Working with categorical data with R and the **vcd** and **vcdExtra** packages

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Abstract

This tutorial describes the creation and manipulation of frequency and contingency tables from categorical variables, along with tests of independence, measures of association, and methods for graphically displaying results. The framework is provided by the R package **vcd**, but other packages are used to help with various tasks. The **vcdExtra** package extends the graphical and statistical methods provided by **vcd**.

This package is now the main support package for the book *Discrete Data Analysis with R: Visualizing and Modeling Techniques for Categorical and Count Data* (Friendly and Meyer 2016). The web page for the book, ddar.datavis.ca, gives further details.

Contents

1 Introduction

This tutorial, part of the **vcdExtra** package, describes how to work with categorical data in the context of fitting statistical models in R and visualizing the results using the **vcd** and **vcdExtra** packages. It focuses first on methods and tools for creating and manipulating R data objects which represent frequency and contingency tables involving categorical variables.

Further sections describe some simple methods for calculating tests of independence and measures of association among categorical variables, and also methods for graphically displaying results.

There is much more to the analysis of categorical data than is described here, where the emphasis is on cross-tabulated tables of frequencies ("contingency tables"), statistical tests, associated loglinear models, and visualization of *how* variables are related.

A more general treatment of graphical methods for categorical data is contained in the book, *Discrete Data Analysis with R: Visualizing and Modeling Techniques for Categorical and Count Data* (Friendly and Meyer 2016). An earlier book using SAS is *Visualizing Categorical Data* (Friendly 2000), for which **vcd** is a partial R companion, covering topics not otherwise available in R. On the other hand, the implementation of graphical methods in **vcd** is more general in many respects than what I provided in SAS. Statistical models for categorical data in R have been extended considerably with the **gnm** package for generalized *nonlinear* models. The **vcdExtra** package extends **vcd** methods to models fit using `glm()` and `gnm()`.

A more complete theoretical description of these statistical methods is provided in Agresti's (2002; 2013) *Categorical Data Analysis*. For this, see the Splus/R companion by Laura Thompson, `http://www.stat.ufl.edu/~aa/cda/Thompson_manual.pdf` and Agresti's support web page, `http://www.stat.ufl.edu/~aa/cda/cda.html`.

2 Creating and manipulating frequency tables

R provides many methods for creating frequency and contingency tables. Several are described below. In the examples below, we use some real examples and some anonymous ones, where the variables `A`, `B`, and `C` represent categorical variables, and `X` represents an arbitrary R data object.

The first thing you need to know is that categorical data can be represented in three different forms in R, and it is sometimes necessary to convert from one form to another, for carrying out statistical tests, fitting models or visualizing the results. Once a data object exists in R, you can examine its complete structure with the `str()` function, or view the names of its components with the `names()` function.

case form a data frame containing individual observations, with one or more factors, used as the classifying variables. In case form, there may also be numeric covariates. The total number of observations is `nrow(X)`, and the number of variables is `ncol(X)`.

Example: The `Arthritis` data is available in case form in the **vcd** package. There are two explanatory factors: `Treatment` and `Sex`. `Age` is a numeric covariate, and `Improved` is the response— an ordered factor, with levels `None < Some < Marked`. Excluding `Age`, we would have a $2 \times 2 \times 3$ contingency table for `Treatment`, `Sex` and `Improved`.

```
> names(Arthritis)      # show the variables

[1] "ID"        "Treatment" "Sex"       "Age"       "Improved"

> str(Arthritis)        # show the structure

'data.frame':        84 obs. of  5 variables:
 $ ID       : int  57 46 77 17 36 23 75 39 33 55 ...
 $ Treatment: Factor w/ 2 levels "Placebo","Treated": 2 2 2 2 2 2 2 2 2 2 ...
 $ Sex      : Factor w/ 2 levels "Female","Male": 2 2 2 2 2 2 2 2 2 2 ...
 $ Age      : int  27 29 30 32 46 58 59 59 63 63 ...
 $ Improved : Ord.factor w/ 3 levels "None"<"Some"<..: 2 1 1 3 3 3 1 3 1 1 ...

> head(Arthritis,5)     # first 5 observations, same as Arthritis[1:5,]
```

```
  ID Treatment  Sex Age Improved
1 57   Treated Male  27     Some
2 46   Treated Male  29     None
3 77   Treated Male  30     None
4 17   Treated Male  32   Marked
5 36   Treated Male  46   Marked
```

frequency form a data frame containing one or more factors, and a frequency variable, often called `Freq` or `count`. The total number of observations is `sum(X$Freq)`, `sum(X[,"Freq"])` or some equivalent form. The number of cells in the table is `nrow(X)`.

Example: For small frequency tables, it is often convenient to enter them in frequency form using `expand.grid()` for the factors and `c()` to list the counts in a vector. The example below, from Agresti (2002) gives results for the 1991 General Social Survey, with respondents classified by sex and party identification.

```
> # Agresti (2002), table 3.11, p. 106
> GSS <- data.frame(
+   expand.grid(sex=c("female", "male"),
+               party=c("dem", "indep", "rep")),
+   count=c(279,165,73,47,225,191))
> GSS

     sex party count
1 female   dem   279
2   male   dem   165
3 female indep    73
4   male indep    47
5 female   rep   225
6   male   rep   191

> names(GSS)

[1] "sex"   "party" "count"

> str(GSS)

'data.frame':        6 obs. of  3 variables:
 $ sex  : Factor w/ 2 levels "female","male": 1 2 1 2 1 2
 $ party: Factor w/ 3 levels "dem","indep",..: 1 1 2 2 3 3
 $ count: num  279 165 73 47 225 191

> sum(GSS$count)

[1] 980
```

table form a matrix, array or table object, whose elements are the frequencies in an n-way table. The variable names (factors) and their levels are given by `dimnames(X)`. The total number of observations is `sum(X)`. The number of dimensions of the table is `length(dimnames(X))`, and the table sizes are given by `sapply(dimnames(X), length)`.

Example: The `HairEyeColor` is stored in table form in **vcd**.

```
> str(HairEyeColor)                          # show the structure
```

```
 'table' num [1:4, 1:4, 1:2] 32 53 10 3 11 50 10 30 10 25 ...
 - attr(*, "dimnames")=List of 3
  ..$ Hair: chr [1:4] "Black" "Brown" "Red" "Blond"
  ..$ Eye : chr [1:4] "Brown" "Blue" "Hazel" "Green"
  ..$ Sex : chr [1:2] "Male" "Female"
```

```
> sum(HairEyeColor)                      # number of cases
```

```
[1] 592
```

```
> sapply(dimnames(HairEyeColor), length) # table dimension sizes
```

```
Hair  Eye  Sex
   4    4    2
```

Example: Enter frequencies in a matrix, and assign `dimnames`, giving the variable names and category labels. Note that, by default, `matrix()` uses the elements supplied by *columns* in the result, unless you specify `byrow=TRUE`.

```
> ## A 4 x 4 table  Agresti (2002, Table 2.8, p. 57) Job Satisfaction
> JobSat <- matrix(c(1,2,1,0, 3,3,6,1, 10,10,14,9, 6,7,12,11), 4, 4)
> dimnames(JobSat) = list(income=c("< 15k", "15-25k", "25-40k", "> 40k"),
+                 satisfaction=c("VeryD", "LittleD", "ModerateS", "VeryS"))
> JobSat
```

```
        satisfaction
income   VeryD LittleD ModerateS VeryS
  < 15k      1       3        10     6
  15-25k     2       3        10     7
  25-40k     1       6        14    12
  > 40k      0       1         9    11
```

`JobSat` is a matrix, not an object of `class("table")`, and some functions are happier with tables than matrices. You can coerce it to a table with `as.table()`,

```
> JobSat <- as.table(JobSat)
> str(JobSat)
```

```
 'table' num [1:4, 1:4] 1 2 1 0 3 3 6 1 10 10 ...
 - attr(*, "dimnames")=List of 2
  ..$ income      : chr [1:4] "< 15k" "15-25k" "25-40k" "> 40k"
  ..$ satisfaction: chr [1:4] "VeryD" "LittleD" "ModerateS" "VeryS"
```

2.1 Ordered factors and reordered tables

In table form, the values of the table factors are ordered by their position in the table. Thus in the `JobSat` data, both `income` and `satisfaction` represent ordered factors, and the *positions* of the values in the rows and columns reflects their ordered nature.

Yet, for analysis, there are time when you need *numeric* values for the levels of ordered factors in a table, e.g., to treat a factor as a quantitative variable. In such cases, you can simply re-assign the `dimnames` attribute of the table variables. For example, here, we assign numeric values to `income` as the middle of their ranges, and treat `satisfaction` as equally spaced with integer scores.

```
> dimnames(JobSat)$income<-c(7.5,20,32.5,60)
> dimnames(JobSat)$satisfaction<-1:4
```

For the HairEyeColor data, hair color and eye color are ordered arbitrarily. For visualizing the data using mosaic plots and other methods described below, it turns out to be more useful to assure that both hair color and eye color are ordered from dark to light. Hair colors are actually ordered this way already, and it is easiest to re-order eye colors by indexing. Again str() is your friend.

```
> HairEyeColor <- HairEyeColor[, c(1,3,4,2), ]
> str(HairEyeColor)

 'table' num [1:4, 1:4, 1:2] 32 53 10 3 10 25 7 5 3 15 ...
 - attr(*, "dimnames")=List of 3
  ..$ Hair: chr [1:4] "Black" "Brown" "Red" "Blond"
  ..$ Eye : chr [1:4] "Brown" "Hazel" "Green" "Blue"
  ..$ Sex : chr [1:2] "Male" "Female"
```

This is also the order for both hair color and eye color shown in the result of a correspondence analysis (Figure 6) below.

