucplot framework*** on which these are based is described in Section 5.3. The graphical extension of mosaic plots to three-way and large tables (Section 5.4) is quite direct. However, the details require a brief introduction to loglinear models and some terminology for different types of "independence" in such tables, also described in this section. Mosaic methods are further extended to all-pairwise plots in Section 5.6 and 3D plots in Section 5.7.

5.2   Two-way tables

{sec:mosaic-twoway}

The mosaic display (Friendly, 1992, 1994, 1997, Hartigan and Kleiner, 1981, 1984) is like a grouped barchart, where the heights (or widths) of the bars show the relative frequencies of one variable, and widths (heights) of the sections in each bar show the conditional frequencies of the second variable, given the first. This gives an area-proportional visualization of the frequencies composed of tiles corresponding to the cells created by successive vertical and horizontal splits of rectangle, representing the total frequency in the table. The construction of the mosaic display, and what it reveals, are most easily understood for two-way tables.

{ex:haireye2a}

EXAMPLE 5.1: Hair color and eye color

Consider the data shown earlier in Table 4.2, showing the relation between hair color and eye color among students in a statistics course. The basic mosaic display for this 4×4 table is shown in Figure 5.1.

```
> data("HairEyeColor", package = "datasets")
> haireye <- margin.table(HairEyeColor, 1 : 2)
> mosaic(haireye, labeling = labeling_values)
```

For such a two-way table, the mosaic in Figure 5.1 is constructed by first dividing a unit square in proportion to the marginal totals of one variable, say, hair color.

For these data, the marginal frequencies and proportions of hair color are calculated below:

```
> (hair <- margin.table(haireye, 1))

Hair
Black Brown   Red Blond
  108   286    71   127

> prop.table(hair)

Hair
  Black   Brown     Red   Blond
0.18243 0.48311 0.11993 0.21453
```
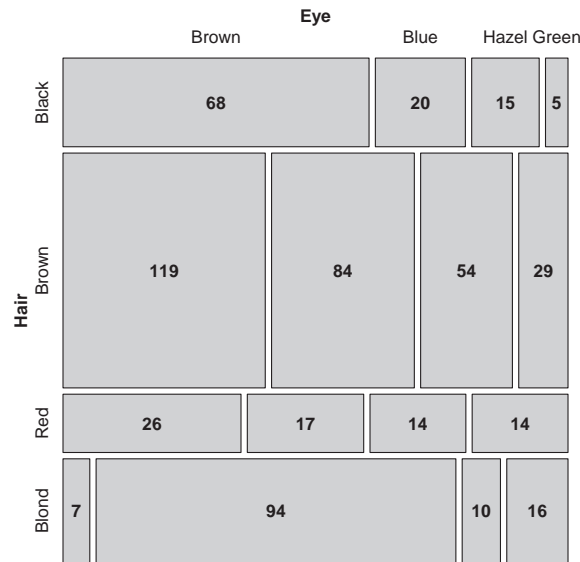
Figure 5.1: Basic mosaic display for hair color and eye color data. The area of each rectangle is proportional to the observed frequency in that cell, shown as numbers.

These frequencies can be shown as the mosaic for the first variable (hair color), with the unit square split according to the marginal proportions as in Figure 5.2 (left). The rectangular tiles are then shaded to show the residuals (deviations) from a particular model as shown in the right panel of Figure 5.2. The details of the calculations for shading are:

- The one-way table of marginal totals can be fit to a model, in this case, the (implausible) model that all hair colors are equally probable. This model has expected frequencies $m_i = 592/4 = 148$:

```
> expected <- rep(sum(hair) / 4, 4)
> names(expected) <- names(hair)
> expected

Black Brown   Red Blond
  148   148   148   148
```

- The Pearson residuals from this model, $r_i = (n_i - m_i)/\sqrt{m_i}$, are:

```
> (residuals <- (hair - expected) / sqrt(expected))

Hair
  Black    Brown      Red    Blond
-3.2880  11.3435  -6.3294  -1.7262
```

and these values are shown by color and shading as shown in the legend in Figure 5.3. The high positive value for brown hair indicates that people with brown hair are much more frequent in this sample than the equiprobability model would predict; the large negative residual for red hair shows that redheads are much less common. Further details of the schemes for shading are described below, but essentially we use increasing intensities of blue (red) for positive (negative) residuals.
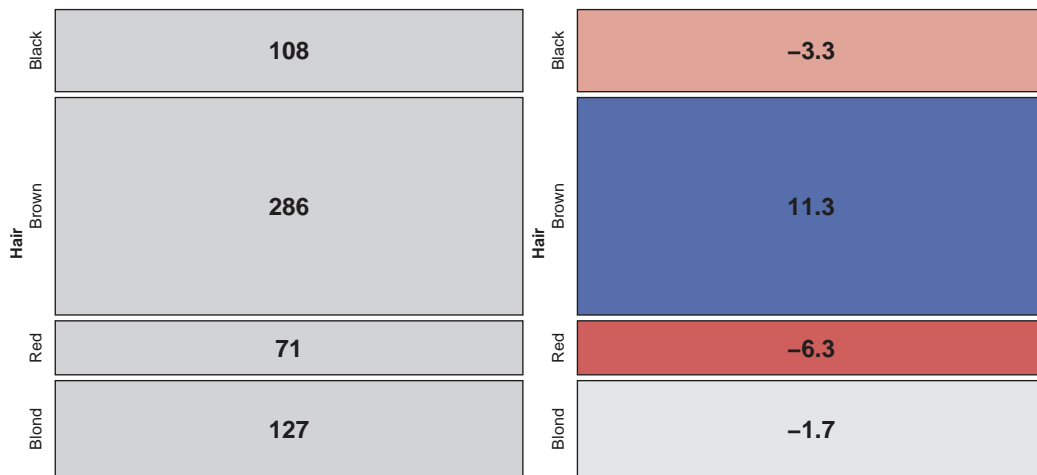
Figure 5.2: First step in constructing a mosaic display. Left: splitting the unit square according to frequencies of hair color; right: shading the tiles according to residuals from a model of equal marginal probabilities.

{fig:haireye-mos4}

In the next step, the rectangle for each hair color is subdivided in proportion to the *relative* (conditional) frequencies of the second variable—eye color, giving the following conditional row proportions:

```
> round(addmargins(prop.table(haireye, 1), 2), 3)

       Eye
Hair     Brown  Blue Hazel Green   Sum
  Black 0.630 0.185 0.139 0.046 1.000
  Brown 0.416 0.294 0.189 0.101 1.000
  Red   0.366 0.239 0.197 0.197 1.000
  Blond 0.055 0.740 0.079 0.126 1.000
```

The proportions in each row determine the width of the tiles in the second mosaic display in Figure 5.3.

- Again, the cells are shaded in relation to standardized Pearson residuals, $r_{ij} = (n_{ij}-m_{ij})/\sqrt{m_{ij}}$, from a model. For a two-way table, the model is that hair color and eye color are independent in the population from which this sample was drawn. These residuals are calculated as shown below using `independence_table()` to calculate the expected values m_{ij} under this model ($m_{ij} = n_{++}\pi_{i+}\pi_{+j}$):

```
> exp <- independence_table(haireye)
> resids <- (haireye - exp) / sqrt(exp)
> round(resids, 2)

       Eye
Hair     Brown  Blue Hazel Green
  Black   4.40 -3.07 -0.48 -1.95
  Brown   1.23 -1.95  1.35 -0.35
  Red    -0.07 -1.73  0.85  2.28
  Blond  -5.85  7.05 -2.23  0.61
```

- Thus, in Figure 5.3, the two tiles shaded deep blue correspond to the two cells, (Black, Brown) and (Blond, Blue), whose residuals are greater than +4, indicating much greater frequency in
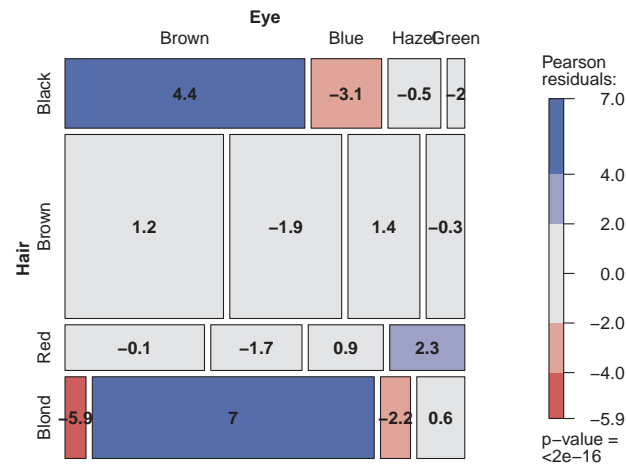
Figure 5.3: Second step in constructing the mosaic display. Each rectangle for hair color is subdivided in proportion to the relative frequencies of eye color, and the tiles are shaded in relation to residuals from the model of independence.

{fig:haireye-mos8}

those cells than would be found if hair color and eye color were independent. The tile shaded deep red, (Blond, Brown), corresponds to the largest negative residual $= -5.85$, indicating this combination is extremely rare under the hypothesis of independence.

- The overall Pearson χ^2 statistic for the independence model is just the sum of squares of the residuals, with degrees of freedom $(r - 1) \times (c - 1)$.

```
> (chisq <- sum(resids ^ 2))

[1] 138.29

> (df <- prod(dim(haireye) - 1))

[1] 9

> pchisq(chisq, df, lower.tail = FALSE)

[1] 2.3253e-25
```

- These results are of course identical to what `chisq.test()` provides. Note that the latter can be used to retrieve the residuals:

```
> chisq.test(haireye)


	Pearson's Chi-squared test

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

```
> round(residuals(chisq.test(haireye)), 2)

        Eye
Hair     Brown  Blue Hazel Green
  Black   4.40 -3.07 -0.48 -1.95
  Brown   1.23 -1.95  1.35 -0.35
  Red    -0.07 -1.73  0.85  2.28
  Blond  -5.85  7.05 -2.23  0.61
```

△

5.2.1   Shading levels

A variety of schemes for shading the tiles are available in the strucplot framework (Section 5.3), but the simplest (and default) shading patterns for the tiles are based on the sign and magnitude of the standardized Pearson residuals, using shades of blue for positive residuals and red for negative residuals, and two threshold values for their magnitudes, $|r_{ij}| > 2$ and $|r_{ij}| > 4$.

Because the standardized residuals are approximately unit-normal $N(0, 1)$ values, this corresponds to highlighting cells whose residuals are *individually* significant at approximately the .05 and .0001 level, respectively. Other shading schemes described later provide tests of significance, but the main purpose of highlighting cells is to draw attention to the *pattern* of departures of the data from the assumed model of independence.

5.2.2   Interpretation and reordering

To interpret the association between hair color and eye color, consider the pattern of positive (blue) and negative (red) tiles in the mosaic display. We interpret positive values as showing cells whose observed frequency is substantially greater than would be found under independence; negative values indicate cells that occur less often than under independence.

The interpretation can often be enhanced by reordering the rows or columns of the two-way table so that the residuals have an *opposite corner* pattern of signs. This usually helps us interpret any systematic patterns of association in terms of the ordering of the row and column categories.

In this example, a more direct interpretation can be achieved by reordering the eye colors as shown in Figure 5.4. Note that in this rearrangement both hair colors and eye colors are ordered from dark to light, suggesting an overall interpretation of the association between hair color and eye color.

```
> # re-order eye colors from dark to light
> haireye2 <- as.table(haireye[, c("Brown", "Hazel", "Green", "Blue")])
> mosaic(haireye2, shade = TRUE)
```

In general, the levels of a factor in mosaic displays are often best reordered by arranging them according to their scores on the first (largest) *correspondence analysis* dimension (Friendly, 1994); see Chapter 6 for details. Friendly and Kwan (2003) use this as one example of ***effect ordering*** for data displays, illustrated in Chapter 1.

Thus, the mosaic in Figure 5.4 shows that the association between hair and eye color is essentially that:

• people with dark hair tend to have dark eyes,
• those with light hair tend to have light eyes,
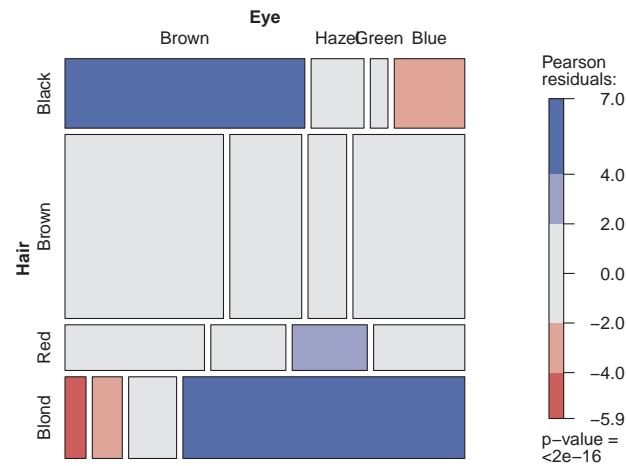• people with red hair and green eyes do not quite fit this pattern.

Figure 5.4: Two-way mosaic for hair color and eye color, reordered. The eye colors were reordered from dark to light, enhancing the interpretation.

{fig:haireye-mos9}

5.3 The strucplot framework

{sec:mosaic-strucplot}

Mosaic displays have much in common with sieve plots and association plots described in Chapter 4 and with related graphical methods such as ***doubledecker plots*** described later in this chapter. The main idea is to visualize a contingency table of frequencies by "tiles" corresponding to the table cells arranged in rectangular form. For multiway tables with more than two factors, the variables are nested into rows and columns using recursive conditional splits, given the table margins. The result is a "flat" representation that can be visualized in ways similar to a two-dimensional representation of a table. The `structable()` function described in Section 2.5 gives the tabular version of a strucplot. The description below follows Meyer et al. (2006), also included as a vignette (accessible from R as `vignette("strucplot", pkg = "vcd")`), in vcd (Meyer et al., 2015).

Rather than implementing each of these methods separately, the ***strucplot framework*** in the vcd package provides a general class of methods of which these are all instances. This framework defines a class of conditional displays, which allows for granular control of graphical appearance aspects, including:

- the content of the tiles, e.g., observed or expected frequencies
- the split direction for each dimension, horizontal or vertical
- the graphical parameters of the tiles' content, e.g., color or other visual attributes
- the spacing between the tiles
- the labeling of the tiles

5.3.1 Components overview

{sec:strucplot_overview}

The strucplot framework is highly modularized: Figure 5.5 shows the hierarchical relationship between the various components. For the most part, you will directly use the convenience and related
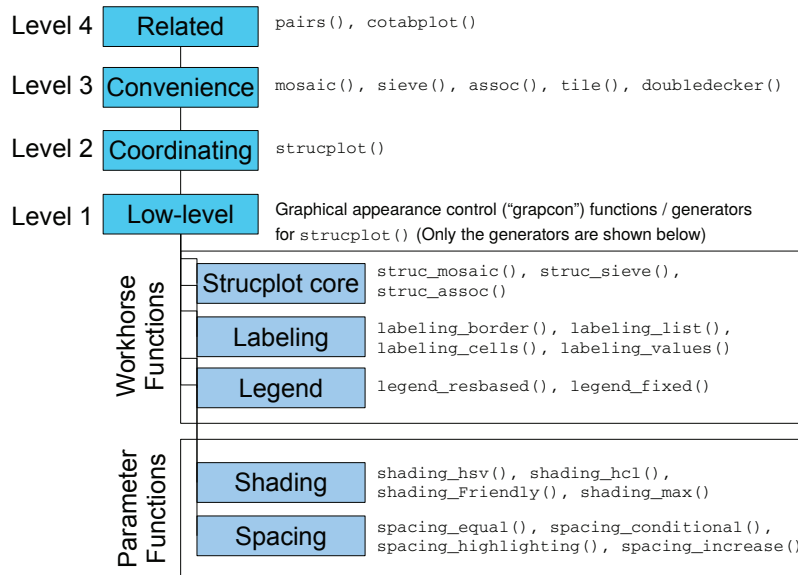
Figure 5.5: Components of the strucplot framework. High-level functions use those at lower levels to provide a general system for tile-based plots of frequency tables.   {fig:struc}

functions at the top of the diagram, but it is more convenient to describe the framework from the bottom up.

1. On the lowest level, there are several groups of workhorse and parameter functions that directly or indirectly influence the final appearance of the plot (see Table 5.1 for an overview). These are examples of *graphical appearance control* functions (called **grapcon functions**). They are created by generating functions (*grapcon generators*), allowing flexible parameterization and extensibility (Figure 5.5 only shows the generators). The generator names follow the naming convention *group_foo()*, where *group* reflects the group the generators belong to (strucplot core, labeling, legend, shading, or spacing).

   • The workhorse functions (created by `struc_foo()`) are `labeling_foo()`, and `legend_foo()`. These functions directly produce graphical output (i.e., "add ink to the canvas"), for labels and legends respectively.
   • The parameter functions (created by `spacing_foo()` and `shading_foo()`) compute graphical parameters used by the others. The grapcon functions returned by `struc_foo()` implement the core functionality, creating the tiles and their content.

2. On the second level of the framework, a suitable combination of the low-level grapcon functions (or, alternatively, corresponding generating functions) is passed as "hyperparameters" to `strucplot()`. This central function sets up the graphical layout using grid viewports, and coordinates the specified core, labeling, shading, and spacing functions to produce the plot.

3. On the third level, vcd provides several convenience functions such as `mosaic()`, `sieve()`, `assoc()`, `tile()`, and `doubledecker()` which interface to `strucplot()` through sensible parameter defaults and support for model formulae.

4. Finally, on the fourth level, there are "related" vcd functions (such as `cotabplot()` and the

Table 5.1: Available graphical appearance control (grapcon) generators in the strucplot framework {tab:grapcons}

Group	Grapcon generator	Description
strucplot core	`struc_assoc()`	core function for association plots
	`struc_mosaic()`	core function for mosaic plots (also used for tile plots)
	`struc_sieve()`	core function for sieve plots
labeling	`labeling_border()`	border labels
	`labeling_cboxed()`	centered labels with boxes, all labels clipped,
		and on top and left border
	`labeling_cells()`	cell labels
	`labeling_conditional()`	border labels for conditioning variables
		and cell labels for conditioned variables
	`labeling_doubledecker()`	draws labels for doubledecker plot
	`labeling_lboxed()`	left-aligned labels with boxes
	`labeling_left()`	left-aligned border labels
	`labeling_left2()`	left-aligned border labels, all labels on top and left border
	`labeling_list()`	draws a list of labels under the plot
	`labeling_residuals()`	show residuals in cells
	`labeling_value()`	show values (observed, expected) in cells
shading	`shading_binary()`	visualizes the sign of the residuals
	`shading_Friendly()`	implements Friendly shading (based on HSV colors)
	`shading_hcl()`	shading based on HCL colors
	`shading_hsv()`	shading based on HSV colors
	`shading_max()`	shading visualizing the maximum test statistic
		(based on HCL colors)
	`shading_sieve()`	implements Friendly shading customized for sieve plots
		(based on HCL colors)
spacing	`spacing_conditional()`	increasing spacing for conditioning variables,
		equal spacing for conditioned variables
	`spacing_dimequal()`	equal spacing for each dimension
	`spacing_equal()`	equal spacing for all dimensions
	`spacing_highlighting()`	increasing spacing, last dimension set to zero
	`spacing_increase()`	increasing spacing
legend	`legend_fixed()`	creates a fixed number of bins (similar to `mosaicplot()`)
	`legend_resbased()`	suitable for an arbitrary number of bins
		(also for continuous shadings)

`pairs()` methods for table objects) arranging collections of plots of the strucplot framework into more complex displays (e.g., by means of panel functions).

5.3.2 Shading schemes

{sec:mosaic-shading}

Unlike other graphics functions in base R, the strucplot framework allows almost full control over the graphical parameters of all plot elements. In particular, in association plots, mosaic plots, and sieve plots, you can modify the graphical appearance of each tile individually.

Built on top of this functionality, the framework supplies a set of shading functions choosing colors appropriate for the visualization of loglinear models. The tiles' graphical parameters are set using the `gp` argument of the functions of the strucplot framework. This argument basically expects an object of class `"gpar"` whose components are arrays of the same shape (length and dimensionality) as the data table.

For added generality, however, you can also supply a `grapcon` function that computes such an object given a vector of residuals, or, alternatively, a *generating function* that takes certain argu-

ments and returns such a grapcon function (see Table 5.1). vcd provides several shading functions, including support for both HSV (hue-saturation-value) and HCL (hue-chroma-luminance) colors, and visualization of significance tests.

5.3.2.1 Specifying graphical parameters for strucplot displays

Strucplot displays in vcd are built using the grid graphics package (Murrell, 2011). There are many graphical parameters that can be set using `gp = gpar(...)` in a call to a high-level strucplot function. Among these, the following are often most useful to control the drawing components:

col	Color for lines and borders.
fill	Color for filling rectangles, polygons, ...
alpha	Alpha channel for transparency of fill color.
lty	Line type for lines and borders.
lwd	Line width for lines and borders.

In addition, a number of parameters control the display of text labels in these displays:

fontsize	The size of text (in points)
cex	Multiplier applied to fontsize
fontfamily	The font family (serif, sans, mono, ...)
fontface	The font face (**bold**, *italic*, ...)

See `help(gpar)` for a complete list and `help(par)` for further details.

We illustrate this capability below using the hair color and eye color data as reordered in Figure 5.4. The following example produces a ***Marimekko chart***, or a "poor-man's mosaic display" as shown in the left panel of Figure 5.6. This is essentially a divided bar chart where the eye colors within each horizontal bar for the hair color group are all given the same color. In the example, the matrix fill_colors is constructed to conform to the haireye2 table, using color values that approximate the eye colors.[1]

```
> # color by hair color
> fill_colors <- c("brown4", "#acba72", "green", "lightblue")
> (fill_colors_mat <- t(matrix(rep(fill_colors, 4), ncol = 4)))

     [,1]     [,2]       [,3]     [,4]
[1,] "brown4" "#acba72" "green" "lightblue"
[2,] "brown4" "#acba72" "green" "lightblue"
[3,] "brown4" "#acba72" "green" "lightblue"
[4,] "brown4" "#acba72" "green" "lightblue"

> mosaic(haireye2, gp = gpar(fill = fill_colors_mat, col = 0))
```

Alternatively, we could have used the convenience function `shading_Marimekko()` in vcd:

```
> mosaic(haireye2, gp = shading_Marimekko(haireye2))
```

Note that because the hair colors and eye colors are both ordered, this shows the decreasing prevalence of light hair color amongst those with brown eyes and the increasing prevalence of light hair with blue eyes.

Alternatively, for some purposes,[2] we might like to use color to highlight the pattern of diagonal cells, and the off-diagonals 1, 2, 3 steps removed. The R function `toeplitz()` returns such a

---

[1]Actually, the fill_colors vector could be directly used since values are recycled as needed by mosaic().

[2]For example, this would be appropriate for a square table, showing agreement between row and column categories, as in Section 4.7.

patterned matrix, and we can use this to calculate the `fill_colors` by indexing the result of the `rainbow_hcl()` palette function in **colorspace** (Ihaka et al., 2015) (generating better colors than `palette()`). The code below produces the right panel in Figure 5.6.