With data in case form or frequency form, when you have ordered factors represented with character values, you must ensure that they are treated as ordered in R.[1]

Imagine that the Arthritis data was read from a text file. By default the Improved will be ordered alphabetically: Marked, None, Some— not what we want. In this case, the function ordered() (and others) can be useful.

```
> Arthritis <- read.csv("arthritis.txt",header=TRUE)
> Arthritis$Improved <- ordered(Arthritis$Improved, levels=c("None", "Some", "Marked"))
```

With this order of Improved, the response in this data, a mosaic display of Treatment and Improved (Figure 1)shows a clearly interpretable pattern.

Finally, there are situations where, particularly for display purposes, you want to re-order the *dimensions* of an n-way table, or change the labels for the variables or levels. This is easy when the data are in table form: aperm() permutes the dimensions, and assigning to names and dimnames changes variable names and level labels respectively. We will use the following version of UCBAdmissions in Section 3.4 below.[2]

```
> UCB <- aperm(UCBAdmissions, c(2, 1, 3))
> dimnames(UCB)[[2]] <- c("Yes", "No")
> names(dimnames(UCB)) <- c("Sex", "Admit?", "Department")
> ftable(UCB)

              Department   A   B   C   D   E   F
Sex    Admit?
Male   Yes               512 353 120 138  53  22
       No                313 207 205 279 138 351
Female Yes                89  17 202 131  94  24
       No                 19   8 391 244 299 317
```

[1]In SAS, many procedures offer the option order = data | internal | formatted to allow character values to be ordered according to (a) their order in the data set, (b) sorted internal value, or (c) sorted formatted representation provided by a SAS format.

[2] Changing Admit to Admit? might be useful for display purposes, but is dangerous— because it is then difficult to use that variable name in a model formula. See Section 5.3 for options labeling_args and set_labels to change variable and level names for displays in the strucplot framework.

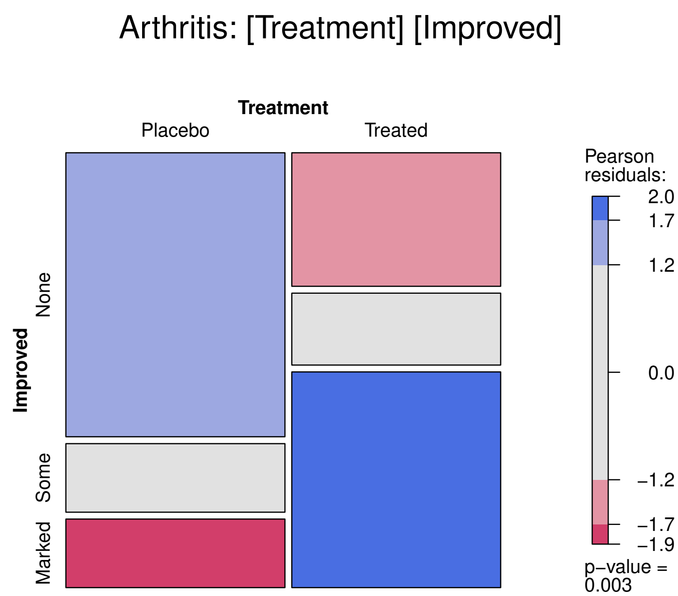


Figure 1: Mosaic plot for the **Arthritis** data, showing the marginal model of independence for Treatment and Improved. Age, a covariate, and Sex are ignored here.

2.2 structable()

For 3-way and larger tables the `structable()` function in **vcd** provides a convenient and flexible tabular display. The variables assigned to the rows and columns of a two-way display can be specified by a model formula.

```
> structable(HairEyeColor)                       # show the table: default

             Eye Brown Hazel Green Blue
Hair  Sex
Black Male          32    10     3   11
      Female        36     5     2    9
Brown Male          53    25    15   50
      Female        66    29    14   34
Red   Male          10     7     7   10
      Female        16     7     7    7
Blond Male           3     5     8   30
      Female         4     5     8   64

> structable(Hair+Sex ~ Eye, HairEyeColor)    # specify col ~ row variables

      Hair Black        Brown         Red         Blond
      Sex   Male Female  Male Female Male Female  Male Female
Eye
Brown         32     36    53     66   10     16     3      4
```

```
Hazel          10      5    25      29    7       7     5       5
Green           3      2    15      14    7       7     8       8
Blue           11      9    50      34   10       7    30      64
```

It also returns an object of class "structable" which may be plotted with mosaic() (not shown here).

```
> HSE < - structable(Hair+Sex ~ Eye, HairEyeColor)   # save structable object
> mosaic(HSE)                                        # plot it
```

2.3 table() and friends

You can generate frequency tables from factor variables using the table() function, tables of proportions using the prop.table() function, and marginal frequencies using margin.table().

```
>  n=500
>  A <- factor(sample(c("a1","a2"), n, rep=TRUE))
>  B <- factor(sample(c("b1","b2"), n, rep=TRUE))
>  C <- factor(sample(c("c1","c2"), n, rep=TRUE))
>  mydata <- data.frame(A,B,C)
```

```
> # 2-Way Frequency Table
> attach(mydata)
> mytable <- table(A,B)   # A will be rows, B will be columns
> mytable                 # print table
> margin.table(mytable, 1) # A frequencies (summed over B)
> margin.table(mytable, 2) # B frequencies (summed over A)
> prop.table(mytable)    # cell percentages
> prop.table(mytable, 1) # row percentages
> prop.table(mytable, 2) # column percentages
```

table() can also generate multidimensional tables based on 3 or more categorical variables. In this case, use the ftable() or structable() function to print the results more attractively.

```
> # 3-Way Frequency Table
> mytable <- table(A, B, C)
> ftable(mytable)
```

table() ignores missing values by default. To include NA as a category in counts, include the table option exclude=NULL if the variable is a vector. If the variable is a factor you have to create a new factor using newfactor <- factor(oldfactor, exclude=NULL).

2.4 xtabs()

The xtabs() function allows you to create cross-tabulations of data using formula style input. This typically works with case-form data supplied in a data frame or a matrix. The result is a contingency table in array format, whose dimensions are determined by the terms on the right side of the formula.

```
> # 3-Way Frequency Table
> mytable <- xtabs(~A+B+C, data=mydata)
> ftable(mytable)    # print table
> summary(mytable)   # chi-square test of indepedence
```

If a variable is included on the left side of the formula, it is assumed to be a vector of frequencies (useful if the data have already been tabulated in frequency form).

```
> (GSStab <- xtabs(count ~ sex + party, data=GSS))
```

```
        party
sex      dem indep rep
  female 279    73 225
  male   165    47 191
```

```
> summary(GSStab)
```

```
Call: xtabs(formula = count ~ sex + party, data = GSS)
Number of cases in table: 980
Number of factors: 2
Test for independence of all factors:
        Chisq = 7.01, df = 2, p-value = 0.03005
```

2.5 Collapsing over table factors: `aggregate()`, `margin.table()` and `apply()`

It sometimes happens that we have a data set with more variables or factors than we want to analyse, or else, having done some initial analyses, we decide that certain factors are not important, and so should be excluded from graphic displays by collapsing (summing) over them. For example, mosaic plots and fourfold displays are often simpler to construct from versions of the data collapsed over the factors which are not shown in the plots.

The appropriate tools to use again depend on the form in which the data are represented— a case-form data frame, a frequency-form data frame (`aggregate()`), or a table-form array or table object (`margin.table()` or `apply()`).

When the data are in frequency form, and we want to produce another frequency data frame, `aggregate()` is a handy tool, using the argument `FUN=sum` to sum the frequency variable over the factors *not* mentioned in the formula.

Example: The data frame `DaytonSurvey` in the **vcdExtra** package represents a 2^5 table giving the frequencies of reported use ("ever used?") of alcohol, cigarettes and marijuana in a sample of high school seniors, also classified by sex and race.

```
> str(DaytonSurvey)
```

```
'data.frame':        32 obs. of  6 variables:
 $ cigarette: Factor w/ 2 levels "Yes","No": 1 2 1 2 1 2 1 2 1 2 ...
 $ alcohol  : Factor w/ 2 levels "Yes","No": 1 1 2 2 1 1 2 2 1 1 ...
 $ marijuana: Factor w/ 2 levels "Yes","No": 1 1 1 1 2 2 2 2 1 1 ...
 $ sex      : Factor w/ 2 levels "female","male": 1 1 1 1 1 1 1 1 2 2 ...
 $ race     : Factor w/ 2 levels "white","other": 1 1 1 1 1 1 1 1 1 1 ...
 $ Freq     : num  405 13 1 1 268 218 17 117 453 28 ...
```

```
> head(DaytonSurvey)
```

```
  cigarette alcohol marijuana    sex  race Freq
1       Yes     Yes       Yes female white  405
2        No     Yes       Yes female white   13
3       Yes      No       Yes female white    1
4        No      No       Yes female white    1
5       Yes     Yes        No female white  268
6        No     Yes        No female white  218
```

To focus on the associations among the substances, we want to collapse over sex and race. The right-hand side of the formula used in the call to `aggregate()` gives the factors to be retained in the new frequency data frame, `Dayton.ACM.df`.

```
> # data in frequency form
> # collapse over sex and race
> Dayton.ACM.df <- aggregate(Freq ~ cigarette+alcohol+marijuana,
+                            data=DaytonSurvey, FUN=sum)
> Dayton.ACM.df

  cigarette alcohol marijuana Freq
1       Yes     Yes       Yes  911
2        No     Yes       Yes   44
3       Yes      No       Yes    3
4        No      No       Yes    2
5       Yes     Yes        No  538
6        No     Yes        No  456
7       Yes      No        No   43
8        No      No        No  279
```

When the data are in table form, and we want to produce another table, `apply()` with `FUN=sum` can be used in a similar way to sum the table over dimensions not mentioned in the `MARGIN` argument. `margin.table()` is just a wrapper for `apply()` using the `sum()` function.