```
> # toeplitz designs
> library(colorspace)
> toeplitz(1 : 4)

     [,1] [,2] [,3] [,4]
[1,]    1    2    3    4
[2,]    2    1    2    3
[3,]    3    2    1    2
[4,]    4    3    2    1

> fill_colors <- rainbow_hcl(8)[1 + toeplitz(1 : 4)]
> mosaic(haireye2, gp = gpar(fill = fill_colors, col = 0))
```
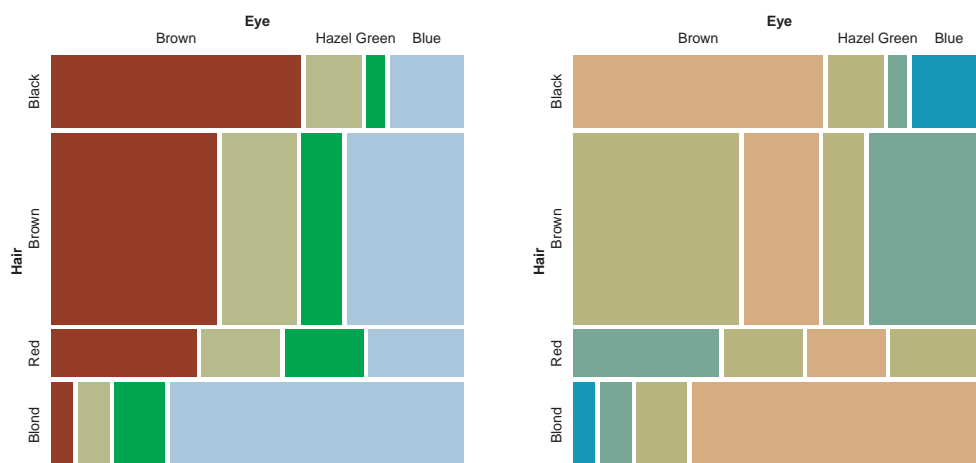

Figure 5.6: Mosaic displays for the `haireye2` data, using custom colors to fill the tiles. Left: Marimekko chart, using colors to reflect the eye colors; right: Toeplitz-based colors, reflecting the diagonal strips in a square table.

{fig:HE-fill}

Again, **vcd** offers a convenience function for this purposes, `shading_diagonal()`:

```
> mosaic(haireye2, gp = shading_diagonal(haireye2))
```

More simply, to shade a mosaic according to the levels of one variable (typically a response variable), you can use the `highlighting` arguments of `mosaic()`. The first call below gives a result similar to the left panel of Figure 5.6. Alternatively, using the formula method for `mosaic()`, specify the response variable as the left-hand side.

```
> mosaic(haireye2, highlighting = "Eye", highlighting_fill = fill_colors)
> mosaic(Eye ~ Hair, data = haireye2, highlighting_fill = fill_colors)
```

5.3.2.2 Residual-based shading

The important idea that differentiates mosaic and other strucplot displays from the "poor-man's," Marimekko versions (Figure 5.6) often shown in other software, is that rather than just using shading

color to *identify* the cells, we can use these attributes to show something more—*residuals* from some model, whose pattern helps to explain the association between the table variables.
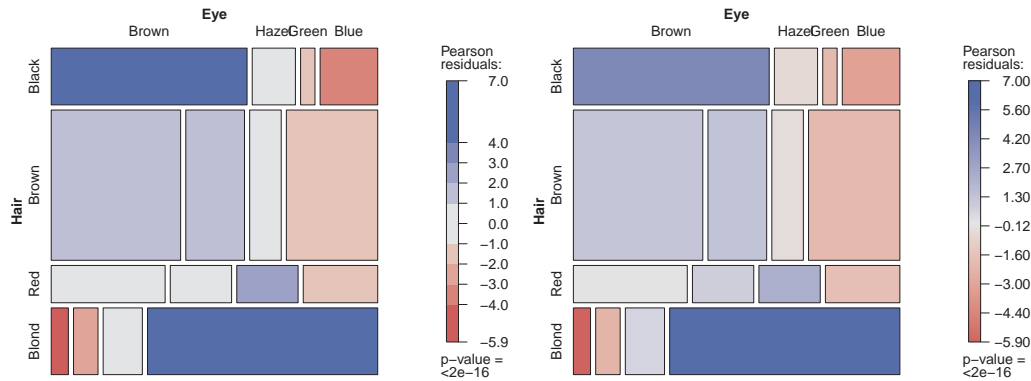
As described above, the strucplot framework includes a variety of `shading_` functions, and these can be customized with optional arguments. Zeileis et al. (2007) describe a general approach to residual-based shadings for area-proportional visualizations, used in the development of the strucplot framework in vcd.

{ex:interp}

EXAMPLE 5.2: Interpolation options

One simple thing to do is to modify the `interpolate` option passed to the default `shading_hcl` function, as shown in Figure 5.7.

```
> # more shading levels
> mosaic(haireye2, shade = TRUE, gp_args = list(interpolate = 1 : 4))
>
> # continuous shading
> interp <- function(x) pmin(x / 6, 1)
> mosaic(haireye2, shade = TRUE, gp_args = list(interpolate = interp))
```


Figure 5.7: Interpolation options for shading levels in mosaic displays. Left: four shading levels; right: continuous shading.

{fig:HE-interp}

For the left panel of Figure 5.7, a numeric vector is passed as `interpolate=1:4`, defining the boundaries of a step function mapping the absolute values of residuals to saturation levels in the HCL color scheme. For the right panel, a user-defined function, `interp()`, is created which maps the absolute residuals to saturation values in a continuous way (up to a maximum of 6).

Note that these two interpolation schemes produce quite similar results, differing mainly in the shading level of residuals within ± 1 and in the legend. In practice, the default discrete interpolation, using cutoffs of $\pm 2, \pm 4$ usually works quite well.   △

{ex:shading}

EXAMPLE 5.3: Shading functions

Alternatively, the names of shading functions can be passed as the `gp` argument, as shown below, producing Figure 5.8. Two shading function are illustrated here:

- The left panel of Figure 5.8 uses the classical Friendly (1994) shading scheme, `shading_Friendly`

with HSV colors[3] of blue and red and default cutoffs for absolute residuals, $\pm 2, \pm 4$, corresponding to `interpolate = c(2, 4)`. In this shading scheme, all tiles use an outline color (`col`) corresponding to the sign of the residual. As well, the border line type (`lty`) distinguishes positive and negative residuals, which is useful if a mosaic plot is printed in black and white.

- The right panel uses the `shading_max()` function, based on the ideas of Zeileis et al. (2007) on residual-based shadings for area-proportional visualizations. Instead of using the cutoffs 2 and 4, it employs the critical values, M_α, for the maximum absolute Pearson residual statistic,

$$M = \max_{i,j} |r_{ij}|,$$

by default at $\alpha = 0.10$ and 0.01.[4] Only those residuals with $|r_{ij}| > M_\alpha$ are colored in the plot, using two levels for Value ("lightness") in HSV color space. Consequently, all color in the plot signals a significant departure from independence at 90% or 99% significance level, respectively.[5]

```
> mosaic(haireye2, gp = shading_Friendly, legend = legend_fixed)
> set.seed(1234)
> mosaic(haireye2, gp = shading_max)
```
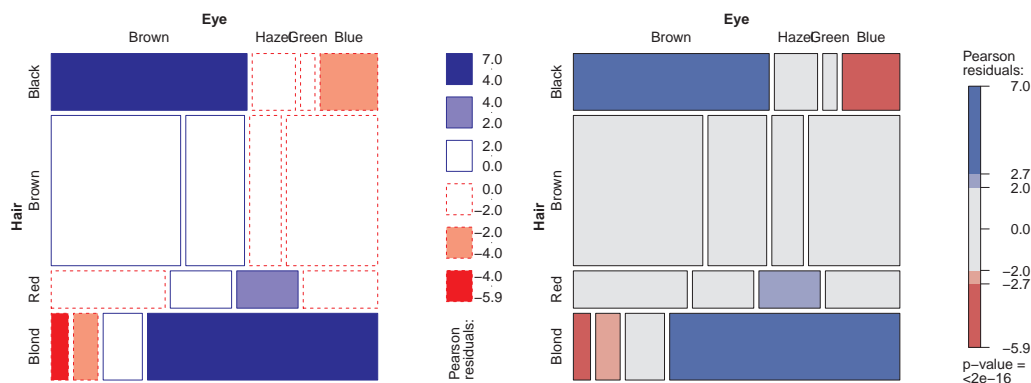

Figure 5.8: Shading functions for mosaic displays. Left: `shading_Friendly` using fixed cutoffs and the "Friendly" color scheme and an alternative legend style (`legend_fixed`); right: `shading_max`, using a permutation-based test to determine significance of residuals.

{fig:HE-shading}

In this example, the difference between these two shading schemes is largely cosmetic, in that the pattern of association is similar in the two panels of Figure 5.8, and the interpretation would be the same. This is not always the case, as we will see in the next example. △

---

[3] `shading_Friendly2()` is a variant based on HCL colors.

[4] These default significance levels were chosen because this leads to displays where fully colored cells are clearly significant ($p < 0.01$), cells without color are clearly non-significant ($p > 0.1$), and cells in between can be considered to be weakly significant ($0.01 \leq p \leq 0.1$).

[5] This computation uses the **vcd** function `coindep_test()` to calculate generalized tests of (conditional) independence by simulation from the marginal distribution of the input table under (conditional) independence. In these examples using `shading_max`, the function `set.seed()` is used to initialize the random number generators to a given state for reproducibility.

EXAMPLE 5.4: Arthritis treatment

This example uses the *Arthritis* data, illustrated earlier (Example 2.2), on the relation between treatment and outcome for rheumatoid arthritis. To confine this example to a two-way table, we use only the (larger) female patient group.

```
> art <- xtabs(~ Treatment + Improved, data = Arthritis,
+              subset = Sex == "Female")
> names(dimnames(art))[2] <- "Improvement"
```

The calls to mosaic() below compare shading_Friendly and shading_max, giving the plots shown in Figure 5.9.

```
> mosaic(art, gp = shading_Friendly, margin = c(right = 1),
+        labeling = labeling_residuals, suppress = 0, digits = 2)
> set.seed(1234)
> mosaic(art, gp = shading_max, margin = c(right = 1))
```
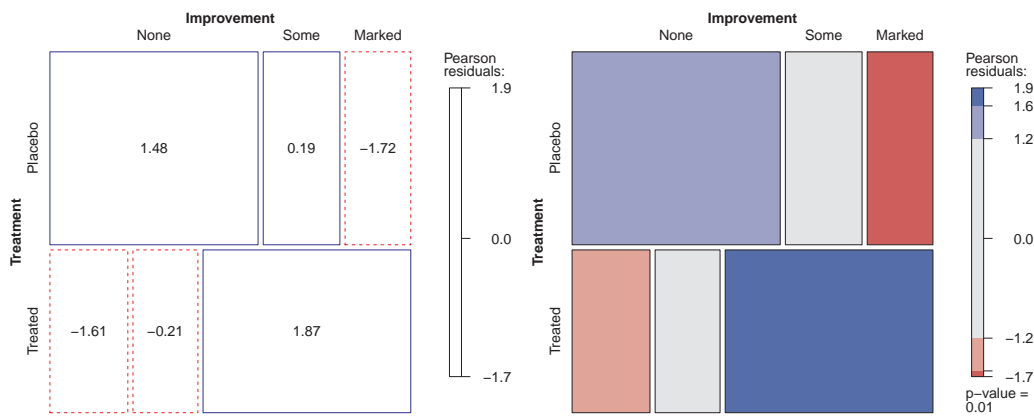

Figure 5.9: Mosaic plots for the female patients in the Arthritis data. Left: Fixed shading levels via shading_Friendly; right: shading levels determined by significant maximum residuals via shading_max.

This data set is somewhat paradoxical, in that the standard chisq.test() for association with these data gives a highly significant result, $\chi^2(2) = 11.3, p = 0.0035$, while the shading pattern using shading_Friendly in the left panel of Figure 5.9 shows all residuals within ± 2, and thus unshaded.

On the other hand, the shading_max shading in the right panel of Figure 5.9 shows that significant deviations from independence occur in the four corner cells, corresponding to more of the treated group showing marked improvement, and more of the placebo group showing no improvement.

Some details behind the shading_max method are shown below. The Pearson residuals for this table are calculated as:

```
> residuals(chisq.test(art))

         Improvement
Treatment      None      Some     Marked
  Placebo  1.47752   0.19267  -1.71734
  Treated -1.60852  -0.20975   1.86960
```

The `shading_max()` function then calls `coindep_test(art)` to generate $n = 1000$ random tables with the same margins, and computes the maximum residual statistic for each. This gives a non-parametric p-value for the test of independence, $p = 0.011$ shown in the legend.

```
> set.seed(1243)
> art_max <- coindep_test(art)
> art_max


Permutation test for conditional independence

data:  art
f(x) = 1.87, p-value = 0.011
```

Finally, the 0.90 and 0.99 quantiles of the simulation distribution are used as shading levels, passed as the value of the `interpolate` argument.

```
> art_max$qdist(c(0.90, 0.99))

   90%     99%
1.2393  1.9167
```

$\triangle$

The converse situation can also arise in practice. An overall test for association using Pearson's χ^2 may not be significant, but the maximum residual test may highlight one or more cells worthy of greater attention, as illustrated in the following example.

{ex:soccer2}

EXAMPLE 5.5: UK soccer scores

In Example 3.9, we examined the distribution of goals scored by the home team and the away team in 380 games in the 1995/96 season by the 20 teams in the UK Football Association, Premier League. The analysis there focused on the distribution of the total goals scored, under the assumption that the number of goals scored by the home team and the away team were independent.

Here, the rows and columns of the table *UKSoccer* are both ordered, so it is convenient and compact to carry out all the CMH tests taking ordinality into account.

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

Cochran-Mantel-Haenszel Statistics for Home by Away

                 AltHypothesis Chisq Df  Prob
cor        Nonzero correlation  1.01  1 0.315
rmeans  Row mean scores differ  5.63  4 0.229
cmeans  Col mean scores differ  7.42  4 0.115
general     General association 18.65 16 0.287
```

All of these are non-significant, so that might well be the end of the story, as far as independence of goals in home and away games is concerned. Yet, one residual, $r_{42} = 3.08$ stands out, corresponding to 4 or more goals by the home team and only 2 goals by the away team, which accounts for nearly half of the $\chi^2(16) = 18.7$ for general association. The mosaic plot is shown in Figure 5.10.

```
> set.seed(1234)
> mosaic(UKSoccer, gp = shading_max, labeling = labeling_residuals,
+        digits = 2)
```
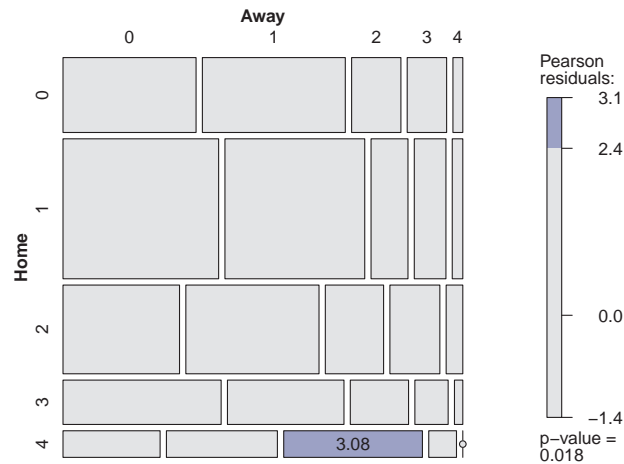

Figure 5.10: Mosaic display for UK soccer scores, highlighting one cell that stands out for further attention.

{fig:UKsoccer-mosaic}

This occurrence may or may not turn out to have some explanation, but at least the mosaic plot draws it to our attention, and is consistent with the (significant) result from `coindep_test()`. △

5.4   Three-way and larger tables

{sec:mosaic-threeway}

The mosaic displays and other graphical methods within the strucplot framework extend quite naturally to three-way and higher-way tables. The essential idea is that for the variables in a multiway table in a given order, each successive variable is used to subdivide the tile(s) in proportion to the relative (conditional) frequencies of that variable, given all previous variables. This process continues recursively until all table variables have been included.

For simplicity, we continue with the running example of hair color and eye color. Imagine that each cell of the two-way table for hair and eye color is further classified by one or more additional variables—sex and level of education, for example. Then each rectangle can be subdivided horizontally to show the proportion of males and females in that cell, and each of those horizontal portions can be subdivided vertically to show the proportions of people at each educational level in the hair–eye–sex group.