$\boxed{\textbf{\textit{Example}}:}$ To illustrate, we first convert the `DaytonSurvey` to a 5-way table using `xtabs()`, giving `Dayton.tab`.

```
> # in table form
> Dayton.tab <- xtabs(Freq~cigarette+alcohol+marijuana+sex+race, data=DaytonSurvey)
> structable(cigarette+alcohol+marijuana ~ sex+race, data=Dayton.tab)

             cigarette Yes             No
             alcohol   Yes     No      Yes     No
             marijuana Yes  No Yes  No Yes  No Yes  No
sex    race
female white           405 268   1  17  13 218   1 117
       other            23  23   0   1   2  19   0  12
male   white           453 228   1  17  28 201   1 133
       other            30  19   1   8   1  18   0  17
```

Then, use `apply()` on `Dayton.tab` to give the 3-way table `Dayton.ACM.tab` summed over sex and race. The elements in this new table are the column sums for `Dayton.tab` shown by `structable()` just above.

```
> # collapse over sex and race
> Dayton.ACM.tab <- apply(Dayton.tab, MARGIN=1:3, FUN=sum)
> Dayton.ACM.tab <- margin.table(Dayton.tab, 1:3)   # same result
> structable(cigarette+alcohol ~ marijuana, data=Dayton.ACM.tab)

          cigarette Yes     No
          alcohol   Yes  No Yes  No
marijuana
Yes                 911   3  44   2
No                  538  43 456 279
```

Many of these operations can be performed using the `**ply()` functions in the **plyr** package. For example, with the data in a frequency form data frame, use `ddply()` to collapse over unmentioned factors, and `plyr::summarise()`[3] as the function to be applied to each piece.

```
> Dayton.ACM.df <- ddply(DaytonSurvey, .(cigarette, alcohol, marijuana),
+                        plyr::summarise, Freq=sum(Freq))
```

2.6 Collapsing table levels: `collapse.table()`

A related problem arises when we have a table or array and for some purpose we want to reduce the number of levels of some factors by summing subsets of the frequencies. For example, we may have initially coded Age in 10-year intervals, and decide that, either for analysis or display purposes, we want to reduce Age to 20-year intervals. The `collapse.table()` function in **vcdExtra** was designed for this purpose.

Example: Create a 3-way table, and collapse Age from 10-year to 20-year intervals. First, we generate a $2 \times 6 \times 3$ table of random counts from a Poisson distribution with mean of 100.

```
> # create some sample data in frequency form
> sex <- c("Male", "Female")
> age <- c("10-19", "20-29",  "30-39", "40-49", "50-59", "60-69")
> education <- c("low", 'med', 'high')
> data <- expand.grid(sex=sex, age=age, education=education)
> counts <- rpois(36, 100)   # random Possion cell frequencies
> data <- cbind(data, counts)
> # make it into a 3-way table
> t1 <- xtabs(counts ~ sex + age + education, data=data)
> structable(t1)
```

```
                 age 10-19 20-29 30-39 40-49 50-59 60-69
sex    education
Male   low              98   105   104    90    90   101
       med              97   105   101    88    97   107
       high             99   101   109    88    99    96
Female low             102   117   101   105    85    88
       med             106    84    92   116   110    96
       high            106    96   121    91   107   102
```

Now collapse `age` to 20-year intervals, and `education` to 2 levels. In the arguments, levels of `age` and `education` given the same label are summed in the resulting smaller table.

```
> # collapse age to 3 levels, education to 2 levels
> t2 <- collapse.table(t1,
+          age=c("10-29", "10-29",  "30-49", "30-49", "50-69", "50-69"),
+          education=c("<high", "<high", "high"))
> structable(t2)
```

```
                 age 10-29 30-49 50-69
sex    education
Male   <high           405   383   395
       high            200   197   195
Female <high           409   414   379
       high            202   212   209
```

[3] Ugh. This **plyr** function clashes with a function of the same name in **vcdExtra**. In this document I will use the explicit double-colon notation to keep them separate.

2.7 Converting among frequency tables and data frames

As we've seen, a given contingency table can be represented equivalently in different forms, but some R functions were designed for one particular representation. Table 1 shows some handy tools for converting from one form to another.

Table 1: Tools for converting among different forms for categorical data

	To this		
From this	Case form	Frequency form	Table form
Case form	noop	`xtabs(~A+B)`	`table(A,B)`
Frequency form	`expand.dft(X)`	noop	`xtabs(count~A+B)`
Table form	`expand.dft(X)`	`as.data.frame(X)`	noop

A contingency table in table form (an object of `class(table)`) can be converted to a data.frame with `as.data.frame()`.[4] The resulting `data.frame` contains columns representing the classifying factors and the table entries (as a column named by the `responseName` argument, defaulting to `Freq`. This is the inverse of `xtabs()`.

Example: Convert the `GSStab` in table form to a data.frame in frequency form.

```
> as.data.frame(GSStab)

     sex party Freq
1 female   dem  279
2   male   dem  165
3 female indep   73
4   male indep   47
5 female   rep  225
6   male   rep  191
```

Example: Convert the `Arthritis` data in case form to a 3-way table of `Treatment` × `Sex` × `Improved`. Note the use of `with()` to avoid having to use `Arthritis$Treatment` etc. within the call to `table()`.[5]

```
> Art.tab <-with(Arthritis, table(Treatment, Sex, Improved))
> str(Art.tab)

 'table' int [1:2, 1:2, 1:3] 19 6 10 7 7 5 0 2 6 16 ...
 - attr(*, "dimnames")=List of 3
  ..$ Treatment: chr [1:2] "Placebo" "Treated"
  ..$ Sex      : chr [1:2] "Female" "Male"
  ..$ Improved : chr [1:3] "None" "Some" "Marked"

> ftable(Art.tab)

                 Improved None Some Marked
Treatment Sex
```

[4] Because R is object-oriented, this is actually a short-hand for the function `as.data.frame.table()`.

[5] `table()` does not allow a `data` argument to provide an environment in which the table variables are to be found. In the examples in Section 2.3 I used `attach(mydata)` for this purpose, but `attach()` leaves the variables in the global environment, while `with()` just evaluates the `table()` expression in a temporary environment of the data.

```
Placebo   Female            19    7     6
          Male              10    0     1
Treated   Female             6    5    16
          Male               7    2     5
```

There may also be times that you will need an equivalent case form `data.frame` with factors representing the table variables rather than the frequency table. For example, the `mca()` function in package **MASS** only operates on data in this format. Marc Schwartz provided code for `expand.dft()` on the Rhelp mailing list for converting a table back into a case form `data.frame`. This function is included in **vcdExtra**.

Example: Convert the `Arthritis` data in table form (`Art.tab`) back to a `data.frame` in case form, with factors `Treatment`, `Sex` and `Improved`.

```
> Art.df <- expand.dft(Art.tab)
> str(Art.df)
```

```
'data.frame':        84 obs. of  3 variables:
 $ Treatment: chr  "Placebo" "Placebo" "Placebo" "Placebo" ...
 $ Sex      : chr  "Female" "Female" "Female" "Female" ...
 $ Improved : chr  "None" "None" "None" "None" ...
```

2.8 A complex example

If you've followed so far, you're ready for a more complicated example. The data file, `tv.dat` represents a 4-way table of size $5 \times 11 \times 5 \times 3$ where the table variables (unnamed in the file) are read as `V1` – `V4`, and the cell frequency is read as `V5`. The file, stored in the `doc/extdata` directory of **vcdExtra**, can be read as follows:

```
> tv.data<-read.table(system.file("extdata","tv.dat", package="vcdExtra"))
> head(tv.data,5)
```

```
  V1 V2 V3 V4 V5
1  1  1  1  1  6
2  2  1  1  1 18
3  3  1  1  1  6
4  4  1  1  1  2
5  5  1  1  1 11
```

For a local file, just use `read.table()` in this form:

```
> tv.data<-read.table("C:/R/data/tv.dat")
```

The data `tv.dat` came from the initial implementation of mosaic displays in R by Jay Emerson. In turn, they came from the initial development of mosaic displays (Hartigan and Kleiner 1984) that illustrated the method with data on a large sample of TV viewers whose behavior had been recorded for the Neilson ratings. This data set contains sample television audience data from Neilsen Media Research for the week starting November 6, 1995.

The table variables are:
`V1`– values 1:5 correspond to the days Monday–Friday;
`V2`– values 1:11 correspond to the quarter hour times 8:00PM through 10:30PM;
`V3`– values 1:5 correspond to ABC, CBS, NBC, Fox, and non-network choices;
`V4`– values 1:3 correspond to transition states: turn the television Off, Switch channels, or Persist in viewing the current channel.

We are interested just the cell frequencies, and rely on the facts that the (a) the table is complete— there are no missing cells, so `nrow(tv.data)`=825; (b) the observations are ordered so that `V1` varies most rapidly and `V4` most slowly. From this, we can just extract the frequency column and reshape it into an array.

```
> TV <- array(tv.data[,5], dim=c(5,11,5,3))
> dimnames(TV) <- list(c("Monday","Tuesday","Wednesday","Thursday","Friday"),
+                  c("8:00","8:15","8:30","8:45","9:00","9:15","9:30",
+                    "9:45","10:00","10:15","10:30"),
+                  c("ABC","CBS","NBC","Fox","Other"), c("Off","Switch","Persist"))
> names(dimnames(TV))<-c("Day", "Time", "Network", "State")
```

More generally (even if there are missing cells), we can use `xtabs()` (or `plyr::daply()`) to do the cross-tabulation, using `V5` as the frequency variable. Here's how to do this same operation with `xtabs()`:

```
> TV <- xtabs(V5 ~ ., data=tv.data)
> dimnames(TV) <- list(Day=c("Monday","Tuesday","Wednesday","Thursday","Friday"),
+                  Time=c("8:00","8:15","8:30","8:45","9:00","9:15","9:30",
+                         "9:45","10:00","10:15","10:30"),
+                  Network=c("ABC","CBS","NBC","Fox","Other"),
+                  State=c("Off","Switch","Persist"))
```

But this 4-way table is too large and awkward to work with. Among the networks, Fox and Other occur infrequently. We can also cut it down to a 3-way table by considering only viewers who persist with the current station.[6]

```
> TV <- TV[,,1:3,]      # keep only ABC, CBS, NBC
> TV <- TV[,,,3]        # keep only Persist -- now a 3 way table
> structable(TV)

                  Time 8:00 8:15 8:30 8:45 9:00 9:15 9:30 9:45 10:00 10:15 10:30
Day       Network
Monday    ABC           146  151  156   83  325  350  386  340   352   280   278
          CBS           337  293  304  233  311  251  241  164   252   265   272
          NBC           263  219  236  140  226  235  239  246   279   263   283
Tuesday   ABC           244  181  231  205  385  283  345  192   329   351   364
          CBS           173  180  184  109  218  235  256  250   274   263   261
          NBC           315  254  280  241  370  214  195  111   188   190   210
Wednesday ABC           233  161  194  156  339  264  279  140   237   228   203
          CBS           158  126  207   59   98  103  122   86   109   105   110
          NBC           134  146  166   66  194  230  264  143   274   289   306
Thursday  ABC           174  183  197  181  187  198  211   86   110   122   117
          CBS           196  185  195  104  106  116  116   47   102    84    84
          NBC           515  463  472  477  590  473  446  349   649   705   747
Friday    ABC           294  281  305  239  278  246  245  138   246   232   233
          CBS           130  144  154   81  129  153  136  126   138   136   152
          NBC           195  220  248  160  172  164  169   85   183   198   204
```

Finally, for some purposes, we might want to collapse the 11 times into a smaller number. Here, we use `as.data.frame.table()` to convert the table back to a data frame, `levels()` to re-assign the values of `Time`, and finally, `xtabs()` to give a new, collapsed frequency table.

[6]This relies on the fact that that indexing an array drops dimensions of length 1 by default, using the argument `drop=TRUE`; the result is coerced to the lowest possible dimension.

```
> TV.df <- as.data.frame.table(TV)
> levels(TV.df$Time) <- c(rep("8:00-8:59",4),rep("9:00-9:59",4), rep("10:00-10:44",3))
> TV2 <- xtabs(Freq ~ Day + Time + Network, TV.df)
> structable(Day ~ Time+Network,TV2)
```

```
                    Day Monday Tuesday Wednesday Thursday Friday
Time        Network
8:00-8:59   ABC            536     861       744      735   1119
            CBS           1167     646       550      680    509
            NBC            858    1090       512     1927    823
9:00-9:59   ABC           1401    1205      1022      682    907
            CBS            967     959       409      385    544
            NBC            946     890       831     1858    590
10:00-10:44 ABC            910    1044       668      349    711
            CBS            789     798       324      270    426
            NBC            825     588       869     2101    585
```

Whew! See Figure 7 for a mosaic plot of the TV2 data.

3 Tests of Independence

3.1 CrossTable

OK, now we're ready to do some analyses. For tabular displays, the CrossTable() function in the **gmodels** package produces cross-tabulations modeled after PROC FREQ in SAS or CROSSTABS in SPSS. It has a wealth of options for the quantities that can be shown in each cell.

```
> # 2-Way Cross Tabulation
> library(gmodels)
> CrossTable(GSStab,prop.t=FALSE,prop.r=FALSE,prop.c=FALSE)
```

```
   Cell Contents
|-------------------------|
|                       N |
| Chi-square contribution |
|-------------------------|


Total Observations in Table:  980


             | party
         sex |       dem |     indep |       rep | Row Total |
-------------|-----------|-----------|-----------|-----------|
      female |       279 |        73 |       225 |       577 |
             |     1.183 |     0.078 |     1.622 |           |
-------------|-----------|-----------|-----------|-----------|
        male |       165 |        47 |       191 |       403 |
             |     1.693 |     0.112 |     2.322 |           |
-------------|-----------|-----------|-----------|-----------|
Column Total |       444 |       120 |       416 |       980 |
-------------|-----------|-----------|-----------|-----------|
```

There are options to report percentages (row, column, cell), specify decimal places, produce Chi-square, Fisher, and McNemar tests of independence, report expected and residual values (pearson, standardized, adjusted standardized), include missing values as valid, annotate with row and column titles, and format as SAS or SPSS style output! See `help(CrossTable)` for details.

3.2 Chi-square test

For 2-way tables you can use `chisq.test()` to test independence of the row and column variable. By default, the p-value is calculated from the asymptotic chi-squared distribution of the test statistic. Optionally, the p-value can be derived via Monte Carlo simulation.

```
> (HairEye <- margin.table(HairEyeColor, c(1, 2)))

       Eye
Hair    Brown Hazel Green Blue
  Black    68    15     5   20
  Brown   119    54    29   84
  Red      26    14    14   17
  Blond     7    10    16   94

> chisq.test(HairEye)

        Pearson's Chi-squared test

data:  HairEye
X-squared = 138.29, df = 9, p-value < 2.2e-16
```

3.3 Fisher Exact Test

`fisher.test(X)` provides an exact test of independence. `X` must be a two-way contingency table in table form. Another form, `fisher.test(X, Y)` takes two categorical vectors of the same length. For tables larger than 2×2 the method can be computationally intensive (or can fail) if the frequencies are not small.

```
> fisher.test(GSStab)

        Fisher's Exact Test for Count Data

data:  GSStab
p-value = 0.03115
alternative hypothesis: two.sided
```

But this does not work because `HairEye` data has n=592 total frequency. An exact test is unnecessary in this case.

```
> fisher.test(HairEye)

Error in fisher.test(HairEye) : FEXACT error 6.
LDKEY is too small for this problem.
Try increasing the size of the workspace.
```

3.4 Mantel-Haenszel test and conditional association

Use the `mantelhaen.test(X)` function to perform a Cochran-Mantel-Haenszel χ^2 chi test of the null hypothesis that two nominal variables are *conditionally independent*, $A \perp B \,|\, C$, in each stratum, assuming that there is no three-way interaction. `X` is a 3 dimensional contingency table, where the last dimension refers to the strata.