{ex:HEC1}

EXAMPLE 5.6: Hair color, eye color, and sex

Figure 5.11 shows the mosaic for the three-way table, with hair and eye color groups divided according to the proportions of males and females. As explained in the next section (Section 5.4.2)

there are now different models for "independence" we could investigate, not just the (mutual) independence of all factors. Here, for example, we could examine whether the additional variable (Sex) is independent from the *joint* relationship between Hair and Eye.

```
> HEC <- HairEyeColor[, c("Brown", "Hazel", "Green", "Blue"),]
> mosaic(HEC, rot_labels = c(right = -45))
```
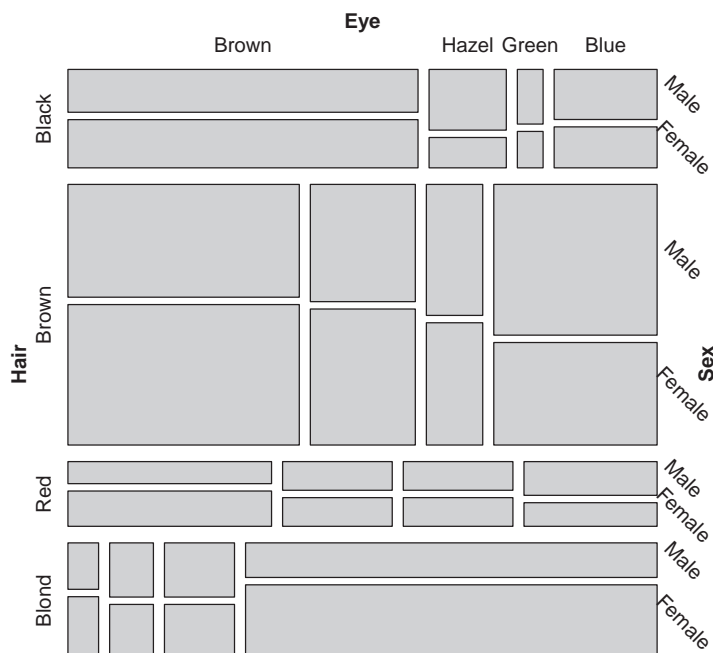

Figure 5.11: Three-way mosaic for hair color, eye color, and sex.   {fig:HEC-mos1b}

In Figure 5.11 it is easy to see that there is no systematic association between sex and the combinations of hair and eye color—the proportion of male/female students is roughly the same in almost all hair/eye color groups. Yet, among blue-eyed blonds, there seems to be an overabundance of females, and the proportion of blue-eyed males with brown hair also looks suspicious.   △

These and other hypotheses are best tested within the framework of ***loglinear model***s, allowing you to flexibly specify various independence models for any number of variables, and analyze them similarly to classical ANOVA models. This general topic is discussed in detail in Chapter 9. For the present purposes, we give a short introduction in the following section.

5.4.1 A primer on loglinear models

{sec:loglinprimer}

The essential idea behind loglinear models is that the multiplicative relationships among expected frequencies under independence (shown as areas in sieve diagrams and mosaic plots) become *additive* models when expressed as models for log frequency, and we briefly explain this connection here for two-way tables.

To see this, consider two discrete variables, A and B, with n_{ij} observations in each cell i, j of an $R \times C$ contingency table, and use $n_{i+} = \Sigma_j n_{ij}$ and $n_{+j} = \Sigma_i n_{ij}$ for the row and column

marginal totals, respectively. The total frequency is $n_{++} = \Sigma_{ij} n_{ij}$. Analogously, we use m_{ij} for the expected frequency under any model and also use a subscript $+$ to represent summation over that dimension.

Then, the hypothesis of independence means that the expected frequencies, m_{ij}, obey

$$m_{ij} = \frac{m_{i+}\, m_{+j}}{m_{++}}\,.$$

This multiplicative model can be transformed to an additive (linear) model by taking logarithms of both sides:

$$\log(m_{ij}) = \log(m_{i+}) + \log(m_{+j}) - \log(m_{++})\,.$$

This is usually re-expressed in an equivalent form in terms of model parameters μ, λ_i^A and λ_j^B

<div style="text-align:left">{eq:lmain0}</div>
$$\log(m_{ij}) = \mu + \lambda_i^A + \lambda_j^B \equiv [A][B]\,. \tag{5.1}$$

Model Eqn. (5.1) asserts that the row and column variables are independent because there is no term that depends on both A and B.

In contrast, a model for a two-way table that allows an arbitrary association between the variables is the ***saturated model***, including an additional term, λ_{ij}^{AB}:

<div style="text-align:left">{eq:lsat0}</div>
$$\log(m_{ij}) = \mu + \lambda_i^A + \lambda_j^B + \lambda_{ij}^{AB} \equiv [AB]\,. \tag{5.2}$$

Except for the difference in notation, model Eqn. (5.2) is formally the same as a two-factor ANOVA model with an interaction, typically expressed as $E(y_{ij}) = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij}$. Hence, associations between variables in loglinear models are analogous to interactions in ANOVA models.[6] In contrast to ANOVA, the "main effects," λ_i^A and λ_j^B, are rarely of interest—a typical log-linear analysis focuses only on the interaction (association) terms.

Models such as Eqn. (5.1) and Eqn. (5.2) are examples of ***hierarchical models***. This means that the model must contain all lower-order terms contained within any high-order term in the model. Thus, the saturated model, Eqn. (5.2) contains λ_{ij}^{AB}, and therefore *must* contain λ_i^A and λ_j^B. As a result, hierarchical models may be identified by the shorthand notation that lists only the high-order terms: model Eqn. (5.2) is denoted $[AB]$, while model Eqn. (5.1) is $[A][B]$.

In R, the most basic function for fitting loglinear models is `loglin()` in the stats package. It is designed to work with the frequency data in table form, and a model specified in terms of the (high-order) table margins to be fitted. For example, the independence model Eqn. (5.1) is specified as

```
> loglin(mytable, margin = list(1, 2))
```

meaning that variables 1 and 2 are independent, whereas the saturated model Eqn. (5.2) would be specified as

```
> loglin(mytable, margin = list(c(1, 2)))
```

The function `loglm()` in MASS (Ripley, 2015) provides a more convenient front-end to `loglin()` to allow loglinear models to be specified using a model formula. With table variables A and B, the independence model can be fit using `loglm()` as

```
> loglm(~ A + B, data = mytable)
```

and the saturated model in either of the following equivalent forms:

---

[6]The use of superscripted symbols, $\lambda_i^A, \lambda_j^B, \lambda_{ij}^{AB}$, rather than separate Greek letters is a convention in loglinear models, and useful mainly for multiway tables.

```
> loglm(~ A + B + A : B, data = mytable)
> loglm(~ A * B, data = mytable)
```

In such model formulas, A:B indicates an interaction term λ_{ij}^{AB}, while A*B is expanded to also include the terms A + B.

EXAMPLE 5.7: Hair color, eye color, and sex

Getting back to our running example of hair and eye color, we start casting the classical test of independence used in Section 5.2 as log-linear model analysis. Using the haireye two-way table, the independence of Hair and Eye is equivalent to the model [Hair][Eye] and formulated in R using loglm() as:

```
> loglm(~ Hair + Eye, data = haireye)

Call:
loglm(formula = ~Hair + Eye, data = haireye)

Statistics:
                      X^2 df P(> X^2)
Likelihood Ratio 146.44   9        0
Pearson          138.29   9        0
```

The output includes both the χ^2 and the deviance test statistics, both significant, indicating strong lack of fit. We now extend the analysis by including Sex, i.e., use the full *HairEyeColor* data set. In the section's introductory example, this was visualized using a mosaic plot, leading to the hypothesis whether Hair and Eye were jointly independent of Sex. To test this formally, we fit the corresponding model [HairEye][Sex] to the data:

```
> HE_S <- loglm(~ Hair * Eye + Sex, data = HairEyeColor)
> HE_S

Call:
loglm(formula = ~Hair * Eye + Sex, data = HairEyeColor)

Statistics:
                      X^2 df P(> X^2)
Likelihood Ratio 19.857  15  0.17750
Pearson          19.567  15  0.18917
```

giving a non-significant Pearson $\chi^2(15) = 19.567, p = 0.189$. The residuals from this model could be retrieved using

```
> residuals(HE_S, type = "pearson")
```

for further inspection. Mosaic plots can conveniently be used for this purpose, either by specifying the residuals with the residuals= argument, or by providing the loglm model formula as the expected= argument, letting mosaic() calculate them by calling loglm(). In the call to mosaic() below, the model of joint independence is specified as expected = ~ Hair * Eye + Sex. The strucplot labeling function labeling_residuals is used to display the residuals in the highlighted cells.

```
> HEC <- HairEyeColor[, c("Brown", "Hazel", "Green", "Blue"),]
> mosaic(HEC, expected = ~ Hair * Eye + Sex,
+        labeling = labeling_residuals,
+        digits = 2, rot_labels = c(right = -45))
```

Although non-significant, the two largest residuals highlighted in the plot account for nearly half $(-2.15^2 + 2.03^2 = 8.74)$ of the lack of fit, and so are worthy of attention here. An easy (probably facile) interpretation is that among the blue-eyed blonds, some of the females benefited from hair products. △
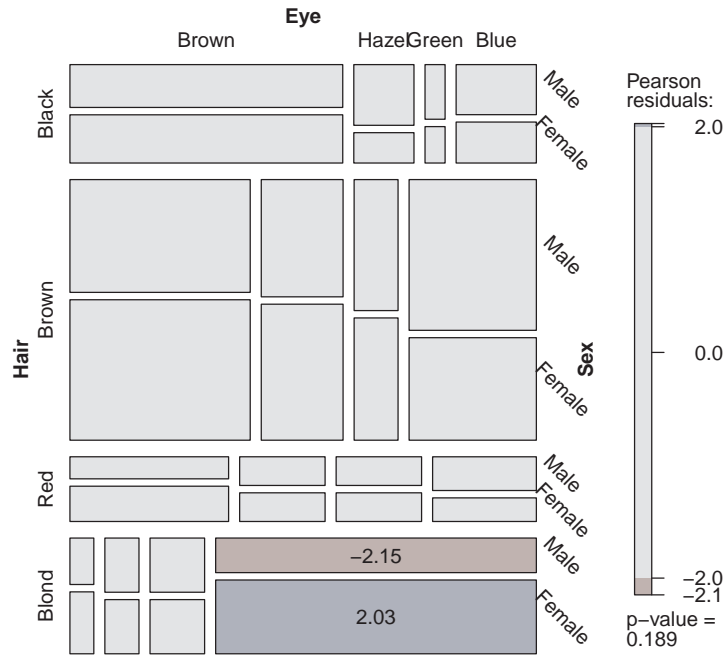
Figure 5.12: Three-way mosaic for hair color, eye color, and sex. Residuals from the model of joint independence, [HE][S] are shown by shading.   {fig:HEC-mos1}

5.4.2 Fitting models

{sec:mosaic-fitting}

When three or more variables are represented in a table, we can fit several different models of types of "independence" and display the residuals from each model. We treat these models as null or ***baseline models***, which may not fit the data particularly well. The deviations of observed frequencies from expected ones, displayed by shading, will often suggest terms to be added to an explanatory model that achieves a better fit.

For a three-way table, with variables A, B and C, some of the hypothesized models that can be fit are described below and summarized in Table 5.2. Here we use $[\bullet]$ notation to list the ***high-order terms*** in a hierarchical loglinear model; these correspond to the margins of the table that are fitted exactly, and which translate directly into R formulas used in `loglm()` and `mosaic(...,  expected=)`.

The notation [AB][AC], for example, is shorthand for the model `loglm(~ A*B + A*C)` that implies
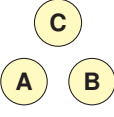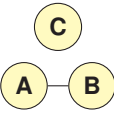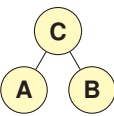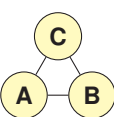
{eq:AB-AC}
$$\log(m_{ijk}) = \mu + \lambda_i^A + \lambda_j^B + \lambda_k^C + \lambda_{ij}^{AB} + \lambda_{ik}^{AC} , \tag{5.3}$$

and reproduces the $\{AB\}$ and $\{AC\}$ marginal subtables.[7] That is, the calculated expected frequencies in these margins are always equal to the corresponding observed frequencies, $m_{ij+} = n_{ij+}$ and $m_{i+k} = n_{i+k}$.

In this table, $A \perp B$ is read, "A is independent of B." The independence interpretation of the model Eqn. (5.3) is $B \perp C \mid A$, which can be read as "B is independent of C, given (conditional on) A." Table 5.2 also depicts the relations among variables as an ***association graph***, where associated

---

[7]The notation here uses curly braces, $\{\bullet\}$ to indicate a marginal subtable summed over all other variables.

Table 5.2: Fitted margins, model symbols, and interpretations for some hypotheses for a three-way

table

Hypothesis	Fitted margins	Model symbol	Independence interpretation	Association graph
H_1	$n_{i++}, n_{+j+}, n_{++k}$	[A][B][C]	$A \perp B \perp C$	
H_2	n_{ij+}, n_{++k}	[AB][C]	$(A, B) \perp C$	
H_3	n_{i+k}, n_{+jk}	[AC][BC]	$A \perp B \mid C$	
H_4	$n_{ij+}, n_{i+k}, n_{+jk}$	[AB][AC][BC]	NA	

variables are connected by an edge and variables that are asserted to be independent are uncon-
nected. In mosaic-like displays, other associations present in the data will appear in the pattern of
residuals.

For a three-way table, there are four general classes of independence models illustrated in Ta-
ble 5.2, as described below.[8] Not included here is the ***saturated model***, [ABC], which fits the
observed data exactly.

H_1**: Complete independence.** The model of complete (mutual) independence, symbolized $A \perp$
$B \perp C$, with model formula ~ A + B + C, asserts that all joint probabilities are products of
the one-way marginal probabilities:

$$\pi_{ijk} = \pi_{i++}\, \pi_{+j+}\, \pi_{++k}\,,$$

for all i, j, k in a three-way table. This corresponds to the log-linear model [A][B][C]. Fit-
ting this model puts all higher terms, and hence all association among the variables, into the
residuals.

H_2**: Joint independence.** Another possibility is to fit the model in which variable C is jointly
independent of variables A and B, $(\{A, B\} \perp C)$, with model formula ~ A*B + C, where

$$\pi_{ijk} = \pi_{ij+}\, \pi_{++k}\,.$$

This corresponds to the loglinear model [AB][C]. Residuals from this model show the extent to
which variable C is related to the combinations of variables A and B but they do not show any

___
[8]For H_2 and H_3, permutation of the variables A, B, and C gives other members of each class.

association between A and B, since that association is fitted exactly. For this model, variable C is also independent of A and B in the marginal $\{AC\}$ table (collapsing over B) and in the marginal $\{BC\}$.

H_3: **Conditional independence.** Two variables, say A and B, are conditionally independent given the third (C) if A and B are independent when we control for C, symbolized as $A \perp B \,|\, C$, and model formula ~ `A*C + B*C` (or ~ `(A + B) * C`). This means that conditional probabilities, $\pi_{ij|k}$ obey

$$\pi_{ij|k} = \pi_{i+|k}\,\pi_{+j|k}\,,$$

where $\pi_{ij|k} = \pi_{ijk}/\pi_{ij+}$, $\pi_{i+|k} = \pi_{i+k}/\pi_{i++}$, and $\pi_{+j|k} = \pi_{+jk}/\pi_{+j+}$. The corresponding loglinear models is denoted [AC][BC]. When this model is fit, the mosaic display shows the conditional associations between variables A and B, controlling for C, but does not show the associations between A and C, or B and C.

H_4: **No three-way interaction.** For this model, no pair is marginally or conditionally independent, so there is *no* independence interpretation. Nor is there a closed-form expression for the cell probabilities. However, the association between any two variables is the same at each level of the third variable. The corresponding loglinear model formula is [AB][AC][BC], indicating that all two-way margins are fit exactly and so only the three-way association is shown in the mosaic residuals.

{ex:HEC3}

EXAMPLE 5.8: Hair color, eye color, and sex

We continue with the analysis of the `HairEyeColor` data from Example 5.6 and Example 5.7. Figure 5.12 showed the fit of the joint-independence model [HairEye][Sex], testing whether the joint distribution of hair color and eye color is associated with sex.

Any other model fit to this table will have the same size tiles in the mosaic since the areas depend on the observed frequencies; the residuals, and hence the shading of the tiles will differ. Figure 5.13 shows mosaics for two other models. Shading in the left panel shows residuals from the model of mutual independence, [Hair][Eye][Sex], and so includes all sources of association among these three variables. The right panel shows the conditional independence model, [HairSex][EyeSex], testing whether hair color and eye color are independent, given sex. Note that the pattern of residuals here is similar to that in the two-way display, Figure 5.4, that collapsed over sex.

```
> abbrev <- list(abbreviate = c(FALSE, FALSE, 1))
> mosaic(HEC, expected = ~ Hair + Eye + Sex, labeling_args = abbrev,
+    main = "Model: ~ Hair + Eye + Sex")
> mosaic(HEC, expected = ~ Hair * Sex + Eye * Sex, labeling_args = abbrev,
+        main="Model: ~ Hair*Sex + Eye*Sex")
```

Compared with Figure 5.12 for the joint independence model, [HairEye][Sex], it is easy to see that both of these models fit very poorly.

We consider loglinear models in more detail in Chapter 9, but for now note that these models are fit using `loglm()` in the MASS package, with the model formula given in the `expected` argument. The details of these models can be seen by fitting these models explicitly, and the fit of several models can be summarized compactly using `LRstats()` in vcdExtra (Friendly, 2015).

```
> library(MASS)
> # three types of independence:
> mod1 <- loglm(~ Hair + Eye + Sex, data = HEC)          # mutual
> mod2 <- loglm(~ Hair * Sex + Eye * Sex, data = HEC)    # conditional
> mod3 <- loglm(~ Hair * Eye + Sex, data = HEC)          # joint
> LRstats(mod1, mod2, mod3)
```
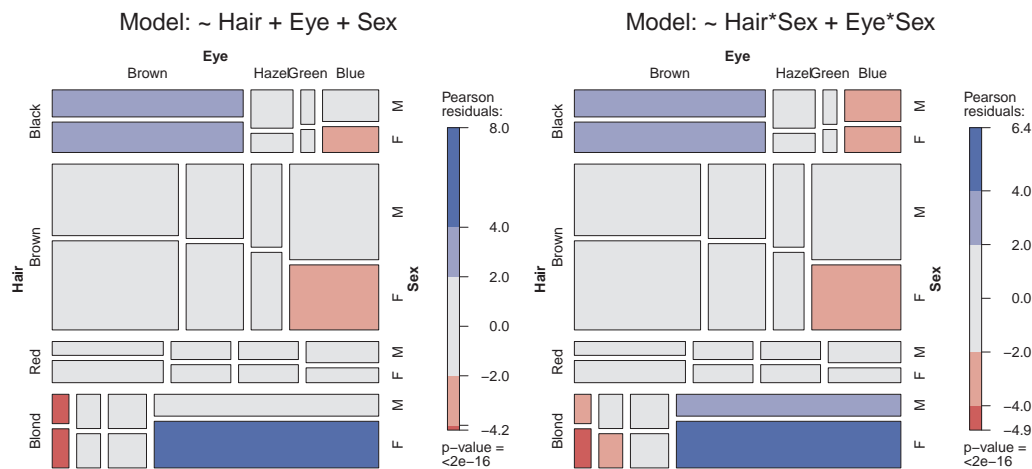
Figure 5.13: Mosaic displays for other models fit to the data on hair color, eye color, and sex. Left: Mutual independence model; right: Conditional independence of hair color and eye color given sex.

{fig:HEC-mos2}

```
Likelihood summary table:
     AIC BIC LR Chisq Df Pr(>Chisq)
mod1 321 333    166.3 24      <2e-16 ***
mod2 324 344    156.7 18      <2e-16 ***
mod3 193 218     19.9 15        0.18
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Alternatively, you can get the Pearson and likelihood ratio (LR) tests for a given model using `anova()`, or compare a set of models using LR tests on the *difference* in LR χ^2 from one model to the next, when a list of models is supplied to `anova()`.

```
> anova(mod1)

Call:
loglm(formula = ~Hair + Eye + Sex, data = HEC)

Statistics:
                   X^2 df P(> X^2)
Likelihood Ratio 166.30 24        0
Pearson          164.92 24        0

> anova(mod1, mod2, mod3, test = "chisq")

LR tests for hierarchical log-linear models

Model 1:
 ~Hair + Eye + Sex
Model 2:
 ~Hair * Sex + Eye * Sex
Model 3:
 ~Hair * Eye + Sex

          Deviance df Delta(Dev) Delta(df) P(> Delta(Dev)
Model 1    166.300 24
Model 2    156.678 18     9.6222         6        0.14149
Model 3     19.857 15   136.8213         3        0.00000
Saturated    0.000  0    19.8566        15        0.17750
```

△

5.5   Model and plot collections

This section describes a few special circumstances in which a collection of mosaic plots and related loglinear models can be used in a complementary fashion to understand the nature of associations in three-way and larger tables.

5.5.1   Sequential plots and models

As described in Section 5.2, we can think of the mosaic display for an n-way table as being constructed in stages, with the variables listed in a given order, and the unit tile decomposed recursively as each variable is entered in turn. This process turns out to have the useful property that it provides an additive (hierarchical) decomposition of the total association in a table, in a way analogous to sequential fitting with Type I sum of squares in regression models.

Typically, we just view the mosaic and fit models to the full n-way table, but it is useful to understand the connection with models for the marginal subtables, defined by summing over all variables not yet entered. For example, for a three-way table with variables A, B, C, the marginal subtables $\{A\}$ and $\{AB\}$ are calculated in the process of constructing the three-way mosaic. The $\{A\}$ marginal table can be fit to a model where the categories of variable A are equiprobable as shown in Figure 5.2 (or some other discrete distribution); the independence model can be fit to the $\{AB\}$ subtable as in Figure 5.2, and so forth.

This connection can be seen in the following formula that decomposes the joint cell probability in an n-way table with variables $v_1, v_2, \ldots v_n$ as a sequential product of conditional probabilities,

$$p_{ijk\ell\ldots} = \overbrace{p_i \times p_{j|i} \times \underbrace{p_{k|ij}}} \times p_{\ell|ijk} \times \cdots \times p_{n|ijk\ldots} \tag{5.4}$$

where the brace above spans $\{v_1 v_2\}$ and the brace below spans $\{v_1 v_2 v_3\}$.

In Eqn. (5.4), the first term corresponds to the one-way mosaic for v_1, the first two terms to the mosaic for v_1 and v_2, the first three terms to the mosaic for v_1, v_2, and v_2, and so forth.

It can be shown (Friendly, 1994) that this sequential product of probabilities corresponds to a set of sequential models of *joint independence*, whose likelihood ratio G^2 statistics provide an additive decomposition of the total association, $G^2_{[v_1][v_2]\ldots[v_n]}$ for the mutual independence model in the full table:

$$G^2_{[v_1][v_2]\ldots[v_n]} = G^2_{[v_1][v_2]} + G^2_{[v_1 v_2][v_3]} + G^2_{[v_1 v_2 v_3][v_4]} + \cdots + G^2_{[v_1 \ldots v_{n-1}][v_n]} . \tag{5.5}$$

For example, for the hair-eye data, the mosaic displays for the [Hair] [Eye] marginal table (Figure 5.4) and the [HairEye] [Sex] table (Figure 5.12) can be viewed as representing the partition of G^2 shown as a table below:

Model	Model symbol	df	G^2
Marginal	[Hair] [Eye]	9	146.44
Joint	[Hair, Eye] [Sex]	15	19.86
Mutual	[Hair] [Eye] [Sex]	24	166.30

The decomposition in this table reflecting Eqn. (5.5) is shown as a visual equation in Figure 5.14. You can see from the shading how the two sequential submodels contribute to overall association in the model of mutual independence.

Although sequential models of joint independence have the nice additive property illustrated
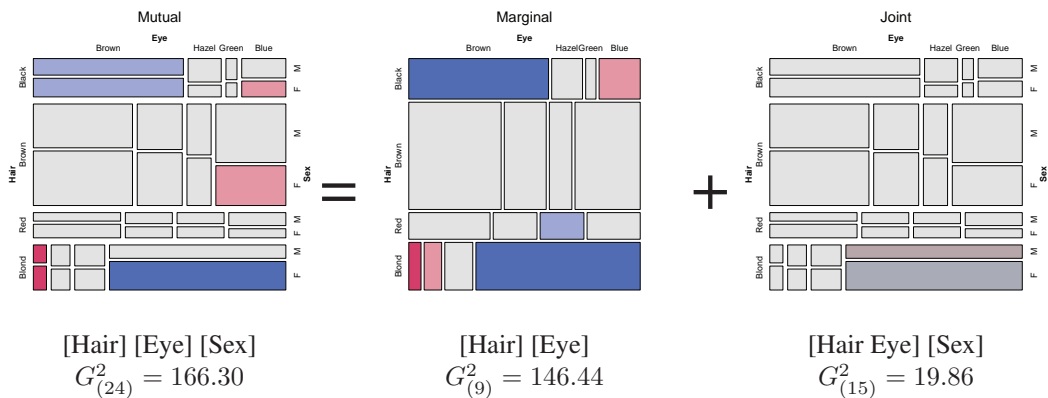
$$[Hair] [Eye] [Sex] \qquad [Hair] [Eye] \qquad [Hair Eye] [Sex]$$
$$G^2_{(24)} = 166.30 \qquad G^2_{(9)} = 146.44 \qquad G^2_{(15)} = 19.86$$

Figure 5.14: Visual representation of the decomposition of the G^2 for mutual independence (total) as the sum of marginal and joint independence.

{fig:HEC-seq}

above, other classes of sequential models are possible, and sometimes of substantive interest. The main types of these models are illustrated in Table 5.3 for 3-, 4-, and 5-way tables, with variables A, B, ..., E. In all cases, the natural model for the one-way margin is the equiprobability model, and that for the two-way margin is [A][B].

{tab:seqmodels} **Table 5.3:** Classes of sequential models for *n*-way tables

function	3-way	4-way	5-way
mutual	[A] [B] [C]	[A] [B] [C] [D]	[A] [B] [C] [D] [E]
joint	[AB] [C]	[ABC] [D]	[ABCE] [E]
joint (with=1)	[A] [BC]	[A] [BCD]	[A] [BCDE]
conditional	[AC] [BC]	[AD] [BD] [CD]	[AE] [BE] [CE] [DE]
conditional (with=1)	[AB] [AC]	[AB] [AC] [AD]	[AB] [AC] [AD] [AE]
markov (order=1)	[AB] [BC]	[AB] [BC] [CD]	[AB] [BC] [CD] [DE]
markov (order=2)	[A] [B] [C]	[ABC] [BCD]	[ABC] [BCD] [CDE]
saturated	[ABC]	[ABCD]	[ABCDE]

The vcdExtra package provides a collection of convenience functions that generate the loglinear model formulae symbolically, as indicated in the **function** column. The functions `mutual()`, `joint()`, `conditional()`, `markov()` and so forth simply generate a list of terms suitable for a model formula for `loglin()`. See `help(loglin-utilities)` for further details.

Wrapper functions `loglin2string()` and `loglin2formula()` convert these to character strings or model formulae, respectively, for use with `loglm()` and `mosaic()`-related functions in vcdExtra. Some examples are shown below.

```
> for(nf in 2 : 5) {
+   print(loglin2string(joint(nf, factors = LETTERS[1:5])))
+ }

[1] "[A] [B]"
[1] "[A,B] [C]"
[1] "[A,B,C] [D]"
[1] "[A,B,C,D] [E]"

> for(nf in 2 : 5) {
```

```
+    print(loglin2string(conditional(nf, factors = LETTERS[1:5]),
+                          sep = ""))
+ }

[1] "[A] [B]"
[1] "[AC] [BC]"
[1] "[AD] [BD] [CD]"
[1] "[AE] [BE] [CE] [DE]"

> for(nf in 2 : 5) {
+   print(loglin2formula(conditional(nf, factors = LETTERS[1:5])))
+ }

~A + B
~A:C + B:C
~A:D + B:D + C:D
~A:E + B:E + C:E + D:E
```

Applied to data, these functions take a `table` argument, and deliver the string or formula representation of a type of model for that table:

```
> loglin2formula(joint(3, table = HEC))

~Hair:Eye + Sex

> loglin2string(joint(3, table = HEC))

[1] "[Hair,Eye] [Sex]"
```

Their main use, however, is within higher-level functions, such as `seq_loglm()`, which fit the collection of sequential models of a given type.

```
> HEC.mods <- seq_loglm(HEC, type = "joint")
> LRstats(HEC.mods)

Likelihood summary table:
        AIC BIC LR Chisq Df Pr(>Chisq)
model.1 194 194    165.6  3      <2e-16 ***
model.2 241 246    146.4  9      <2e-16 ***
model.3 193 218     19.9 15        0.18
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In this section we have described a variety of models that can be fit to higher-way tables, some relations among those models, and the aspects of lack of fit that are revealed in the mosaic displays. The following discussion illustrates the process of model fitting, using the mosaic as an interpretive guide to the nature of associations among the variables. In general, we start with a minimal baseline model.[9] The pattern of residuals in the mosaic will suggest associations to be added to an adequate explanatory model. As the model achieves better fit to the data, the degree of shading decreases, so we may think of the process of model fitting as "cleaning the mosaic."

5.5.2   Causal models

The sequence of models of joint independence has another interpretation when the ordering of the variables is based on a set of ordered hypotheses involving causal relationships among variables

---

[9]When one variable, R, is a response, this normally is the model of joint independence, $[E_1 E_2 \ldots] [R]$, where $E_1, E_2, \ldots$ are the explanatory variables. Better-fitting models will often include associations of the form $[E_i R]$, $[E_i E_j R] \ldots$.

(Goodman, 1973, Fienberg, 1980, Section 7.2). Suppose, for example, that the causal ordering of four variables is $A \to B \to C \to D$, where the arrow means "is antecedent to." Goodman suggests that the conditional joint probabilities of B, C, and D given A can be characterized by a set of recursive logit models that treat (a) B as a response to A, (b) C as a response to A and B jointly, and (c) D as a response to A, B and C.

These are equivalent to the loglinear models that we fit as the sequential baseline models of joint independence, namely [A][B], [AB][C], and [ABC][D]. The combination of these models with the marginal probabilities of A gives a characterization of the joint probabilities of all four variables, as in Eqn. (5.4). In application, residuals from each submodel show the associations that remain unexplained.

{ex:marital1}

EXAMPLE 5.9: Marital status and pre- and extramarital sex

A study of divorce patterns in relation to premarital and extramarital sex by Thornes and Collard (1979) reported the 2^4 table shown below, and included in vcd as $PreSex$.

```
> data("PreSex", package = "vcd")
> structable(Gender + PremaritalSex + ExtramaritalSex ~ MaritalStatus,
+            data = PreSex)

              Gender         Women             Men
              PremaritalSex    Yes       No      Yes       No
              ExtramaritalSex  Yes  No Yes  No Yes  No Yes   No
MaritalStatus
Divorced                       17  54  36 214  28  60  17   68
Married                         4  25   4 322  11  42   4  130
```

These data were analyzed by Agresti (2013, Section 6.1.7) and by Friendly (1994, 2000), from which this account draws. A sample of about 500 people who had petitioned for divorce, and a similar number of married people, were asked two questions regarding their pre- and extramarital sexual experience: (1) "Before you married your (former) husband/wife, had you ever made love with anyone else?," (2) "During your (former) marriage (did you) have you had any affairs or brief sexual encounters with another man/woman?" The table variables are thus gender (G), reported premarital (P) and extramarital (E) sex, and current marital status (M).

In this analysis we consider the variables in the order G, P, E, and M, and first reorder the table variables for convenience.

```
> PreSex <- aperm(PreSex, 4 : 1)   # order variables G, P, E, M
```

That is, the first stage treats P as a response to G and examines the [Gender][Pre] mosaic to assess whether gender has an effect on premarital sex. The second stage treats E as a response to G and P jointly; the mosaic for [Gender, Pre] [Extra] shows whether extramarital sex is related to either gender or premarital sex. These are shown in Figure 5.15.

```
> # (Gender Pre)
> mosaic(margin.table(PreSex, 1 : 2), shade = TRUE,
+                 main = "Gender and Premarital Sex")
>
> ## (Gender Pre)(Extra)
> mosaic(margin.table(PreSex, 1 : 3),
+        expected = ~ Gender * PremaritalSex + ExtramaritalSex,
+        main = "Gender*Pre + ExtramaritalSex")
```

Finally, the mosaic for [Gender, Pre, Extra] [Marital] is examined for evidence of the dependence of marital status on the three previous variables jointly. As noted above, these models are equivalent to the recursive logit models whose path diagram is $G \to P \to E \to M$.[10] The G^2

---

[10]Agresti (2013, Figure 6.1) considers a slightly more complex, but more realistic model in which premarital sex affects both the propensity to have extramarital sex and subsequent marital status.
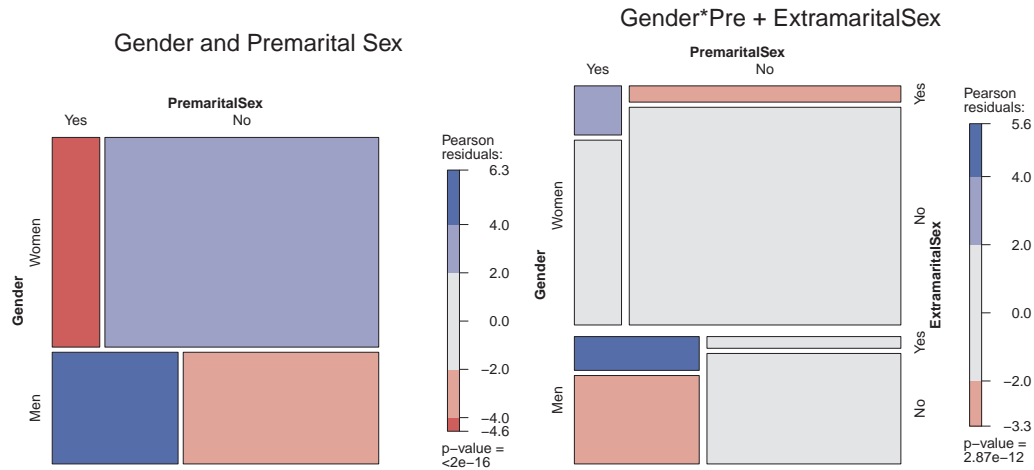
Figure 5.15: Mosaic displays for the first two marginal tables in the PreSex data. Left: Gender and premarital sex; right: fitting the model of joint independence with extramarital sex, [GP][E].

{fig:presex2}

values for these models shown below provide a decomposition of the G^2 for the model of complete independence fit to the full table.

Model	df	G^2
[G] [P]	1	75.259
[GP] [E]	3	48.929
[GPE] [M]	7	107.956
[G] [P] [E] [M]	11	232.142

The [Gender] [Pre] mosaic in the left panel of Figure 5.15 shows that men are much more likely to report premarital sex than are women; the sample odds ratio is 3.7. We also see that women are about twice as prevalent as men in this sample. The mosaic for the model of joint independence, [Gender Pre] [Extra] in the right panel of Figure 5.15, shows that extramarital sex depends on gender and premarital sex jointly. From the pattern of residuals in Figure 5.15 we see that men and women who have reported premarital sex are far more likely to report extramarital sex than those who have not. In this three-way marginal table, the conditional odds ratio of extramarital sex given premarital sex is nearly the same for both genders (3.61 for men and 3.56 for women). Thus, extramarital sex depends on premarital sex, but not on gender.

```
> loddsratio(margin.table(PreSex, 1 : 3), stratum = 1, log = FALSE)

 odds ratios for Gender and PremaritalSex by ExtramaritalSex

    Yes      No
0.28269 0.28611
```

Four-way mosaic plots for two models are shown in Figure 5.16.

```
> ## (Gender Pre Extra)(Marital)
> mosaic(PreSex,
+        expected = ~ Gender * PremaritalSex * ExtramaritalSex
+                   + MaritalStatus,
+        main = "Gender*Pre*Extra + MaritalStatus")
```

```
> ## (GPE)(PEM)
> mosaic(PreSex,
+        expected = ~ Gender * PremaritalSex * ExtramaritalSex
+                   + MaritalStatus * PremaritalSex * ExtramaritalSex,
+        main = "G*P*E + P*E*M")
```
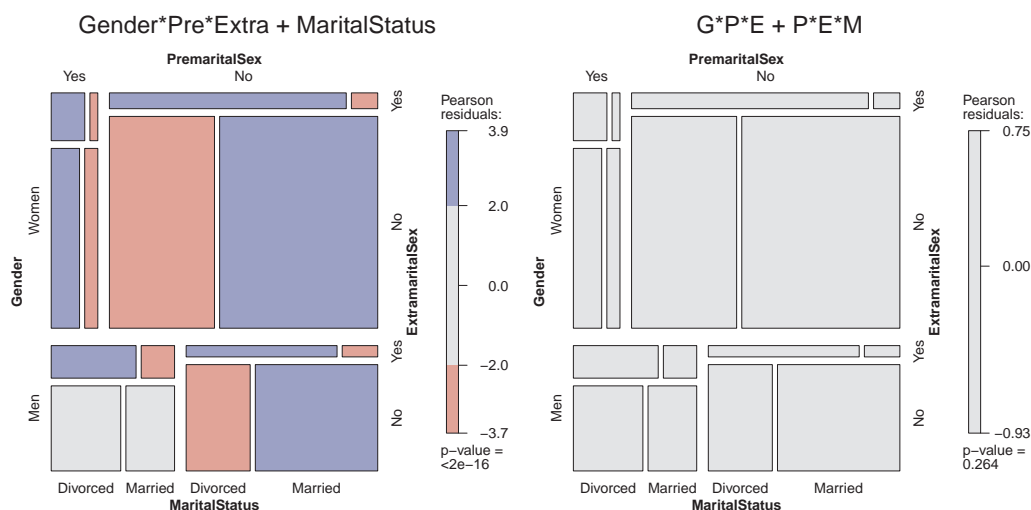

Figure 5.16: Four-way mosaics for the PreSex data. The left panel fits the model [GPE][M]. The pattern of residuals suggests other associations with marital status. The right panel fits the model [GPE][PEM].

{fig:presex3}

△

5.5.3 Partial association

{sec:mospart}

In a three-way (or larger) table it may be that two variables, say A and B, are associated at some levels of the third variable, C, but not at other levels of C. More generally, we may wish to explore whether and how the association among two (or more) variables in a contingency table varies over the levels of the remaining variables. The term ***partial association*** refers to the association among some variables within the levels of the other variables.

Partial association represents a useful "divide and conquer" statistical strategy: it allows you to refine the question you want to answer for complex relations by breaking it down to smaller, easier questions.[11] It is a statistically happy fact that an answer to the larger, more complex question can be expressed as an algebraic sum of the answers to the smaller questions, just as was the case with sequential models of joint independence.

For concreteness, consider the case where you want to understand the relationship between *attitude* toward corporal punishment of children by parents or teachers (Never, Moderate use OK) and *memory* that the respondent had experienced corporal punishment as a child (Yes, No). But you also have measured other variables on the respondents, including their level of *education* and *age* category. In this case, the question of association among all the table variables may be complex, but we can answer a highly relevant, specialized question precisely, "Is there an association between attitude and memory, *controlling for education and age*?" The answer to this question can be

---

[11]This is an analog, for categorical data, of the ANOVA strategy for "probing interactions" by testing ***simple effects*** at the levels of one or more of the factors involved in a two- or higher-way interaction.

thought of as the sum of the answers to the simpler question of association between attitude and memory across all combinations of the education and age categories.

A simpler version of this idea is considered first below (Example 5.10): among workers who were laid off due to either the closure of a plant or business vs. replacement by another worker, the (conditional) relationship of employment status (new job vs. still unemployed) and duration of unemployment can be studied as a sum of the associations between these focal variables over the separate tables for cause of layoff.

To make this idea precise, consider for example the model of conditional independence, $A \perp B \,|\, C$ for a three-way table. This model asserts that A and B are independent within *each* level of C. Denote the hypothesis that A and B are independent at level $C(k)$ by $A \perp B \,|\, C(k), k = 1, \ldots K$. Then one can show (Andersen, 1991) that

$$G^2_{A \perp B \,|\, C} = \sum_k^K G^2_{A \perp B \,|\, C(k)} . \tag{5.6}$$

That is, the overall likelihood ratio G^2 for the conditional independence model with $(I-1)(J-1)K$ degrees of freedom is the sum of the values for the ordinary association between A and B over the levels of C (each with $(I-1)(J-1)$ degrees of freedom). The same additive relationship holds for the Pearson χ^2 statistics: $\chi^2_{A \perp B \,|\, C} = \sum_k^K \chi^2_{A \perp B \,|\, C(k)}$.