The `UCBAdmissions` serves as an example of a $2 \times 2 \times 6$ table, with `Dept` as the stratifying variable.

```
> ## UC Berkeley Student Admissions
> mantelhaen.test(UCBAdmissions)

        Mantel-Haenszel chi-squared test with continuity correction

data:  UCBAdmissions
Mantel-Haenszel X-squared = 1.4269, df = 1, p-value = 0.2323
alternative hypothesis: true common odds ratio is not equal to 1
95 percent confidence interval:
 0.7719074 1.0603298
sample estimates:
common odds ratio
        0.9046968
```

The results show no evidence for association between admission and gender when adjusted for department. However, we can easily see that the assumption of equal association across the strata (no 3-way association) is probably violated. For $2 \times 2 \times k$ tables, this can be examined from the odds ratios for each 2×2 table (`oddsratio()`), and tested by using `woolf_test()` in **vcd**.

```
> oddsratio(UCBAdmissions, log=FALSE)

 odds ratios for Admit and Gender by Dept

        A         B         C         D         E         F
0.3492120 0.8025007 1.1330596 0.9212838 1.2216312 0.8278727

> lor <- oddsratio(UCBAdmissions)  # capture log odds ratios
> summary(lor)

z test of coefficients:

   Estimate Std. Error z value  Pr(>|z|)
A -1.052076   0.262708 -4.0047 6.209e-05 ***
B -0.220023   0.437593 -0.5028    0.6151
C  0.124922   0.143942  0.8679    0.3855
D -0.081987   0.150208 -0.5458    0.5852
E  0.200187   0.200243  0.9997    0.3174
F -0.188896   0.305164 -0.6190    0.5359
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> woolf_test(UCBAdmissions)
```

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

data:  UCBAdmissions
X-squared = 17.902, df = 5, p-value = 0.003072
```

We can visualize the odds ratios of Admission for each department with fourfold displays using `fourfold()`. The cell frequencies n_{ij} of each 2×2 table are shown as a quarter circle whose radius is proportional to $\sqrt{n_{ij}}$, so that its area is proportional to the cell frequency. Confidence rings for the odds ratio allow a visual test of the null of no association; the rings for adjacent quadrants overlap *iff* the observed counts are consistent with the null hypothesis. In the extended version (the default), brighter colors are used where the odds ratio is significantly different from 1. The following lines produce Figure 2.[7]

```
> col <- c("#99CCFF", "#6699CC", "#F9AFAF", "#6666A0", "#FF0000", "#000080")
> fourfold(UCB,mfrow=c(2,3), color=col)
```

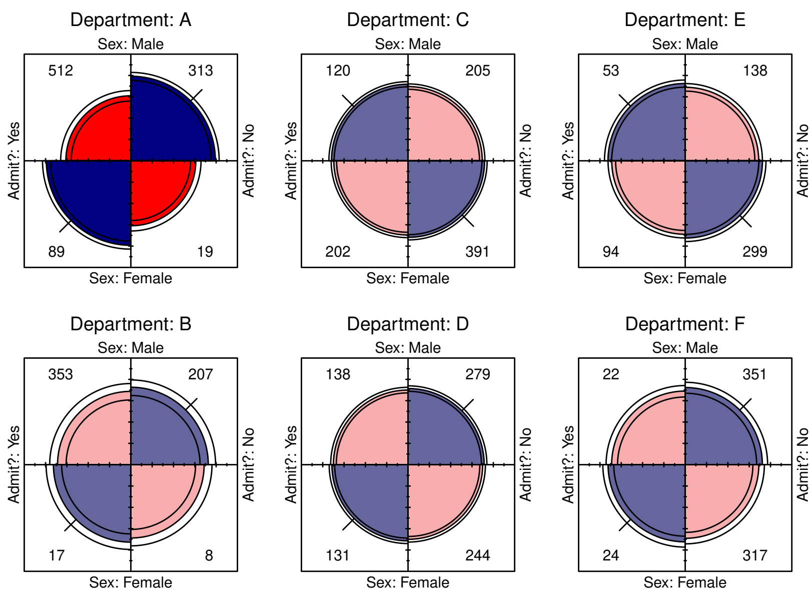


Figure 2: Fourfold display for the `UCBAdmissions` data. Where the odds ratio differs significantly from 1.0, the confidence bands do not overlap, and the circle quadrants are shaded more intensely.

Another **vcd** function, `cotabplot()`, provides a more general approach to visualizing conditional associations in contingency tables, similar to trellis-like plots produced by `coplot()` and lattice graphics. The `panel` argument supplies a function used to render each conditional subtable. The following gives a display (not shown) similar to Figure 2.

```
> cotabplot(UCB, panel = cotab_fourfold)
```

When we want to view the conditional probabilities of a response variable (e.g., `Admit`) in relation to several factors, an alternative visualization is a `doubledecker()` plot. This plot is a specialized

[7] The color values `col[3:4]` were modified from their default values to show a greater contrast between significant and insignificant associations here.

version of a mosaic plot, which highlights the levels of a response variable (plotted vertically) in relation to the factors (shown horizontally). The following call produces Figure 3, where we use indexing on the first factor (`Admit`) to make `Admitted` the highlighted level.

In this plot, the association between `Admit` and `Gender` is shown where the heights of the highlighted conditional probabilities do not align. The excess of females admitted in Dept A stands out here.

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

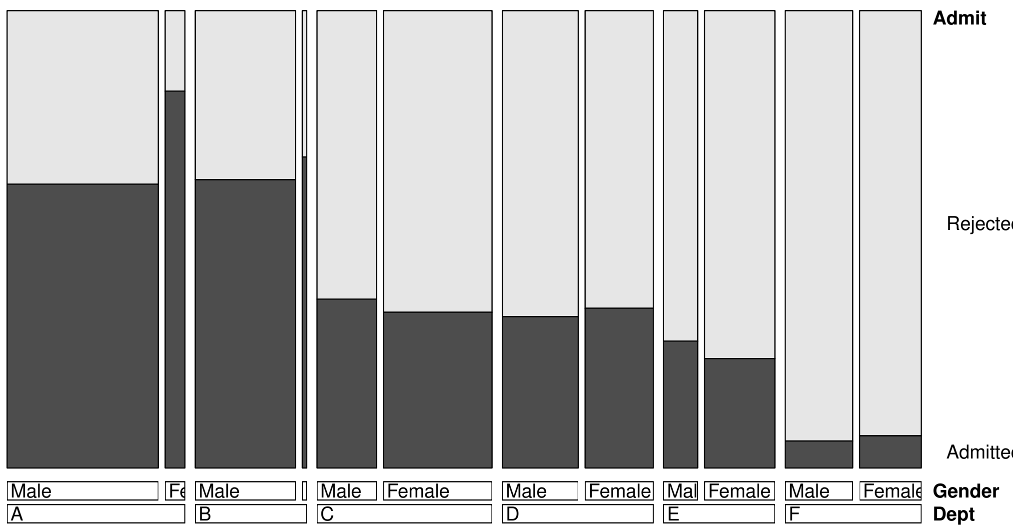


Figure 3: Doubledecker display for the `UCBAdmissions` data. The heights of the highlighted bars show the conditional probabilities of `Admit`, given `Dept` and `Gender`.

Finally, the there is a `plot()` method for `oddsratio` objects. By default, it shows the 95% confidence interval for the log odds ratio. Figure 4 is produced by:

```
> plot(lor, xlab="Department", ylab="Log Odds Ratio (Admit | Gender)")
```

3.5 Cochran-Mantel-Haenszel tests for ordinal factors

The standard χ^2 tests for association in a two-way table treat both table factors as nominal (unordered) categories. When one or both factors of a two-way table are quantitative or ordinal, more powerful tests of association may be obtaianed by taking ordinality into account, using row and or column scores to test for linear trends or differences in row or column means.

More general versions of the CMH tests (Landis etal., 1978) are provided by assigning numeric scores to the row and/or column variables. For example, with two ordinal factors (assumed to be equally spaced), assigning integer scores, `1:R` and `1:C` tests the linear $\times$ linear component of association. This is statistically equivalent to the Pearson correlation between the integer-scored table variables, with $\chi^2 = (n-1)r^2$, with only 1 *df* rather than $(R-1) \times (C-1)$ for the test of general association.

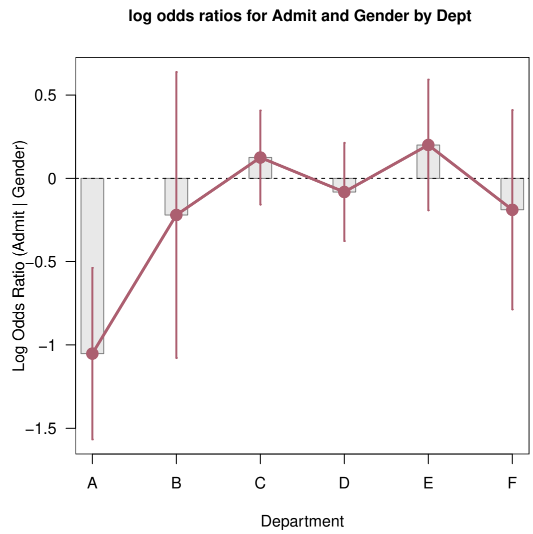


Figure 4: Log odds ratio plot for the `UCBAdmissions` data.

When only one table variable is ordinal, these general CMH tests are analogous to an ANOVA, testing whether the row mean scores or column mean scores are equal, again consuming fewer *df* than the test of general association.

The `CMHtest()` function in **vcdExtra** now calculates these various CMH tests for two possibly ordered factors, optionally stratified other factor(s).

Example: Recall the 4 × 4 table, `JobSat` introduced in Section 2,

```
> JobSat
```

```
        satisfaction
income   VeryD LittleD ModerateS VeryS
  < 15k      1       3        10     6
  15-25k     2       3        10     7
  25-40k     1       6        14    12
  > 40k      0       1         9    11
```

Treating the `satisfaction` levels as equally spaced, but using midpoints of the `income` categories as row scores gives the following results:

```
> CMHtest(JobSat, rscores=c(7.5,20,32.5,60))
```

```
Cochran-Mantel-Haenszel Statistics for income by satisfaction

                 AltHypothesis  Chisq Df     Prob
cor        Nonzero correlation 3.8075  1 0.051025
rmeans  Row mean scores differ 4.4774  3 0.214318
cmeans  Col mean scores differ 3.8404  3 0.279218
general    General association 5.9034  9 0.749549
```

Note that with the relatively small cell frequencies, the test for general give no evidence for association. However, the the `cor` test for linear x linear association on 1 df is nearly significant. The **coin** contains the functions `cmh_test()` and `lbl_test()` for CMH tests of general association and linear x linear association respectively.

3.6 Measures of Association

There are a variety of statistical measures of *strength* of association for contingency tables— similar in spirit to r or r^2 for continuous variables. With a large sample size, even a small degree of association can show a significant χ^2, as in the example below for the `GSS` data.

The `assocstats()` function in **vcd** calculates the ϕ contingency coefficient, and Cramer's V for an $r \times c$ table. The input must be in table form, a two-way $r \times c$ table. It won't work with `GSS` in frequency form, but by now you should know how to convert.