Thus, (a) the overall G^2 (χ^2) may be decomposed into portions attributable to the AB association in the layers of C, and (b) the collection of mosaic displays for the dependence of A and B for each of the levels of C provides a natural visualization of this decomposition. These provide an analog, for categorical data, of the conditioning plot, or ***coplot***, that Cleveland (1993) has shown to be an effective display for quantitative data. See Friendly (1999a) for further details.

Mosaic and other displays in the strucplot framework for partial association can be produced in several different ways. One way is to use a model formula in the call to mosaic() which lists the conditioning variables after the "|" (given) symbol, as in

```
~ Memory + Attitude | Age + Education
```

Another way is to use cotabplot(). This takes the same kind of conditioning model formula, but presents each panel for the conditioning variables in a separate frame within a trellis-like grid.[12]

EXAMPLE 5.10: Employment status data

Data from a 1974 Danish study of 1,314 employees who had been laid off are given in the data table *Employment* in **vcd** (from Andersen (1991, Table 5.12)). The workers are classified by: (a) their employment status, on January 1, 1975 ("NewJob" or still "Unemployed"), (b) the length of their employment at the time of layoff, (c) the cause of their layoff ("Closure", etc., or "Replaced").

```
> data("Employment", package = "vcd")
> structable(Employment)

                          EmploymentLength <1Mo 1-3Mo 3-12Mo 1-2Yr 2-5Yr >5Yr
EmploymentStatus LayoffCause
NewJob           Closure                      8    35     70    62    56   38
                 Replaced                    40    85    181    85   118   56
Unemployed       Closure                     10    42     86    80    67   35
                 Replaced                    24    42     41    16    27   10
```

In this example, it is natural to regard EmploymentStatus (variable A) as the response variable, and EmploymentLength (B) and LayoffCause (C) as predictors. In this case, the

---

[12]Depending on your perspective, this has the advantage of adjusting for the total frequency in each conditional panel, or the disadvantage of ignoring these differences.

minimal baseline model is the joint independence model, $[A][BC]$, which asserts that employment status is independent of both length and cause. This model fits quite poorly, as shown in the output from `loglm()` below.

```
> loglm(~ EmploymentStatus + EmploymentLength * LayoffCause,
+       data = Employment)

Call:
loglm(formula = ~EmploymentStatus + EmploymentLength * LayoffCause,
    data = Employment)

Statistics:
                  X^2 df P(> X^2)
Likelihood Ratio 172.28 11        0
Pearson          165.70 11        0
```

The residuals, shown in Figure 5.17, indicate an opposite pattern for the two categories of `LayoffCause`: those who were laid off as a result of a closure are more likely to be unemployed, regardless of length of time they were employed. Workers who were replaced, however, apparently are more likely to be employed, particularly if they were employed for 3 months or more.

```
> # baseline model [A][BC]
> mosaic(Employment, shade = TRUE,
+       expected = ~ EmploymentStatus + EmploymentLength * LayoffCause,
+       main = "EmploymentStatus + Length * Cause")
```
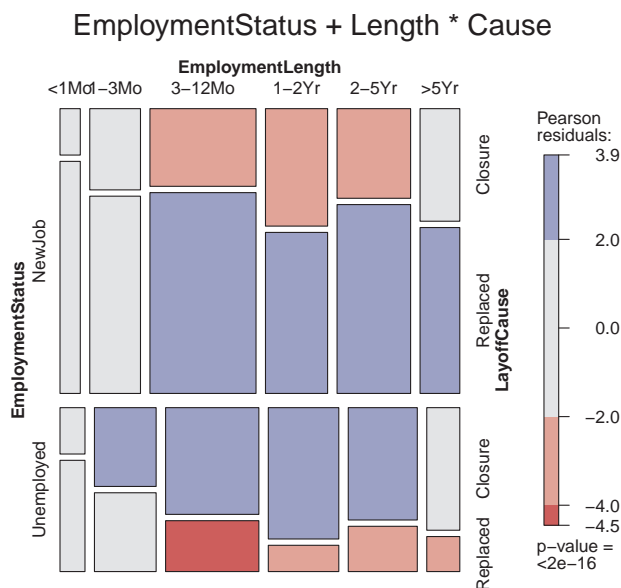

Figure 5.17: Mosaic display for the employment status data, fitting the baseline model of joint independence.

Beyond this baseline model, it is substantively more meaningful to consider the conditional independence model, $A \perp B \mid C$, (or [AC][BC] in shorthand notation), which asserts that employment status is independent of length of employment, given the cause of layoff. We fit this model as shown below:

```
> loglm(~ EmploymentStatus * LayoffCause + EmploymentLength * LayoffCause,
+       data = Employment)

Call:
loglm(formula = ~EmploymentStatus * LayoffCause + EmploymentLength *
    LayoffCause, data = Employment)

Statistics:
                      X^2 df  P(> X^2)
Likelihood Ratio 24.630 10 0.0060927
Pearson          26.072 10 0.0036445
```

This model fits far better ($G^2(10) = 24.63$), but the lack of fit is still significant. The residuals, shown in Figure 5.18, still suggest that the pattern of association between employment and length is different for replaced workers and those laid off due to closure of their workplace.

```
> mosaic(Employment, shade = TRUE, gp_args = list(interpolate = 1 : 4),
+        expected = ~ EmploymentStatus * LayoffCause +
+                     EmploymentLength * LayoffCause,
+        main = "EmploymentStatus * Cause + Length * Cause")
```
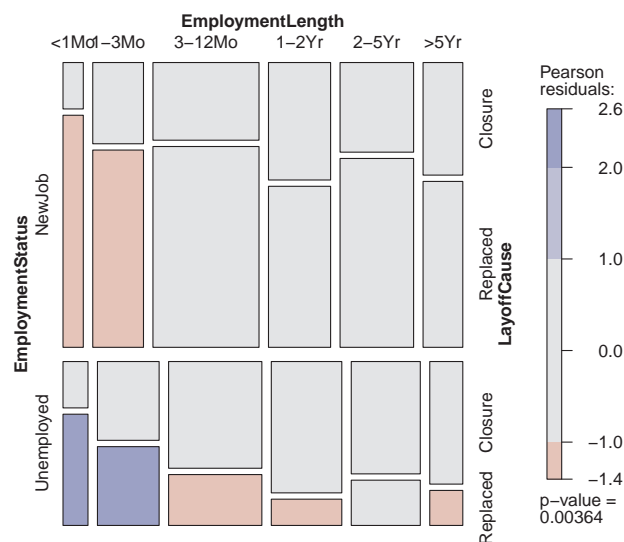

Figure 5.18: Mosaic display for the employment status data, fitting the model of conditional independence, [AC][BC].

{fig:employ-mos2}

To explain this result better, we can fit separate models for the *partial* relationship between `EmploymentStatus` and `EmploymentLength` for the two levels of `LayoffCause`. In R, with the `Employment` data as in table form, this is easily done using `apply()` over the `LayoffCause` margin, giving a list containing the two `loglm()` models.

```
> mods.list <-
+   apply(Employment, "LayoffCause",
+         function(x) loglm(~ EmploymentStatus + EmploymentLength,
+                           data = x))
> mods.list
```

```
$Closure
Call:
loglm(formula = ~EmploymentStatus + EmploymentLength, data = x)

Statistics:
                    X^2 df P(> X^2)
Likelihood Ratio 1.4786  5  0.91553
Pearson          1.4835  5  0.91497

$Replaced
Call:
loglm(formula = ~EmploymentStatus + EmploymentLength, data = x)

Statistics:
                    X^2 df   P(> X^2)
Likelihood Ratio 23.151  5 0.00031578
Pearson          24.589  5 0.00016727
```

Extracting the model fit statistics for these partial models and adding the fit statistics for the overall model of conditional independence, [AC][BC], gives the table below, illustrating the additive property of G^2 and χ^2 (Eqn. (5.6)).

Model	df	G^2	χ^2
$A \perp B \mid C_1$	5	1.49	1.48
$A \perp B \mid C_2$	5	23.15	24.59
$A \perp B \mid C$	10	24.63	26.07

One simple way to visualize these results is to call `mosaic()` separately for each of the layers corresponding to `LayoffCause`. The result is shown in Figure 5.19.

```
> mosaic(Employment[,,"Closure"], shade = TRUE,
+        gp_args = list(interpolate = 1 : 4),
+        margin = c(right = 1), main = "Layoff: Closure")
> mosaic(Employment[,,"Replaced"], shade = TRUE,
+        gp_args = list(interpolate = 1 : 4),
+        margin = c(right = 1), main = "Layoff: Replaced")
```
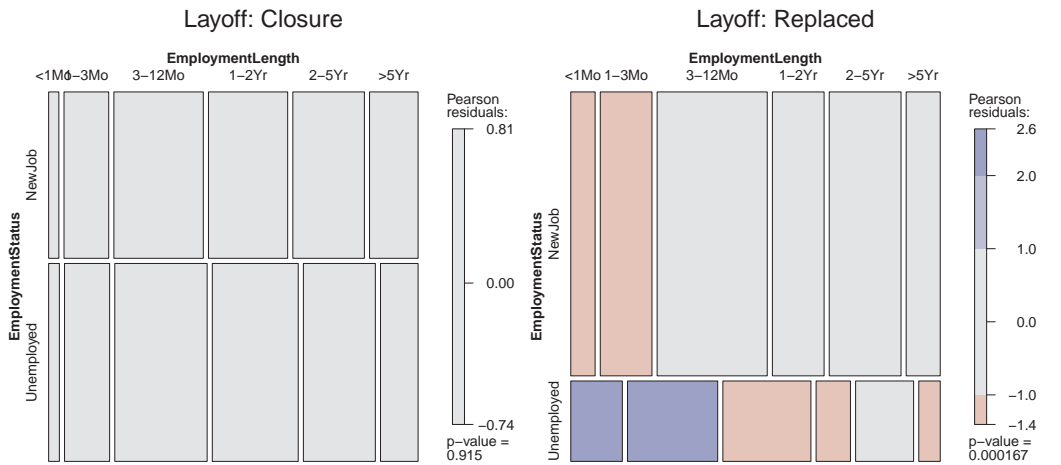

Figure 5.19: Mosaic displays for the employment status data, with separate panels for cause of layoff.

{fig:employ-mos3}

The simple summary from this example is that for workers laid off due to closure of their company, length of previous employment is unrelated to whether or not they are re-employed. However, for workers who were replaced, there is a systematic pattern: those who had been employed for three months or less are likely to remain unemployed, while those with longer job tenure are somewhat more likely to have found a new job.   △

The statistical methods and R techniques described above for three-way tables extend naturally to higher-way tables, as can be seen in the next example.

{ex:punish}

EXAMPLE 5.11: Corporal punishment data

Here we use the *Punishment* data from vcd, which contains the results of a study by the Gallup Institute in Denmark in 1979 about the attitude of a random sample of 1,456 persons towards corporal punishment of children (Andersen, 1991, pp. 207–208). As shown below, this data set is a frequency data frame representing a $2 \times 2 \times 3 \times 3$ table, with table variables (a) attitude toward use of corporal punishment (approve of "moderate" use or "no" approval); (b) memory of whether the respondent had experienced corporal punishment as a child (yes/no); (c) education level of respondent (elementary, secondary, high); and (d) age category of respondent.

```
> data("Punishment", package = "vcd")
> str(Punishment, vec.len = 2)

'data.frame':  36 obs. of  5 variables:
 $ Freq     : num  1 3 20 2 8 ...
 $ attitude : Factor w/ 2 levels "no","moderate": 1 1 1 1 1 ...
 $ memory   : Factor w/ 2 levels "yes","no": 1 1 1 1 1 ...
 $ education: Factor w/ 3 levels "elementary","secondary",..: 1 1 1 2 2 ...
 $ age      : Factor w/ 3 levels "15-24","25-39",..: 1 2 3 1 2 ...
```

Of main interest here is the association between attitude toward corporal punishment as an adult (A) and memory of corporal punishment as a child (B), controlling for age (C) and education (D); that is, the model $A \perp B \mid (C, D)$, or [ACD][BCD] in shorthand notation.

As noted above, this conditional independence hypothesis can be decomposed into the 3×3 partial tests of $A \perp B \mid (C_k, D_\ell)$.

These tests and the associated graphics are somewhat easier to carry out with the data in table form (pun) constructed below. While we're at it, we recode the variable names and factor levels for nicer graphical displays.

```
> pun <- xtabs(Freq ~ memory + attitude + age + education,
+              data = Punishment)
> dimnames(pun) <- list(
+   Memory = c("yes", "no"),
+   Attitude = c("no", "moderate"),
+   Age = c("15-24", "25-39", "40+"),
+   Education = c("Elementary", "Secondary", "High"))
```

Then, the overall test of conditional independence can be carried using loglm() out as

```
> (mod.cond <- loglm(~ Memory * Age * Education +
+                      Attitude * Age * Education, data = pun))

Call:
loglm(formula = ~Memory * Age * Education + Attitude * Age *
    Education, data = pun)

Statistics:
                    X^2 df   P(> X^2)
Likelihood Ratio 39.679  9 8.6851e-06
Pearson          34.604  9 6.9964e-05
```

Alternatively, `coindep_test()` in **vcd** provides tests of conditional independence of two variables in a contingency table by simulation from the marginal permutation distribution of the input table. The version reporting a Pearson χ^2 statistic is given by

```
> set.seed(1071)
> coindep_test(pun, margin = c("Age", "Education"),
+              indepfun = function(x) sum(x ^ 2), aggfun = sum)


Permutation test for conditional independence

data:  pun
f(x) = 34.6, p-value <2e-16
```

These tests all show substantial association between attitude and memory of corporal punishment. How can we understand and explain this?
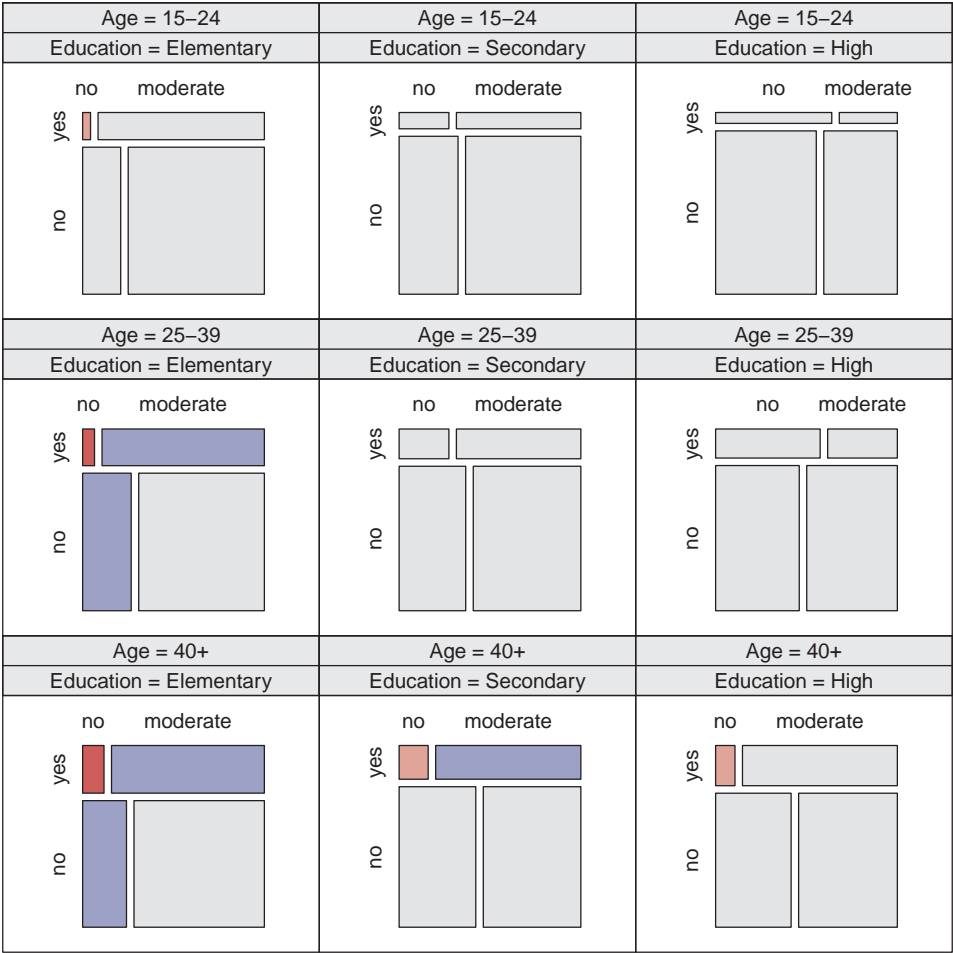

Figure 5.20: Conditional mosaic plot of the Punishment data for the model of conditional independence of attitude and memory, given age and education. Shading of tiles is based on the sum of squares statistic.

{fig:punish-cond1-bis}

As in Example 5.10, we can partition the overall G^2 or χ^2 to show the contributions to this association from the combinations of age and education. The call to `apply()` below fits an independence model for `Memory` and `Attitude` for each stratum defined by the combinations of `Age` and `Education`, and extracts the Pearson χ^2 statistics. The result is returned as a 3×3 matrix.

```
> mods.list <- apply(pun, c("Age", "Education"),
+         function(x) loglm(~ Memory + Attitude, data = x)$pearson)
```

One visual analog of this table of χ^2 statistics is a `cotabplot()` of the (conditional) association of attitude and memory over the age and education cells, shown in Figure 5.20. `cotabplot()` is very general, allowing a variety of functions of the residuals to be used for shading (Zeileis et al., 2007). Here we use the (Pearson) sum of squares statistic, $\sum_{k,\ell} \chi^2_{k,\ell}$.

```
> set.seed(1071)
> pun_cotab <- cotab_coindep(pun, condvars = 3 : 4, type = "mosaic",
+    varnames = FALSE, margins = c(2, 1, 1, 2),
+    test = "sumchisq", interpolate = 1 : 2)
> cotabplot(~ Memory + Attitude | Age + Education,
+           data = pun, panel = pun_cotab)
```

Alternatively, the pattern of conditional association can be shown somewhat more directly in a conditional mosaic plot (Figure 5.21), using the same model formula to condition on age and education. This simply organizes the display to split on the conditioning variables first, with larger spacings.

```
> mosaic(~ Memory + Attitude | Age + Education, data = pun,
+         shade = TRUE, gp_args = list(interpolate = 1 : 4))
```

Both Figure 5.20 and Figure 5.21 reveal that the association between attitude and memory becomes stronger with increasing age among those with the lowest education (first column). Among those in the highest age group (bottom row), the strength of association *decreases* with increasing education. These two displays differ in that in the `cotabplot()` of Figure 5.20, the marginal frequencies of age and education are not shown, whereas in the `mosaic()` of Figure 5.21 they determine the relative sizes of the tiles for the combinations of age and education.

The divide-and-conquer strategy of partial association using statistical tests and visual displays now provides a simple, coherent explanation for this table: memory of experienced violence as a child tends to engender a more favorable attitude toward corporal punishment as an adult, but this association varies directly with both age and education.   △

5.6   Mosaic matrices for categorical data

One reason for the wide usefulness of graphs of quantitative data has been the development of effective, general techniques for dealing with high-dimensional data sets. The ***scatterplot matrix*** shows all pairwise (marginal) views of a set of variables in a coherent display, whose design goal is to show the interdependence among the collection of variables as a whole. It combines multiple views of the data into a single display, which allows detection of patterns that could not readily be discerned from a series of separate graphs. In effect, a multivariate data set in p dimensions (variables) is shown as a collection of $p(p-1)$ two-dimensional scatterplots, each of which is the projection of the cloud of points on two of the variable axes. These ideas can be readily extended to categorical data.