```
> assocstats(GSStab)

                    X^2 df P(> X^2)
Likelihood Ratio 7.0026  2 0.030158
Pearson          7.0095  2 0.030054

Phi-Coefficient   : NA
Contingency Coeff.: 0.084
Cramer's V        : 0.085
```

For tables with ordinal variables, like `JobSat`, some people prefer the Goodman-Kruskal γ statistic (Agresti (2002, §2.4.3)) based on a comparison of concordant and discordant pairs of observations in the case-form equivalent of a two-way table.

```
> GKgamma(JobSat)

gamma        : 0.221
std. error   : 0.117
CI           : -0.009 0.451
```

A web article by Richard Darlington, http://www.psych.cornell.edu/Darlington/crosstab/TABLE0.HTM gives further description of these and other measures of association.

3.7 Measures of Agreement

The `Kappa()` function in the **vcd** package calculates Cohen's κ and weighted κ for a square two-way table with the same row and column categories (Cohen 1960).[8] Normal-theory z-tests are obtained by dividing κ by its asymptotic standard error (ASE). A `confint()` method for `Kappa` objects provides confidence intervals.

```
> (K <- Kappa(SexualFun))

            value     ASE     z Pr(>|z|)
Unweighted 0.1293 0.06860 1.885 0.059387
Weighted   0.2374 0.07832 3.031 0.002437

> confint(K)
```

[8] Don't confuse this with `kappa()` in base R that computes something entirely different (the condition number of a matrix).

```
Kappa                 lwr       upr
  Unweighted -0.005120399 0.2637809
  Weighted    0.083883432 0.3908778
```

A visualization of agreement, both unweighted and weighted for degree of departure from exact agreement is provided by the `agreementplot()` function. Figure 5 shows the agreementplot for the `SexualFun` data, produced as shown below. The Bangdiwala measures represent the proportion of the shaded areas of the diagonal rectangles, using weights w_1 for exact agreement, and w_2 for partial agreement one step from the main diagonal.

```
> agree <- agreementplot(SexualFun, main="Is sex fun?")
> unlist(agree)
```

```
         Bangdiwala Bangdiwala_Weighted            weights1            weights2
          0.1464624           0.4981723           1.0000000           0.8888889
```

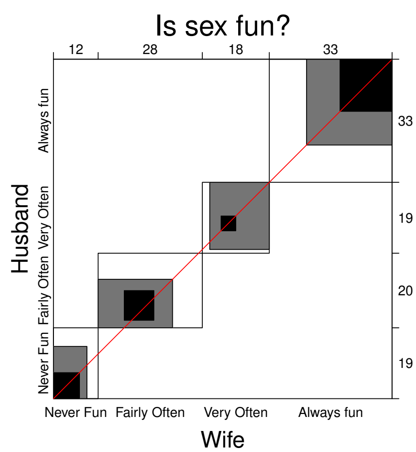


Figure 5: Agreement plot for the `SexualFun` data.

In other examples, the agreement plot can help to show *sources* of disagreement. For example, when the shaded boxes are above or below the diagonal (red) line, a lack of exact agreement can be attributed in part to different frequency of use of categories by the two raters– lack of *marginal homogeneity*.

3.8 Correspondence analysis

Use the **ca** package for correspondence analysis for visually exploring relationships between rows and columns in contingency tables. For an $r \times c$ table, the method provides a breakdown of the Pearson χ^2 for association in up to $M = \min(r-1, c-1)$ dimensions, and finds scores for the row (x_{im}) and column (y_{jm}) categories such that the observations have the maximum possible correlations.[9]

Here, we carry out a simple correspondence analysis of the `HairEye` data. The printed results show that nearly 99% of the association between hair color and eye color can be accounted for in 2 dimensions, of which the first dimension accounts for 90%.

[9] Related methods are the non-parametric CMH tests using assumed row/column scores (Section 3.5), the analogous `glm()` model-based methods (Section 3.5), and the more general RC models which can be fit using `gnm()`. Correspondence analysis differs in that it is a primarily descriptive/exploratory method (no significance tests), but is directly tied to informative graphic displays of the row/column categories.

```
> library(ca)
> ca(HairEye)

 Principal inertias (eigenvalues):
           1        2        3
Value      0.208773 0.022227 0.002598
Percentage 89.37%   9.52%    1.11%


 Rows:
            Black     Brown       Red    Blond
Mass     0.182432  0.483108  0.119932 0.214527
ChiDist  0.551192  0.159461  0.354770 0.838397
Inertia  0.055425  0.012284  0.015095 0.150793
Dim. 1  -1.104277 -0.324463 -0.283473 1.828229
Dim. 2   1.440917 -0.219111 -2.144015 0.466706


 Columns:
            Brown     Hazel     Green     Blue
Mass     0.371622  0.157095  0.108108 0.363176
ChiDist  0.500487  0.288654  0.385727 0.553684
Inertia  0.093086  0.013089  0.016085 0.111337
Dim. 1  -1.077128 -0.465286  0.354011 1.198061
Dim. 2   0.592420 -1.122783 -2.274122 0.556419
```

The resulting `ca` object can be plotted just by running the `plot()` method on the `ca` object, giving the result in Figure 6. `plot.ca()` does not allow labels for dimensions; these can be added with `title()`. It can be seen that most of the association is accounted for by the ordering of both hair color and eye color along Dimension 1, a dark to light dimension.

```
> plot(ca(HairEye), main="Hair Color and Eye Color")
> title(xlab="Dim 1 (89.4%)", ylab="Dim 2 (9.5%)")
```

4 Loglinear Models

You can use the `loglm()` function in the **MASS** package to fit log-linear models. Equivalent models can also be fit (from a different perspective) as generalized linear models with the `glm()` function using the `family='poisson'` argument, and the **gnm** package provides a wider range of generalized *nonlinear* models, particularly for testing structured associations. The visualization methods for these models were originally developed for models fit using `loglm()`, so this approach is emphasized here. Some extensions of these methods for models fit using `glm()` and `gnm()` are contained in the **vcdExtra** package and illustrated in Section 4.2.

Assume we have a 3-way contingency table based on variables A, B, and C. The possible different forms of loglinear models for a 3-way table are shown in Table 2. The **Model formula** column shows how to express each model for `loglm()` in R.[10] In the **Interpretation** column, the symbol "$\perp$" is to be read as "is independent of," and "$|$" means "conditional on," or "adjusting for," or just "given".

[10] For `glm()`, or `gnm()`, with the data in the form of a frequency data.frame, the same model is specified in the form `glm(Freq ~ ..., family="poisson")`, where `Freq` is the name of the cell frequency variable and `...` specifies the **Model formula**.

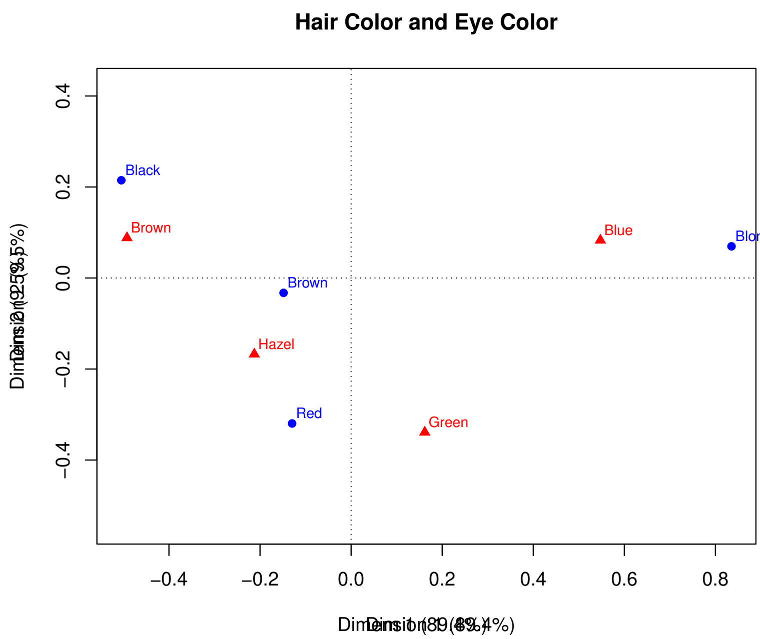


Figure 6: Correspondence analysis plot for the `HairEye` data.

For example, the formula `~A + B + C` specifies the model of *mutual independence* with no associations among the three factors. In standard notation for the expected frequencies m_{ijk}, this corresponds to

$$\log(m_{ijk}) = \mu + \lambda_i^A + \lambda_j^B + \lambda_k^C \equiv \texttt{A + B + C}$$

The parameters λ_i^A, λ_j^B and λ_k^C pertain to the differences among the one-way marginal frequencies for the factors A, B and C.

Similarly, the model of *joint independence*, $(A\,B) \perp C$, allows an association between A and B, but specifies that C is independent of both of these and their combinations,

$$\log(m_{ijk}) = \mu + \lambda_i^A + \lambda_j^B + \lambda_k^C + \lambda_{ij}^{AB} \equiv \texttt{A * B + C}$$

where the parameters λ_{ij}^{AB} pertain to the overall association between A and B (collapsing over C).

Table 2: Log-linear Models for Three-Way Tables

Model	**Model formula**	**Symbol**	**Interpretation**
Mutual independence	`~A + B + C`	$[A][B][C]$	$A \perp B \perp C$
Joint independence	`~A*B + C`	$[AB][C]$	$(A\,B) \perp C$
Conditional independence	`~(A+B)*C`	$[AC][BC]$	$(A \perp B) \mid C$
All two-way associations	`~A*B + A*C + B*C`	$[AB][AC][BC]$	homogeneous association
Saturated model	`~A*B*C`	$[ABC]$	3-way association

In the literature or text books, you will often find these models expressed in shorthand symbolic notation, using brackets, `[ ]` to enclose the *high-order terms* in the model. Thus, the joint independence model can be denoted `[AB][C]`, as shown in the **Symbol** column in Table 2.

Models of *conditional independence* allow (and fit) two of the three possible two-way associations. There are three such models, depending on which variable is conditioned upon. For a given conditional independence model, e.g., `[AB][AC]`, the given variable is the one common to all terms, so this example has the interpretation $(B \perp C) \mid A$.

4.1 Fitting with `loglm()`

For example, we can fit the model of mutual independence among hair color, eye color and sex in `HairEyeColor` as

```
> library(MASS)
> ## Independence model of hair and eye color and sex.
> hec.1 <- loglm(~Hair+Eye+Sex, data=HairEyeColor)
> hec.1

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

Statistics:
                      X^2 df P(> X^2)
Likelihood Ratio 166.3001 24        0
Pearson          164.9247 24        0
```

Similarly, the models of conditional independence and joint independence are specified as

```
> ## Conditional independence
> hec.2 <- loglm(~(Hair + Eye) * Sex, data=HairEyeColor)
> hec.2

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

Statistics:
                      X^2 df P(> X^2)
Likelihood Ratio 156.6779 18        0
Pearson          147.9440 18        0

> ## Joint independence model.
> hec.3 <- loglm(~Hair*Eye + Sex, data=HairEyeColor)
> hec.3

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

Statistics:
                      X^2 df  P(> X^2)
Likelihood Ratio 19.85656 15 0.1775045
Pearson          19.56712 15 0.1891745
```

Note that printing the model gives a brief summary of the goodness of fit. A set of models can be compared using the anova() function.

```
> anova(hec.1, hec.2, hec.3)

LR tests for hierarchical log-linear models

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

           Deviance df Delta(Dev) Delta(df) P(> Delta(Dev)
Model 1   166.30014 24
Model 2   156.67789 18    9.62225         6        0.14149
Model 3    19.85656 15  136.82133         3        0.00000
Saturated   0.00000  0   19.85656        15        0.17750
```

4.2 Fitting with glm() and gnm()

The glm() approach, and extensions of this in the **gnm** package allows a much wider class of models for frequency data to be fit than can be handled by loglm(). Of particular importance are models for ordinal factors and for square tables, where we can test more structured hypotheses about the patterns of association than are provided in the tests of general association under loglm(). These are similar in spirit to the non-parametric CMH tests described in Section 3.5.

Example: The data Mental in the **vcdExtra** package gives a two-way table in frequency form classifying young people by their mental health status and parents' socioeconomic status (SES), where both of these variables are ordered factors.

```
> str(Mental)

'data.frame':        24 obs. of  3 variables:
 $ ses   : Ord.factor w/ 6 levels "1"<"2"<"3"<"4"<..: 1 1 1 1 2 2 2 2 3 3 ...
 $ mental: Ord.factor w/ 4 levels "Well"<"Mild"<..: 1 2 3 4 1 2 3 4 1 2 ...
 $ Freq  : int  64 94 58 46 57 94 54 40 57 105 ...

> xtabs(Freq ~ mental+ses, data=Mental)   # display the frequency table

          ses
mental       1   2   3   4   5   6
  Well      64  57  57  72  36  21
  Mild      94  94 105 141  97  71
  Moderate  58  54  65  77  54  54
  Impaired  46  40  60  94  78  71
```

Simple ways of handling ordinal variables involve assigning scores to the table categories, and the simplest cases are to use integer scores, either for the row variable ("column effects" model), the column variable ("row effects" model), or both ("uniform association" model).

```
> indep <- glm(Freq ~ mental + ses, family = poisson, data = Mental)  # independence model
```

To fit more parsimonious models than general association, we can define numeric scores for the row and column categories

```
> # Use integer scores for rows/cols
> Cscore <- as.numeric(Mental$ses)
> Rscore <- as.numeric(Mental$mental)
```

Then, the row effects model, the column effects model, and the uniform association model can be fit as follows:

```
> # column effects model (ses)
> coleff <- glm(Freq ~ mental + ses + Rscore:ses, family = poisson, data = Mental)
> # row effects model (mental)
> roweff <- glm(Freq ~ mental + ses + mental:Cscore, family = poisson, data = Mental)
> # linear x linear association
> linlin <- glm(Freq ~ mental + ses + Rscore:Cscore, family = poisson, data = Mental)
```

The `Summarize()` in **vcdExtra** provides a nice, compact summary of the fit statistics for a set of models, collected into a "glmlist" object. Smaller is better for AIC and BIC.

```
> # compare models using AIC, BIC, etc
> vcdExtra::LRstats(glmlist(indep, roweff, coleff, linlin))

Likelihood summary table:
          AIC    BIC LR Chisq Df Pr(>Chisq)
indep  209.59 220.19   47.418 15  3.155e-05 ***
roweff 174.45 188.59    6.281 12     0.9013
coleff 179.00 195.50    6.829 10     0.7415
linlin 174.07 185.85    9.895 14     0.7698
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

For specific model comparisons, we can also carry out tests of *nested* models with `anova()` when those models are listed from smallest to largest. Here, there are two separate paths from the most restrictive (independence) model through the model of uniform association, to those that allow only one of row effects or column effects.

```
> anova(indep, linlin, coleff, test="Chisq")

Analysis of Deviance Table

Model 1: Freq ~ mental + ses
Model 2: Freq ~ mental + ses + Rscore:Cscore
Model 3: Freq ~ mental + ses + Rscore:ses
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1        15     47.418
2        14      9.895  1   37.523 9.035e-10 ***
3        10      6.829  4    3.066    0.5469
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova(indep, linlin, roweff, test="Chisq")
```

```
Analysis of Deviance Table

Model 1: Freq ~ mental + ses
Model 2: Freq ~ mental + ses + Rscore:Cscore
Model 3: Freq ~ mental + ses + mental:Cscore
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1        15     47.418
2        14      9.895  1   37.523 9.035e-10 ***
3        12      6.281  2    3.614    0.1641
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The model of linear by linear association seems best on all accounts. For comparison, one might try the CMH tests on these data:

```
> CMHtest(xtabs(Freq~ses+mental, data=Mental))

Cochran-Mantel-Haenszel Statistics for ses by mental

                 AltHypothesis  Chisq Df       Prob
cor        Nonzero correlation 37.156  1 1.0907e-09
rmeans  Row mean scores differ 40.297  5 1.3012e-07
cmeans  Col mean scores differ 40.666  3 7.6971e-09
general    General association 45.958 15 5.4003e-05
```

4.3 Non-linear terms

The strength of the **gnm** package is that it handles a wide variety of models that handle non-linear terms, where the parameters enter the model beyond a simple linear function. The simplest example is the Goodman RC(1) model, which allows a multiplicative term to account for the association of the table variables. In the notation of generalized linear models with a log link, this can be expressed as

$$\log \mu_{ij} = \alpha_i + \beta_j + \gamma_i \delta_j$$

where the row-multiplicative effect parameters γ_i and corresponding column parameters δ_j are estimated from the data.[11] Similarly, the RC(2) model adds two multiplicative terms to the independence model,

$$\log \mu_{ij} = \alpha_i + \beta_j + \gamma_{i1} \delta_{j1} + \gamma_{i2} \delta_{j2}$$

In the **gnm** package, these models may be fit using the `Mult()` to specify the multiplicative term, and `instances()` to specify several such terms.

Example: For the `Mental` data, we fit the RC(1) and RC(2) models, and compare these with the independence model.

```
> RC1 <- gnm(Freq ~ mental + ses + Mult(mental,ses), data=Mental,
+              family=poisson, , verbose=FALSE)
> RC2 <- gnm(Freq ~ mental+ses + instances(Mult(mental,ses),2), data=Mental,
+              family=poisson, verbose=FALSE)
> anova(indep, RC1, RC2, test="Chisq")
```

[11] This is similar in spirit to a correspondence analysis with a single dimension, but as a statistical model.