A multiway contingency table of p categorical variables, $A, B, C, \ldots$, contains the interdependence among the collection of variables as a whole. The saturated loglinear model, $[ABC \ldots]$ fits this interdependence perfectly, but is often too complex to describe or understand.
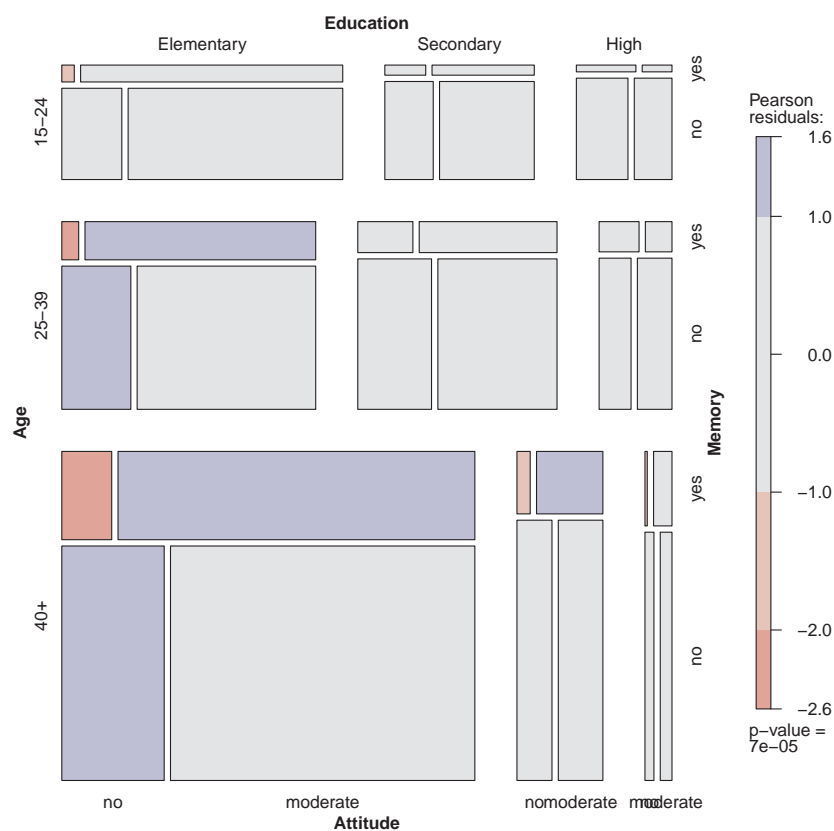
Figure 5.21: Conditional mosaic plot of the Punishment data for the model of conditional independence of attitude and memory, given age and education. This plot explicitly shows the total frequencies in the cells of age and education by the areas of the main blocks for these variables.

{fig:punish-cond2}

By summing the table over all variables except two, A and B, say, we obtain a two-variable (marginal) table, showing the bivariate relationship between A and B, which is also a projection of the p-variable relation into the space of two (categorical) variables. If we do this for all $p(p-1)$ unordered pairs of categorical variables and display each two-variable table as a mosaic, we have a categorical analog of the scatterplot matrix, called a ***mosaic matrix***. Like the scatterplot matrix, the mosaic matrix can accommodate any number of variables in principle, but in practice is limited by the resolution of our display to three or four variables.

In R, the main implementation of this idea is in the generic function `pairs()`. The vcd package extends this to mosaic matrices with methods for "table" and "structable" objects. The gpairs (Emerson and Green, 2014) package provides a ***generalized pairs plot***, with appropriate graphics for a mixture of quantitative and categorical variables.

5.6.1 Mosaic matrices for pairwise associations

{sec:bartlett}{ex:bartlettpairassoc}

EXAMPLE 5.12: Bartlett data on plum-root cuttings

The simplest example of what you can see in a mosaic matrix is provided by the $2 \times 2 \times 2$ table used by Bartlett (1935) to illustrate a method for testing for no three-way interaction in a contingency table (hypothesis H_4 in Table 5.2).

The data set `Bartlett` in vcdExtra gives the result of an agricultural experiment to investi-

gate the survival of plum-root cuttings (`Alive`) in relation to two factors: `Time` of planting and the `Length` of the cutting. In this experiment, 240 cuttings were planted for each of the 2×2 combinations of these factors, and their survival (Alive, Dead) was later recorded.
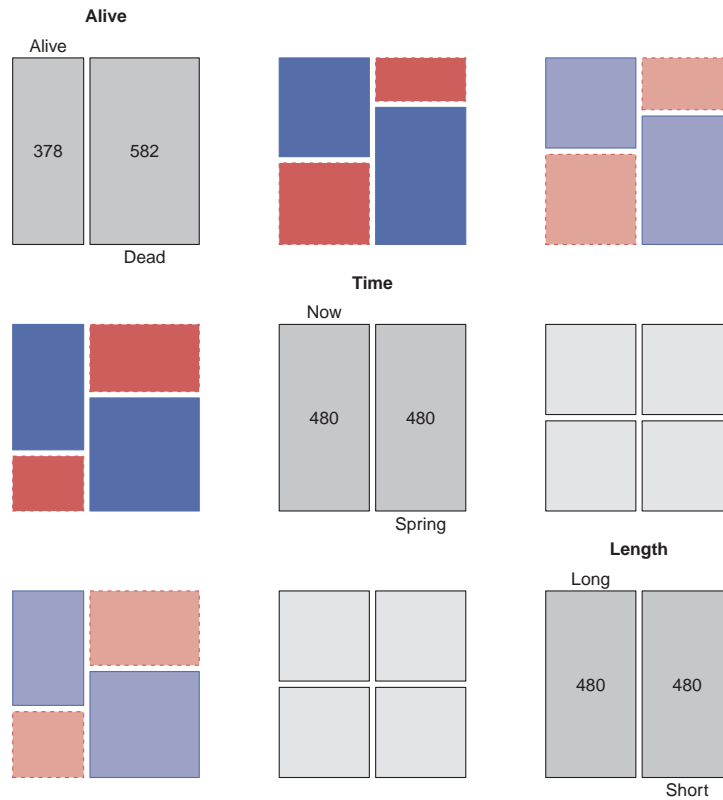
```
> pairs(Bartlett, gp = shading_Friendly2)
```


Figure 5.22: Mosaic pairs plot for the Bartlett data. Each panel shows the bivariate marginal relation between the row and column variables.

{fig:bartlett-pairs}

The mosaic matrix for these data, showing all two-way marginal relations, is shown in Figure 5.22. It can immediately be seen that `Time` and `Length` are independent by the design of the experiment; we use `gp=shading_Friendly` here to emphasize this.

The top row and left column show the relation of survival to each of time of planting and cutting length. It is easily seen that greater survival is associated with cuttings taken now (vs. spring) and those cut long (vs. short), and the degree of association is stronger for planting time than for cutting length.   △

{ex:marital2}

EXAMPLE 5.13: Marital status and pre- and extramarital sex

In Example 5.9 we examined a series of models relating marital status to reported premarital and extramarital sexual activity and gender in the *PreSex* data. Figure 5.23 shows the mosaic matrix for these data. The diagonal panels show the labels for the category levels as well as the one-way marginal totals.

```
> data("PreSex", package = "vcd")
> pairs(PreSex, gp = shading_Friendly2, space = 0.25,
+       gp_args = list(interpolate = 1 : 4))
```
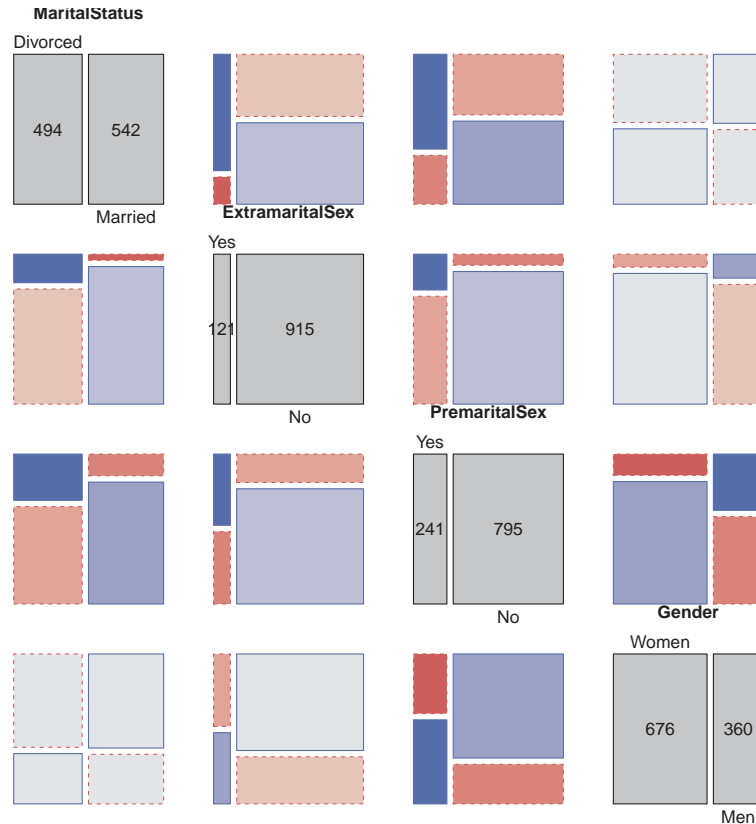

Figure 5.23: Mosaic pairs plot for the PreSex data. Each panel shows the bivariate marginal relation between the row and column variables.

{fig:marital-pairs}

If we view gender, premarital sex, and extramarital sex as explanatory, and marital status (Divorced vs. still Married) as the response, then the mosaics in row 1 (and in column 1)[13] show how marital status depends on each predictor marginally. The remaining panels show the relations within the set of explanatory variables.

Thus, we see in row 1, column 4, that marital status is independent of gender (all residuals equal zero, here), by design of the data collection. In the (1, 3) panel, we see that reported premarital sex is more often followed by divorce, while non-report is more prevalent among those still married. The (1, 2) panel shows a similar, but stronger relation between extramarital sex and marriage stability. These effects pertain to the associations of P and E with marital status (M)—the terms [PM] and [EM] in the loglinear model. We saw earlier that an interaction of P and E (the term [PEM]) is required to fully account for these data. This effect is not displayed in Figure 5.23.

Among the background variables (the loglinear term [GPE]), the (2, 3) panel shows a strong relation between premarital sex and subsequent extramarital sex, while the (2, 4) and (3, 4) panels

---

[13]Rows and columns in a mosaic matrix are identified as in a table or numerical matrix, with row 1, column 1 in the upper left corner.

show that men are far more likely to report premarital sex than women in this sample, and also more likely to report extramarital sex.

Even though the mosaic matrix shows only pairwise, bivariate associations, it provides an integrated view of all of these together in a single display.

△

{ex:berkeley4}

EXAMPLE 5.14: Berkeley admissions

In Chapter 4 we examined the relations among the variables Admit, Gender, and Department in the Berkeley admissions data (Example 4.1, Example 4.11, Example 4.15) using fourfold displays (Figure 4.5 and Figure 4.6) and sieve diagrams (Figure 4.13). These displays showed either a marginal relation (e.g., Admit, Gender) or the full three-way table.

In contrast, Figure 5.24 shows all pairwise marginal relations among these variables, produced using pairs(). Some additional arguments are used to control the details of labels for the diagonal and off-diagonal panels.

```
> largs <- list(labeling = labeling_border(varnames = FALSE,
+               labels = c(T, T, F, T), alternate_labels = FALSE))
> dargs <- list(gp_varnames = gpar(fontsize = 20), offset_varnames = -1,
+               labeling = labeling_border(alternate_labels = FALSE))
> pairs(UCBAdmissions, shade = TRUE, space = 0.25,
+       diag_panel_args = dargs,
+       upper_panel_args = largs, lower_panel_args = largs)
```
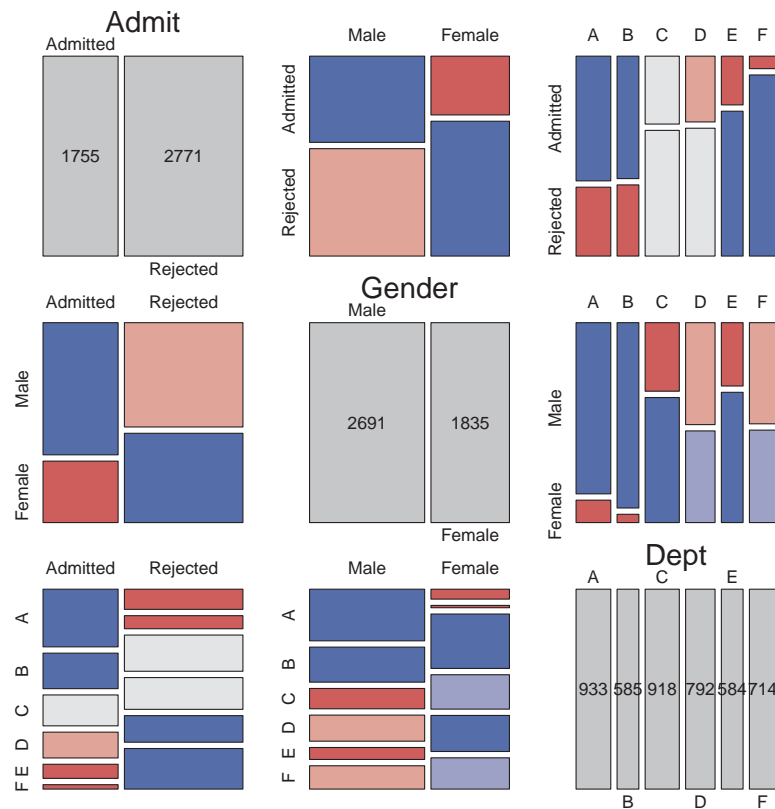

{fig:berk-pairs1} **Figure 5.24:** Mosaic matrix of the UCBAdmissions data showing bivariate marginal relations.

The panel in row 2, column 1 shows that Admission and Gender are strongly associated marginally, as we saw in Figure 4.5, and overall, males are more often admitted. The diagonally opposite panel (row 1, column 2) shows the same relation, splitting first by gender.[14]

The panels in the third column (and third row) provide the explanation for the paradoxical result (see Figure 4.6) that, within all but department A, the likelihood of admission is equal for men and women, yet, overall, there appears to be a bias in favor of admitting men (see Figure 4.5). The (1, 3) and (3, 1) panels show the marginal relation between Admission and Department; that is, how admission rate varies across departments. Departments A and B have the greatest overall admission rate, departments E and F the least. The (2, 3) and (3, 2) panels show how men and women apply differentially to the various departments. It can be seen that men apply in much greater numbers to departments A and B, with higher admission rates, while women apply in greater numbers to the departments C–F, with the lowest overall rate of admission.

△

5.6.2 Generalized mosaic matrices and pairs plots

{sec:condmat}

We need not show only the marginal relation between each pair of variables in a mosaic matrix. Friendly (1999b) describes the extension of this idea to conditional, partial, and other views of a contingency table.

In `pairs.table()`, different ***panel functions*** can be used to specify what is displayed in the upper, lower, and diagonal panels. For the off-diagonal panels, a `type` argument can be used to plot mosaics showing various kinds of independence relations:

`type = "pairwise"` – Shows bivariate marginal relations, collapsed over all other variables.
`type = "total"` – Shows mosaic plots for mutual independence.
`type = "conditional"` – Shows mosaic plots for conditional independence given all other variables.
`type = "joint"` – Shows mosaic plots for joint independence of all pairs of variables from the others.

{ex:berkeley4b}

EXAMPLE 5.15: Berkeley admissions

Figure 5.25 shows the generalized mosaic matrix for the *UCBAdmissions* data, using 3-way mosaics for all the off-diagonal cells. The observed frequencies, of course, are the same in all these cells. However, in the lower panels, the tiles are shaded according to models of joint independence, while in the upper panels, they are shaded according to models of mutual independence.

```
> pairs(UCBAdmissions, space = 0.2,
+       lower_panel = pairs_mosaic(type = "joint"),
+       upper_panel = pairs_mosaic(type = "total"))
```

In this example, it is more useful to fit and display the models of conditional independence for each pair of row, column variables given the remaining one, as shown in Figure 5.26.

```
> pairs(UCBAdmissions, type = "conditional", space = 0.2)
```

Thus, the shading in the (1, 2) and (2, 1) panels shows the fit of the model [Admit, Dept] [Gender, Dept], which asserts that Admission and Gender are independent, given (controlling for) Department. Except for Department A, this model fits quite well, again indicating lack of gender

---

[14]Note that this is different than just the transpose or interchange of horizontal and vertical dimensions as in a scatterplot matrix, because the mosaic display splits the total frequency first by the horizontal variable and then (conditionally) by the vertical variable. The areas of all corresponding tiles are the same in each diagonally opposite pair, however, as are the residuals shown by color and shading.
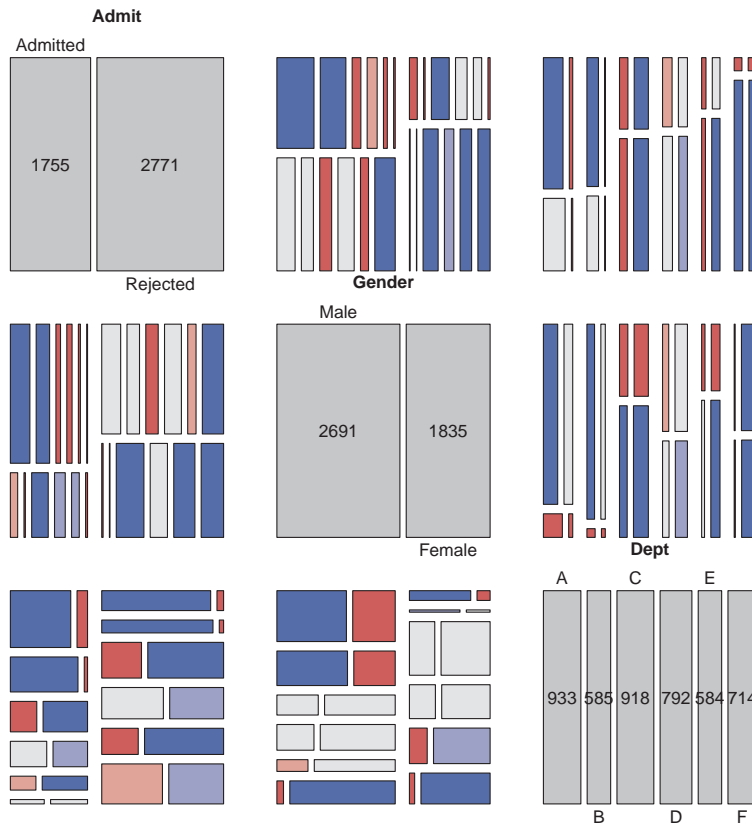
Figure 5.25: Generalized mosaic matrix of the UCBAdmissions data. The above-diagonal plots fit models of joint independence; below-diagonal plots fit models of mutual independence.   {fig:berk-pairs2}

bias. The (1, 3) and (3, 1) panels show the relation between admission and department controlling for gender, highlighting the differential admission rates across departments.

△

Beyond this, the framework of pairs plots can be further generalized to *mixtures* of quantitative and categorical variables, as first described in Friendly (2003) and then in a wider context by Emerson et al. (2013) and Friendly (2013). The essential idea is to consider the combination of two variables, each of which can be either categorical (**C**) or quantitative (**Q**), and various ways to *render* that combination in a graphical display:

CC: mosaic display, sieve diagram, doubledecker plot, faceted or divided bar chart;
CQ: side-by-side boxplots, stripplots, faceted histograms, aligned density plots;
QQ: scatterplot, corrgram, data ellipses, etc.

In R some of these possibilities are provided in the gpairs package (using grid graphics and the vcd strucplot framework), and the GGally (Schloerke et al., 2014) package (an extension to ggplot2 (Wickham and Chang, 2015)).

{ex:arthritis-gpairs}

EXAMPLE 5.16: Arthritis treatment
We illustrate these ideas with the `Arthritis` data using the gpairs package in Figure 5.27. In this data, the variables `Treatment`, `Sex`, and `Improved` are categorical, and `Age` is quantitative.
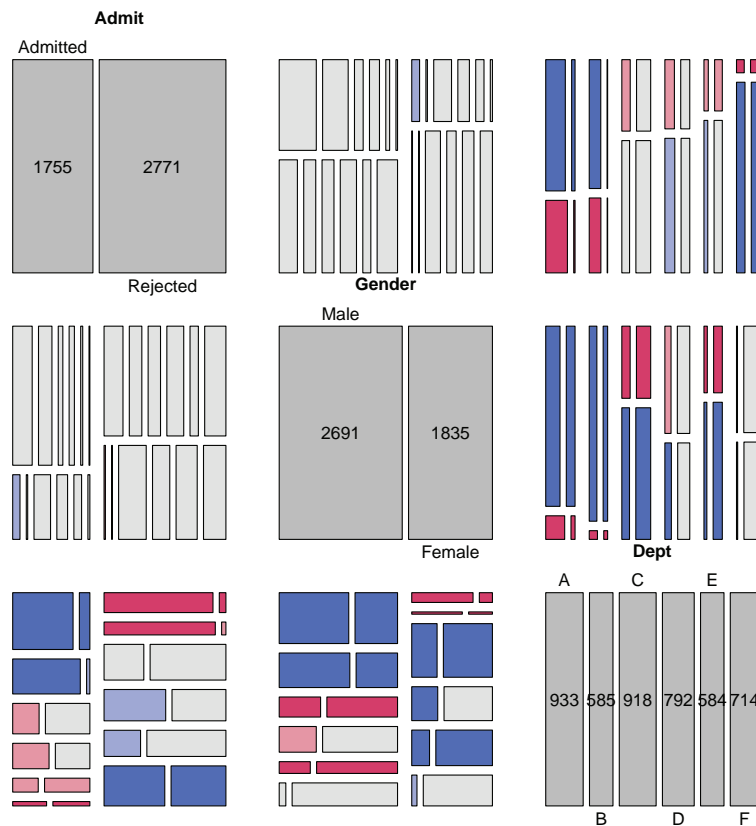
Figure 5.26: Generalized mosaic matrix of the UCBAdmissions data. The off-diagonal plots fit models of conditional indpendence.

{fig:berk-pairs3}

The call to gpairs() below reorders the variables to put the response variable Improved in row 1, column 1. Various options can be passed to mosaic() using the mosaic.pars argument.

```
> library(gpairs)
> data("Arthritis", package = "vcd")
> gpairs(Arthritis[,c(5, 2, 3, 4)],
+        diag.pars = list(fontsize = 20),
+        mosaic.pars = list(gp = shading_Friendly,
+                           gp_args = list(interpolate = 1 : 4)))
```

gpairs() provides a variety of options for the **CQ** and **QQ** combinations, as well as the diagonal cells, but only the defaults are used here. The bottom row, corresponding to Age, uses boxplots to show the distributions of age for each of the categorical variables. The last column shows these same variables as stripplots (or "barcodes"), which show all the individual observations. In the (1, 4) and (4, 1) panels, it can be seen that younger patients are more likely to report no improvement. The other panels in the first row (and column) show that improvement is more likely in the treated condition and greater among women than men.   △
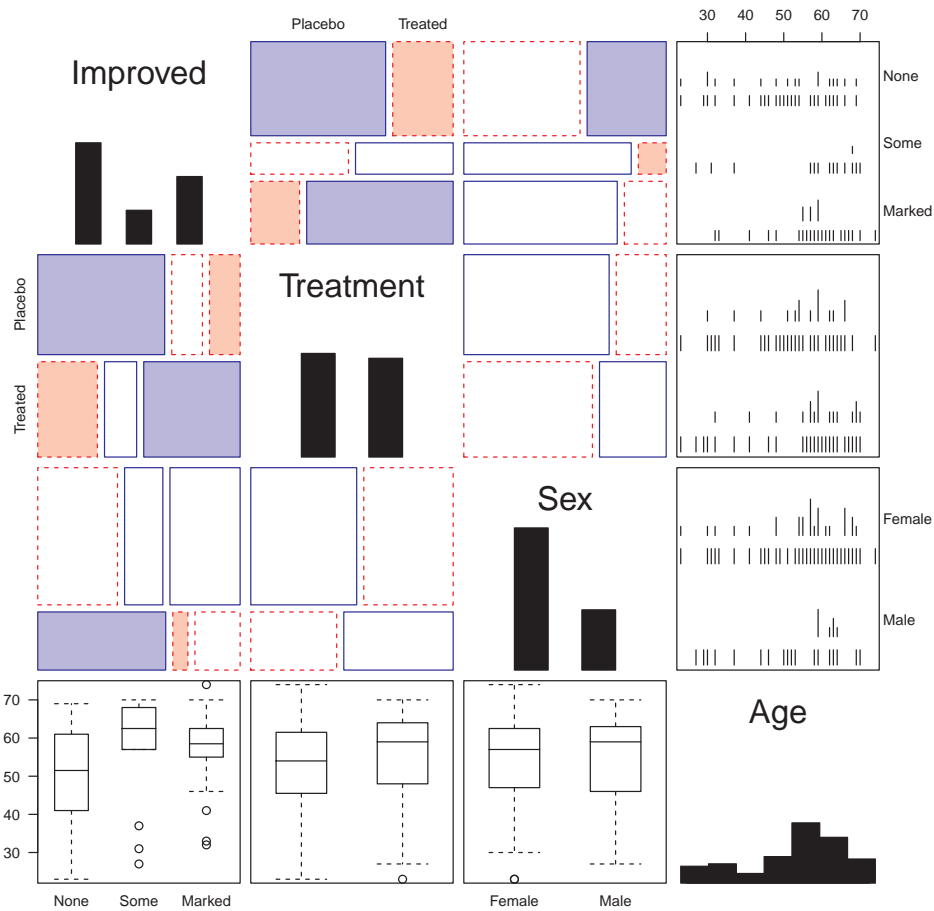
Figure 5.27: Generalized pairs plot of the Arthritis data. Combinations of categorical and quantitative variables can be rendered in various ways.

5.7   3D mosaics

Mosaic-like displays use the idea of recursive partitioning of a unit square to portray the frequencies in an *n*-way table by the area of rectangular tiles with (x, y) coordinates. The same idea extends naturally to a 3D graphic. This starts with a unit cube, which is successively subdivided into 3D cuboids along (x, y, z) dimensions, and the frequency in a table cell is then represented by volume.

As in the 2D versions, each cuboid can be shaded to represent some other feature of the data, typically the residual from some model of independence. In principle, the display can accommodate more than 3 variables by using a sequence of split directions along the (x, y, z) axes.

One difficulty in implementing this method is that, short of using a 3D printer, the canvas for a 3D plot on a screen or printer is still projected on a two-dimensional surface, and graphical elements (volumes, lines, text) toward the front of the view will obscure those in the back. In R, a major advance in 3D graphics is available in the rgl (Adler and Murdoch, 2014) package, which mitigates these problems by: (a) providing an interactive graphic window that can be zoomed and rotated manually with the mouse; (b) allowing dynamic graphics under program control, for example to

animate a plot or make a movie; (c) providing control of the details of 3D rendering, including transparency of shapes, surface shading, lighting, and perspective.

The vcdExtra package implements 3D mosaics using rgl graphics. `mosaic3d()` provides methods for "loglm" as well as "table" (or "structable") objects. At the time of writing, only some features of 2D mosaics are available.

{ex:bartlett-3d}

EXAMPLE 5.17: Bartlett data on plum-root cuttings

In Example 5.12 we showed the mosaic matrix for the *Bartlett*, fitting the model of mutual independence to show all associations among the table variables, Alive, Time of planting, and Length of cutting. Figure 5.28 shows the 3D version, produced using `mosaic3d()`:
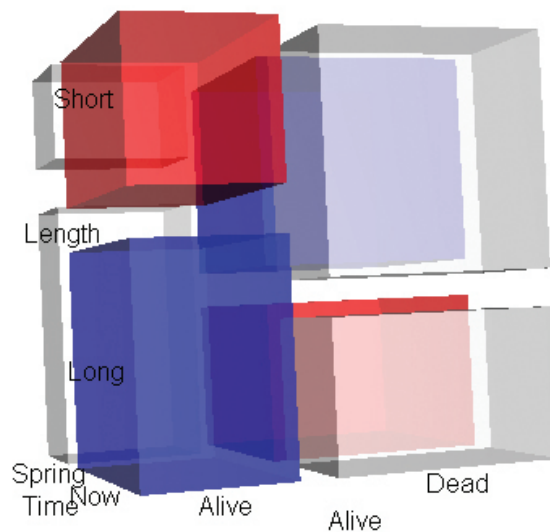
```
> mosaic3d(Bartlett)
```


Figure 5.28: 3D mosaic plot of the Bartlett data, according to the model of mutual independence. {fig:mos3d-bartlett}

In the view of this figure, it can be seen that cuttings are more likely to be alive when planted Now and when cut Long. These relations can more easily be appreciated by rotating the 3D display.

△

5.8 Visualizing the structure of loglinear models

{sec:mosaic-struc}

For quantitative response data, it is easy to visualize a fitted model—for linear regression, this is just a plot of the fitted line; for multiple regression or nonlinear regression with two predictors, this is a plot of the fitted response surface. For a categorical response variable, an analog of such plots is provided by effect plots, described later in this book.

For contingency table data, mosaic displays can be used in a similar manner to illuminate the relations among variables in a contingency table represented in various loglinear models, a point described by Theus and Lauer (1999). In fact, each of the model types depicted in Table 5.2 has a characteristic shape and structure in a mosaic display. This, in turn, leads to a clearer understanding

of the structure that appears in real data when a given model fits, the relations among the models, and the use of mosaic displays. The essential idea is a simple extension of what we do for more traditional models: show the *expected* (fitted) frequencies under a given model rather than observed frequencies in a mosaic-like display.

To illustrate, we use some artificial data on the relations among age, sex, and symptoms of some disease shown in the $2 \times 2 \times 2$ table `struc` below.

```
> struc <- array(c(6, 10, 312, 44,
+                   37, 31, 192, 76),
+   dim = c(2, 2, 2),
+   dimnames = list(Age = c("Young", "Old"),
+                   Sex = c("F", "M"),
+                   Disease = c("No", "Yes"))
+   )
> struc <- as.table(struc)
> structable(struc)

            Sex   F   M
Age    Disease
Young  No          6 312
       Yes        37 192
Old    No         10  44
       Yes        31  76
```

First, note that there are substantial associations in this table, as shown in Figure 5.29, fitting the (default) mutual independence model.

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

The first split by `Age` shows strong partial associations between `Sex` and `Disease` for both young and old. However, the residuals have an opposite pattern for young and old, suggesting a more complex relationship among these variables.
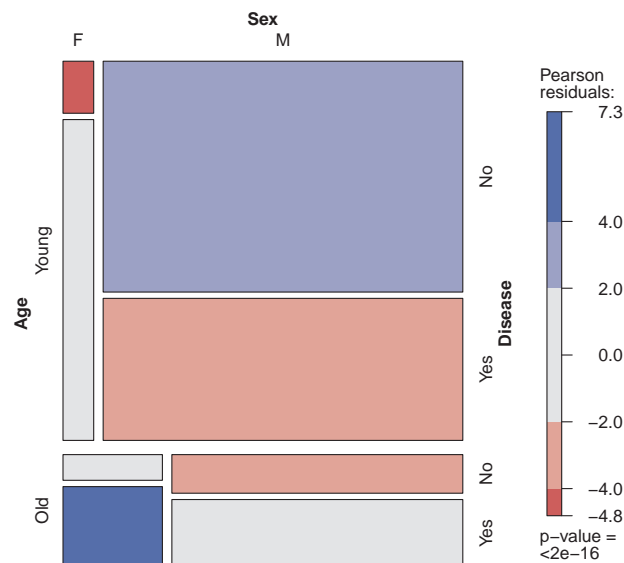

Figure 5.29: Mosaic display for the data on age, sex, and disease. Observed frequencies are shown in the plot, and residuals reflect departure from the model of mutual independence.

In this section we are asking a different question: what would mosaic displays look like if the data were in accord with simpler models? One way to do this is simply to use the expected frequencies to construct the tiles, as in sieve diagrams. The result, in Figure 5.30, shows that the tiles for sex and disease align for each of the age groups, but it is harder to see the relations among all three variables in this plot.
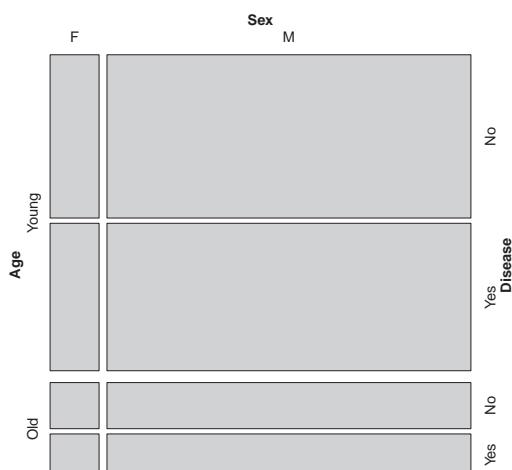
```
> mosaic(struc, type = "expected")
```


Figure 5.30: Mosaic display for the data on age, sex, and disease, using expected frequencies under mutual independence.

{fig:struc-mos2}

We can visualize the model-implied relations among all variables together more easily using mosaic matrices.

5.8.1 Mutual independence

For example, to show the structure of a table that exactly fits the model of mutual independence, H_1, use the loglm() to find the fitted values, fit, as shown below. The function fitted() extracts these from the "loglm" object.

```
> mutual <- loglm(~ Age + Sex + Disease, data = struc, fitted = TRUE)
> fit <- as.table(fitted(mutual))
> structable(fit)

            Sex          F          M
Age   Disease
Young No           34.0991 253.3077
      Yes          30.7992 228.7940
Old   No           10.0365  74.5567
      Yes           9.0652  67.3416
```

These fitted frequencies then have the same one-way margins as the data in *struc*, but have no two-way or higher associations. Then pairs() for this table, using type="total", shows the three-way mosaic for each pair of variables, giving the result in Figure 5.31. We use gp=shading_Friendly to explicitly indicate the zero residuals in the display,

```
> pairs(fit, gp = shading_Friendly2, type = "total")
```
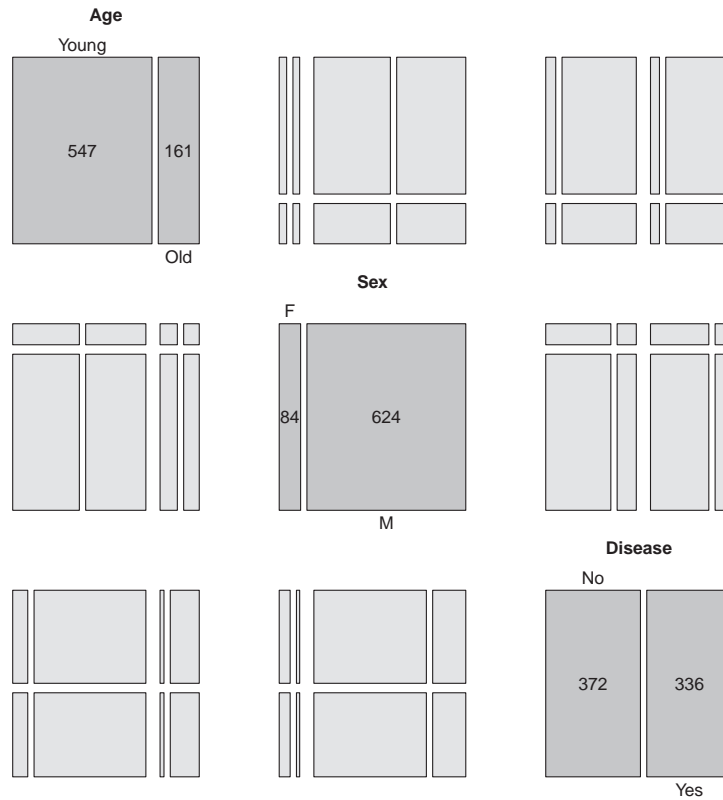

Figure 5.31: Mosaic matrix for fitted values under mutual independence. In all panels the joint frequencies conform to the one-way margins.

{fig:struc-mos3}

In this figure the same data are shown in all the off-diagonal panels and the mutual independence model was fitted in each case, but with the table variables permuted. All residuals are exactly zero in all cells, by construction. We see that in each view, the four large tiles corresponding to the first two variables align, indicating that these two variables are marginally independent. For example, in the (1, 2) panel, age and sex are independent, collapsed over disease.

Moreover, comparing the top half to the bottom half in any panel we see that the divisions by the third variable are the same for both levels of the second variable. In the (1, 2) panel, for example, age and disease are independent for both males and females. This means that age and sex are conditionally independent given disease (age $\perp$ sex | disease).

Because this holds in all six panels, we see that mutual independence implies that *all pairs* of variables are conditionally independent, given the remaining one, $(X \perp Y \mid Z)$ for all permutations of variables. A similar argument can be used to show that joint independence also holds, i.e., $((X, Y) \perp Z)$ for all permutations of variables.

Alternatively, you can also visualize these relationships interactively in a 3D mosaic using `mosaic3d()` that allows you to rotate the mosaic to see all views. In Figure 5.32, all of the 3D tiles are unshaded and you can see that the 3D unit cube has been sliced according to the marginal frequencies.
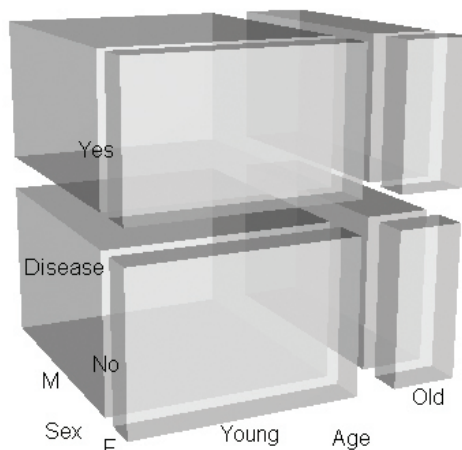
```
> mosaic3d(fit)
```


Figure 5.32: 3D mosaic plot of frequencies according to the model of mutual independence. The one-way margins are slices through the unit cube.

{fig:struct-mos3d1}

5.8.2 Joint independence

The model of joint independence, $H_2 : (A, B) \perp C$, or equivalently, the loglinear model $[AB][C]$ may be visualized similarly by a mosaic matrix in which the data are replaced by fitted values under this model. We illustrate this for the model [Age Sex][Disease], calculating the fitted values in a similar way as before.

```
> joint <- loglm(~ Age * Sex + Disease, data = struc, fitted = TRUE)
> fit <- as.table(fitted(joint))
> structable(fit)

             Sex        F       M
Age   Disease
Young No          22.593 264.814
      Yes         20.407 239.186
Old   No          21.542  63.051
      Yes         19.458  56.949
```

The `pairs.table()` plot, now using simpler pairwise plots (`type="pairwise"`), is shown in Figure 5.33.

```
> pairs(fit, gp = shading_Friendly2)
```

This shows, in row 3 and column 3, the anticipated independence of both age and sex with disease, collapsing over the remaining variable. The (1, 2) and (2, 1) panels show that age and sex are still associated when disease is ignored.
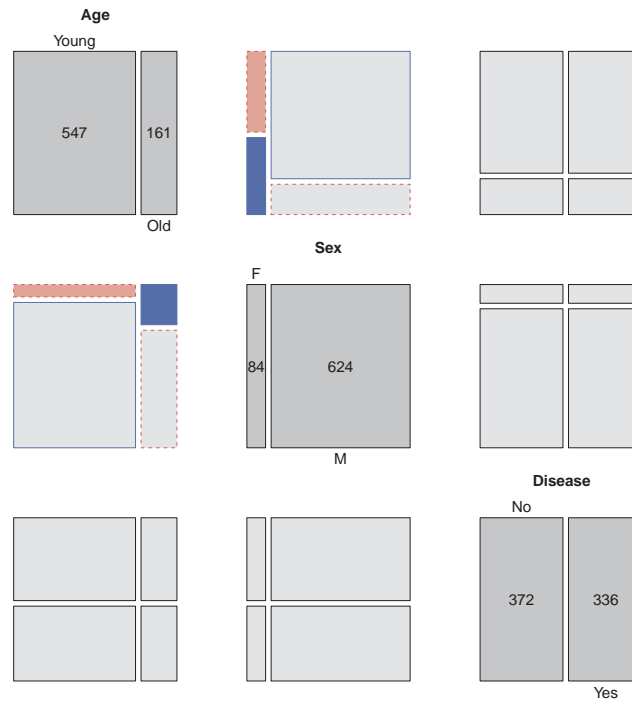
Figure 5.33: Mosaic matrix for fitted values under joint independence for the model [Age Sex][Disease].

{fig:struc-mos4}

5.9 Related visualization methods

{sec:related}

A variety of other graphical methods provide the means for visualizing relationships in multiway frequency tables. We briefly describe a few of these here, without much detail, to give a sense of some alternatives.

5.9.1 Doubledecker plots

{sec:doubledecker}

Doubledecker plots visualize the dependence of one categorical (typically binary) variable on further categorical variables. Formally, they are mosaic plots with vertical splits for all dimensions (predictors) except the last one, which represents the dependent variable (outcome). The last variable is visualized by horizontal splits, no space between the tiles, and separate colors for the levels.

They have the advantage of making it easier to "read" the differences among the conditional response proportions in relation to combinations of the explanatory variables. Moreover, for a binary response, the difference in these conditional proportions for any two columns has a direct relation to the odds ratio for a positive response in relation to those predictor levels (Hofmann, 2001).

The `doubledecker()` function in **vcd** takes a formula argument of the form `R ~ E1 + E2 + ...` where `R` is the response variable and `E1, E2, ...` are the predictors in the contingency table in array form. The shorthand notation, `R ~ .` means that all variables other than `R` are taken as predictors, in their order in the array.

{ex:berkeley-ddecker}

EXAMPLE 5.18: Berkeley admissions

Figure 5.34 shows the doubledecker plot for the *UCBAdmissions* data. By default, the levels

of the response (Admit) are taken in their order in the array and shaded to highlight the *last* level (Rejected). We want to highlight Admitted, so we reverse this dimension in the call below.

```
> doubledecker(Admit ~ Dept + Gender, data = UCBAdmissions[2:1, , ])
```
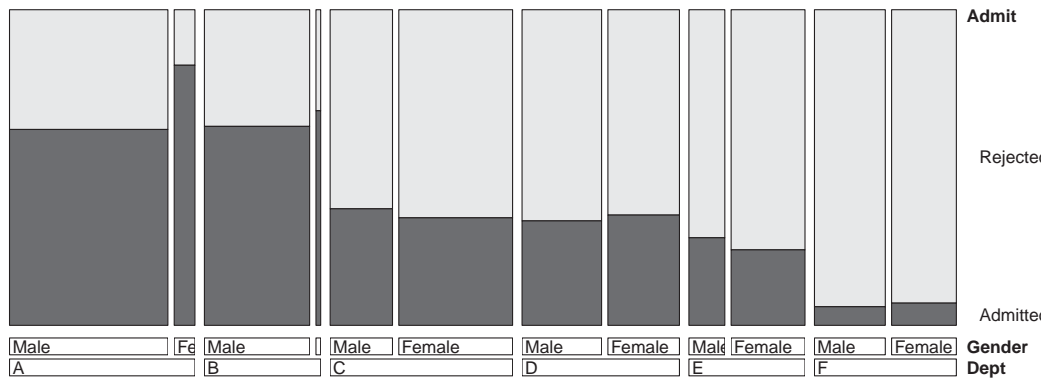

Figure 5.34: Doubledecker plot for the UCBAdmissions data.   {fig:berkeley-doubledecker}

In Figure 5.34, it is easy to see the effects of both Dept and Gender on Admit. Admission rate declines across departments A–E, and within departments, the proportion admitted is roughly the same, except for department A, where more female applicants are admitted.   △

{ex:titanic-ddecker}

EXAMPLE 5.19: Titanic data

Figure 5.35 shows the doubledecker plot for the *Titanic* data. The levels of the response (Survived) are shaded in increasing grey levels, highlighting the proportions of survival.

```
> doubledecker(Survived ~ Class + Age + Sex, Titanic)
```
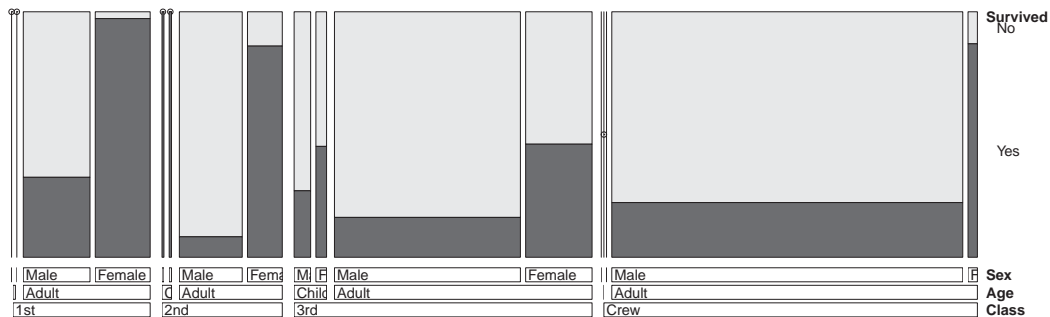

Figure 5.35: Doubledecker plot for the Titanic data.   {fig:titanic-doubledecker}

This order of variables makes it easiest to compare survival of men and women within each age–class combination, but you can also see that survival of adult women decreases with class, and survival among men was greatest in first class. Some additional visualizations of these relationships are illustrated using the next topic in Example 5.21.
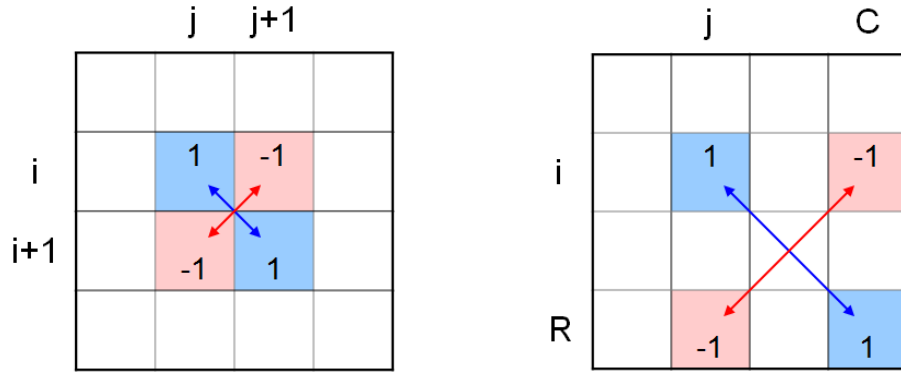
△

Figure 5.36: Generalized odds ratios for an $R \times C$ table. Left: local odds ratios for adjacent categories. Right: odds ratios with respect to a reference category (the last). Each log odds ratio is a contrast of the log frequencies, shown by the cell weights.

{fig:lor}

5.9.2 Generalized odds ratios*

{sec:oddsratio}

In Example 4.12, we used fourfold displays (Figure 4.7) to analyze the odds ratio between breathlessness and wheeze in coal miners as a function of age. Figure 4.8 showed that a plot of the odds ratio directly against age gave a simplified description of this three-way relationship.

Odds ratios for 2×2 tables can be generalized to $R \times C$ tables in a variety of ways, and these can also be calculated for *n*-way tables by treating all but the first two dimensions as strata. Plots of these generalized odds ratios can be quite informative, perhaps more so than in the $2 \times 2 \times k$ case.

Consider an $R \times C$ table with frequencies n_{ij}. Then a set of $(R-1) \times (C-1)$ **local odds ratio**s, $\theta_{i,j}$, can be calculated as the odds ratios for adjacent pairs of rows and columns as shown in the left panel of Figure 5.36.

$$\theta_{ij} = \frac{n_{ij}/n_{i+1,j}}{n_{i,j+1}/n_{i+1,j+1}} = \frac{n_{ij} \times n_{i+1,j+1}}{n_{i+1,j} \times n_{i,j+1}}, \quad \begin{array}{l} i = 1,2,\ldots,R-1 \\ j = 1,2,\ldots,C-1 \end{array}.$$

These odds ratios correspond to "profile contrasts" (or sequential contrasts or successive differences) for ordered categories. Similarly, if one row category and one column category (say, the last) are considered baseline or reference categories, odds ratios with respect to contrasts with those categories (Figure 5.36, right panel) are defined as

$$\theta_{ij} = \frac{n_{i,j} \times n_{R,C}}{n_{i,C} \times n_{R,j}}, \quad \begin{array}{l} i = 1,2,\ldots,R-1 \\ j = 1,2,\ldots,C-1 \end{array}.$$

Note that all such parameterizations are equivalent, in that one can derive all other possible odds ratios from any non-redundant set, but substance-driven contrasts will be easier to interpret.

This calculation is simple in terms of log odds ratios, because it corresponds to a contrast among the log frequencies, with weights ± 1 for the four relevant cells. For local odds ratios, these are

$$\log(\theta_{ij}) = \begin{pmatrix} 1 & -1 & -1 & 1 \end{pmatrix} \log \begin{pmatrix} n_{ij} & n_{i+1,j} & n_{i,j+1} & n_{i+1,j+1} \end{pmatrix}^{\mathsf{T}}.$$

Consider an $R \times C \times K_1 \times K_2 \times \ldots$ frequency table $n_{ij\ldots}$, with factors $K_1, K_2 \ldots$ taken as strata. Let $\boldsymbol{n} = \mathrm{vec}(n_{ij\ldots})$ be the $N \times 1$ vectorization of the frequency table. Then, all log odds ratios and their asymptotic covariance matrix can be calculated as:

$$\begin{aligned} \log(\widehat{\boldsymbol{\theta}}) &= \boldsymbol{C} \log(\boldsymbol{n}) \\ \boldsymbol{S} \equiv \mathcal{V}[\log(\boldsymbol{\theta})] &= \boldsymbol{C} \operatorname{diag}(\boldsymbol{n})^{-1} \boldsymbol{C}^{\mathsf{T}} \end{aligned}$$

where C is an N-column matrix containing all zeros, except for two $+1$ elements and two -1 elements in each row that select the four cells involved in each log lodds ratio.[15]

The function `loddsratio()` in **vcd** calculates these values for the categories of the first two dimensions of an n-way table, together with their asymptotic covariance matrix. Additional dimensions are treated as strata. The `as.array()` and `as.data.frame()` methods can be used to convert a `loddsratio` object to a form suitable for plotting or further analysis.

{ex:punish2}

EXAMPLE 5.20: Corporal punishment data

Example 5.11 used mosaic displays to describe the relationship between attitude toward corporal punishment of children in relationship to memory of having experienced that as a child and education and age of the respondent. Given that `attitude` is the response, we could examine the odds ratios among this variable and any one predictor, treating the other variables as strata. Continuing the analysis of Example 5.11, we calculate log odds ratios for the association of `attitude` and `memory`, stratified by `age` and `education`.

```
> data("Punishment", package = "vcd")
> pun_lor <- loddsratio(Freq ~ memory + attitude | age + education,
+                       data = Punishment)
```

The `as.data.frame()` method converts this to a data frame, and adds standard errors (ASE).

```
> pun_lor_df <- as.data.frame(pun_lor)
```

The plot method for `loddsratio` objects conveniently plots the log odds ratio (LOR) against the strata variables, `age` or `education`, and by default also adds error bars. The result is shown in Figure 5.37.

```
> plot(pun_lor)
```
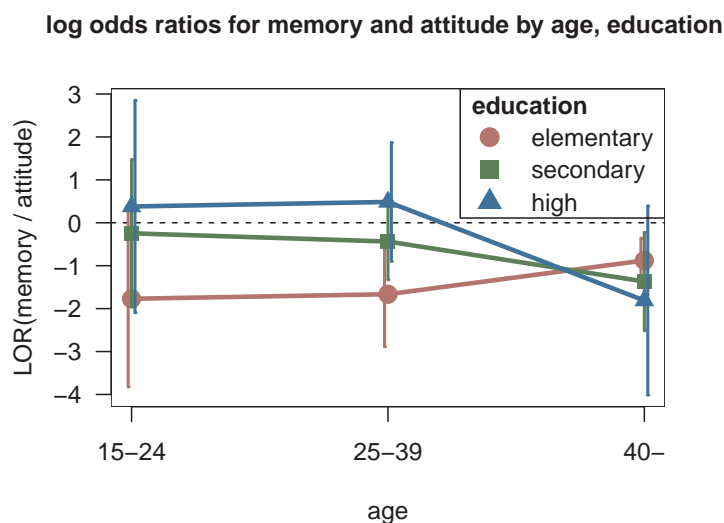

Figure 5.37: Log odds ratio for the association between attitude and memory of corporal punishment, stratified by age and education. Error bars show ± 1 standard error.

{fig:pun-lor-plot}

---

[15]Some additional theory and applications of generalized odds ratios for ordered variables is given by Goodman (1983). Hofmann (2001) describes some connections between odds ratios, loglinear models, and visual modeling using doubledecker plots and mosaic plots.

Compared to Figure 5.20, the differences among the age and education groups are now clear. For respondents less than age 40, increasing education increases the association (log odds ratio) between attitude and memory: those who remembered corporal punishment as a child are more likely to approve of it as their education increases. This result is reversed for those over 40, where all log odds ratios are negative: memory of corporal punishment makes it *less* likely to approve, and this effect becomes stronger with increased education.

Because log odds ratios have an approximate normal distribution under the null hypothesis that all $\log \theta_{ij} = 0$, you can treat these values as data, and carry out a rough analysis of the effects of the stratifying variables using ANOVA, with weights inversely proportional to the estimated sampling variances.[16] In the analysis shown below, we have treated age and education as ordered (numeric) variables.

```
> pun_mod <- lm(LOR ~ age * education, data = pun_lor_df,
+               weights = 1 / ASE^2)
> anova(pun_mod)

Analysis of Variance Table

Response: LOR
              Df Sum Sq Mean Sq F value Pr(>F)
age            1   1.04    1.04    2.72  0.160
education      1   1.84    1.84    4.79  0.080 .
age:education  1   5.04    5.04   13.13  0.015 *
Residuals      5   1.92    0.38
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

This confirms the interaction of age and education on the association between attitude and memory that we described from visual inspection of Figure 5.37.   △

{ex:titanic-lor}

EXAMPLE 5.21: Titanic data

For the `Titanic` data, it is useful to examine the odds ratios for survival in relation to age or sex, using the remaining variables as strata. Some preprocessing is nececessary first: These data contain **structural zeros** as there were no children in the crew. Accordingly, we set the corresponding cell entries to `NA` to avoid the calculation of nonsensical values. (Problems of zero frequencies in frequency tables are discussed in more detail in Section 9.5). Additionally, we reverse the order of the levels so that `Survived=="Yes"` and `Age=="Adult"` are first. The values calculated below then give the log odds of survival for an adult compared to a child in the combinations sex and class.

```
> Titanic2 <- Titanic[, , 2:1, 2:1]
> Titanic2["Crew", , "Child", ] <- NA
> titanic_lor1 <- loddsratio(~ Survived + Age | Class + Sex,
+                            data = Titanic2)
> titanic_lor1

log odds ratios for Survived and Age by Class, Sex

       Sex
Class      Male    Female
  1st  -3.12102  2.342518
  2nd  -5.50154 -1.510269
  3rd  -0.66874  0.031104
  Crew       NA        NA
```

---

[16]This ignores the covariances among the log odds ratios, which are not independent. A proper analysis uses generalized least squares with a weight matrix $\boldsymbol{S}^{-1}$, where $\boldsymbol{S} = \mathcal{V}[\log(\boldsymbol{\theta})]$ is the covariance matrix.

Similarly, for survival and sex, we obtain the log odds ratios of survival for males versus females, for the combinations of age and class.

```
> titanic_lor2 <- loddsratio(~ Survived + Sex | Class + Age,
+                            data = Titanic2)
> titanic_lor2

log odds ratios for Survived and Sex by Class, Age

      Age
Class    Adult    Child
  1st  -4.1643  1.29928
  2nd  -4.1516 -0.16034
  3rd  -1.4786 -0.77879
  Crew -3.0156       NA
```

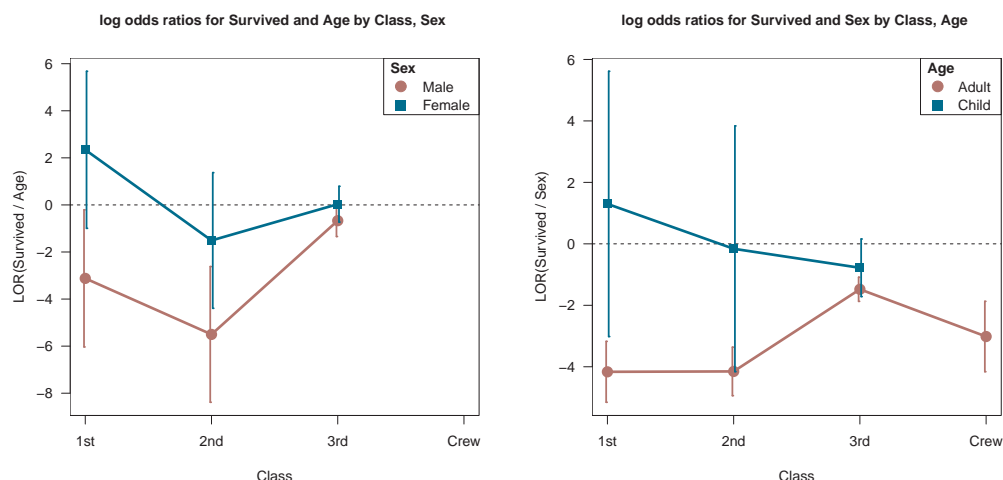The plots for both tables are shown in Figure 5.38.

Figure 5.38: Log odds ratio plots for the Titanic data. Left: Odds ratios for survival and age, by sex and class. Right: for survival and sex, by age and class. Error bars show ± 1 standard error.

In the left panel of Figure 5.38 you can see that the odds ratio of survival for adults relative to children was always greater for females as compared to males, but much less so in 3rd class. In the right panel, the odds ratio of survival for males versus females was always greater for children than adults, again less so in 3rd class. $\triangle$

Other examples and plots for log odds ratios are shown in `help(loddsratio)`.

5.10   Chapter summary

- The mosaic display depicts the frequencies in a contingency table by a collection of rectangular "tiles" whose area is proportional to the cell frequency. The residual from a specified model is portrayed by shading the tile to show the sign and magnitude of the deviation from the model.

- For two-way tables, the tiles for the second variable align at each level of the first variable when the two variables are independent (see Figure 5.10).

- The perception and understanding of *patterns of association* (deviations from independence) are enhanced by reordering the rows or columns to give the shading of the residuals a more coherent pattern. An opposite-corner pattern "explains" the association in terms of the ordering of the factor levels.

- For three-way and larger tables, a variety of models can be fit and visualized. Starting with a minimal baseline model, the pattern of residuals will often suggest additional terms that must be added to "clean the mosaic."

- It is often useful to examine the *sequential* mosaic displays for the marginal subtables with the variables in a given order. Sequential models of joint independence provide a breakdown of the total association in the full table, and are particularly appropriate when the last variable is a response.

- Partial association, which refers to the associations among a subset of variables, within the levels of other variables, may be easily studied by constructing separate mosaics for the subset variables for the levels of the other, "given" variables. These displays provide a breakdown of a model of conditional association for the whole table, and serve as an analog of coplots for quantitative data.

- Mosaic matrices, consisting of all pairwise plots of an *n*-way table, provide a way to visualize all marginal, joint, or conditional relations simultaneously. Doubledecker plots and plots of generalized odds ratios provide other methods to visualize *n*-way tables.

- The structural relations among model terms in various loglinear models themselves can also be visualized by mosaic matrices showing the expected, rather than observed, frequencies under different models.

- Related visualization techniques include doubledecker plots for binary response models and line plots for generalized odds ratios.

5.11 Lab exercises

{lab:mosaic-criminal}
{sec:mosaic-lab}

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

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

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

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

(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.

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.

(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")

(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.

Exercise 5.3 The **Lahman** (Friendly, 2014) package contains comprehensive data on baseball statistics for Major League Baseball from 1871 through 2012. For all players, the *Master* table records the handedness of players, in terms of throwing (L, R) and batting (B, L, R), where B indicates "both." The table below was generated using the following code:

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

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

- Use the code above, or else enter these data into a frequency table in R.
- Construct mosaic displays showing the relation of batting and throwing handedness, split first by batting and then by throwing.
- From these displays, what can be said about players who throw with their left or right hands in terms of their batting handedness?

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.

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

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

(d) Is there anything you can say about positions that have very few left-handed players?

{lab:5.5}

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.

{lab:5.6}

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

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

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

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

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

{lab:5.7}

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

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

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

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

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

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

(d) Create a mosaic display for this data.

{lab:5.8}

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

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

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

{lab:mosaic-accident}

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

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

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

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

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

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

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

{lab:mosaic-vietnam}

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.

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

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

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

{lab:5.11}

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

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

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

{lab:mosaic.titanic}{lab:5.12}

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

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

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

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

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

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