```
Analysis of Deviance Table

Model 1: Freq ~ mental + ses
Model 2: Freq ~ mental + ses + Mult(mental, ses)
Model 3: Freq ~ mental + ses + Mult(mental, ses, inst = 1) + Mult(mental,
    ses, inst = 2)
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1        15     47.418
2         9     40.230  6    7.188   0.3038
3         3      0.523  6   39.707  5.2e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

5 Mosaic plots

Mosaic plots provide an ideal method both for visualizing contingency tables and for visualizing the fit— or more importantly— lack of fit of a loglinear model. For a two-way table, `mosaic()` fits a model of independence, $[A][B]$ or `~A+B` as an R formula. For n-way tables, `mosaic()` can fit any loglinear model, and can also be used to plot a model fit with `loglm()`. See Friendly (1994, 1999) for the statistical ideas behind these uses of mosaic displays in connection with loglinear models.

The essential idea is to recursively sub-divide a unit square into rectangular "tiles" for the cells of the table, such that the are area of each tile is proportional to the cell frequency. For a given loglinear model, the tiles can then be shaded in various ways to reflect the residuals (lack of fit) for a given model. The pattern of residuals can then be used to suggest a better model or understand *where* a given model fits or does not fit.

`mosaic()` provides a wide range of options for the directions of splitting, the specification of shading, labeling, spacing, legend and many other details. It is actually implemented as a special case of a more general class of displays for n-way tables called `strucplot`, including sieve diagrams, association plots, double-decker plots as well as mosaic plots. For details, see `help(strucplot)` and the "See also" links, and also Meyer, Zeileis, and Hornik (2006), which is available as an R vignette via `vignette("strucplot", package="vcd")`.

Figure 1, showing the association between `Treatment` and `Improved` was produced with the following call to `mosaic()`.

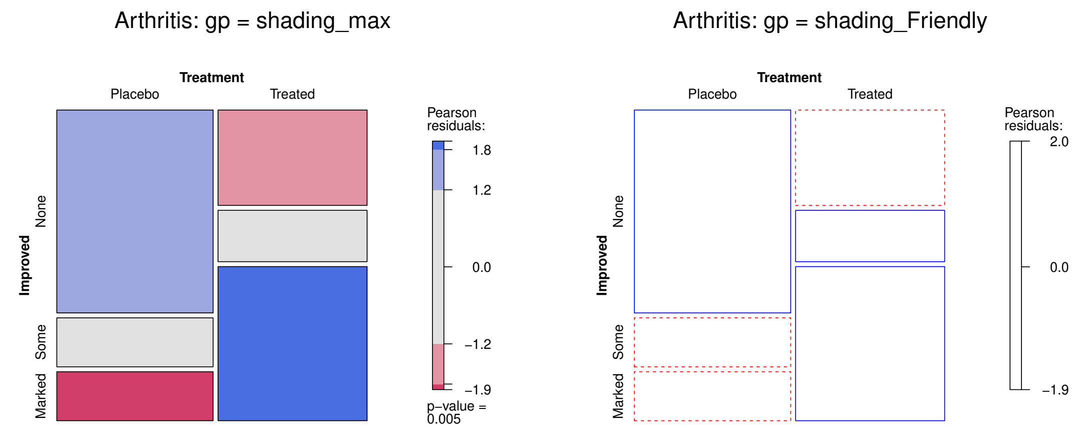
```
> mosaic(art, gp = shading_max, split_vertical = TRUE,
+        main="Arthritis: [Treatment] [Improved]")
```

Note that the residuals for the independence model were not large (as shown in the legend), yet the association between `Treatment` and `Improved` is highly significant.

```
> summary(art)

Call: xtabs(formula = ~Treatment + Improved, data = Arthritis)
Number of cases in table: 84
Number of factors: 2
Test for independence of all factors:
        Chisq = 13.055, df = 2, p-value = 0.001463
```

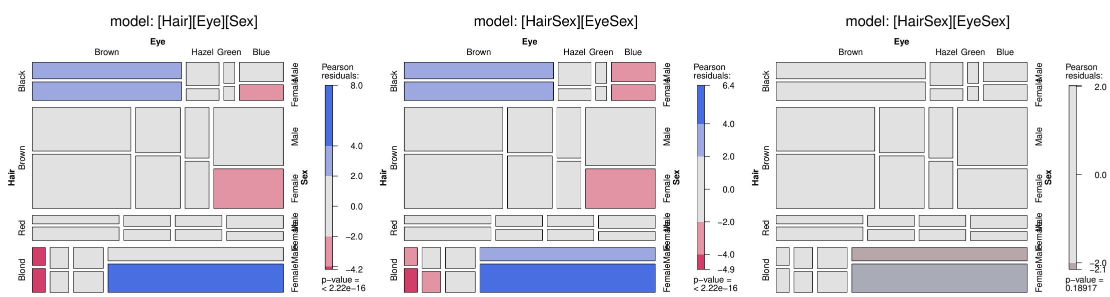
In contrast, one of the other shading schemes, from Friendly (1994) (use: `gp = shading_Friendly`), uses fixed cutoffs of $\pm 2, \pm 4$, to shade cells which are *individually* significant at approximately $\alpha = 0.05$ and $\alpha = 0.001$ levels, respectively. The right panel below uses `gp = shading_Friendly`.



5.1 Mosaics for loglinear models

When you have fit a loglinear model using `loglm()`, and saved the result (as a `loglm` object) the simplest way to display the results is to use the `plot()` method for the `loglm` object. Calling `mosaic(loglm.object)` has the same result. In Section 4.1 above, we fit several different models to the `HairEyeColor` data. We can produce mosaic displays of each just by plotting them:

```
> # mosaic plots, using plot.loglm() method
> plot(hec.1, main="model: [Hair][Eye][Sex]")
> plot(hec.2, main="model: [HairSex][EyeSex]")
> plot(hec.3, main="model: [HairEye][Sex]")
```



Alternatively, you can supply the model formula to `mosaic()` with the `expected` argument. This is passed to `loglm()`, which fits the model, and returns residuals used for shading in the plot.

For example, here we examine the `TV2` constructed in Section 2.8 above. The goal is to see how Network choice depends on (varies with) Day and Time. To do this:

- We fit a model of joint independence of `Network` on the combinations of `Day` and `Time`, with the model formula `~Day:Time + Network`.
- To make the display more easily read, we place `Day` and `Time` on the vertical axis and `Network` on the horizontal,
- The `Time` values overlap on the right vertical axis, so we use `level()` to abbreviate them. `mosaic()` also supports a more sophisticated set of labeling functions. Instead of changing the

data table, we could have used `labeling_args = list(abbreviate = c(Time = 2))` for a similar effect.

The following call to `mosaic()` produces Figure 7:

```
> dimnames(TV2)$Time <- c("8", "9", "10")      # re-level for mosaic display
> mosaic(~ Day + Network + Time, data=TV2, expected=~Day:Time + Network,
+           legend=FALSE, gp=shading_Friendly)
```

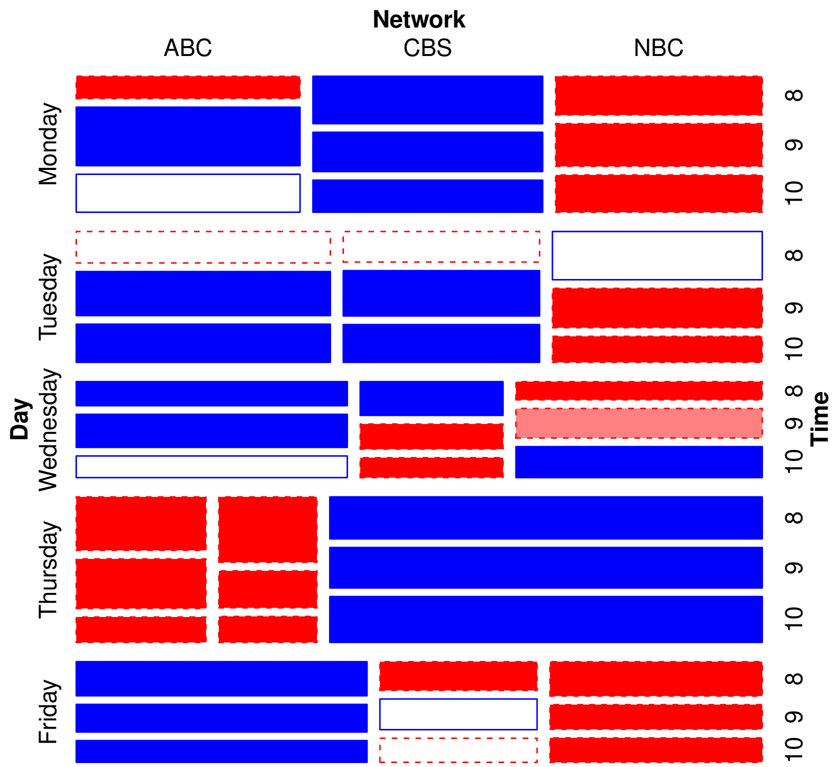


Figure 7: Mosaic plot for the `TV` data showing model of joint independence, `Day:Time + Network`.

From this, it is easy to read from the display how network choice varies with day and time. For example, CBS dominates in all time slots on Monday; ABC and NBC dominate on Tuesday, particularly in the later time slots; Thursday is an NBC day, while on Friday, ABC gets the greatest share.

In interpreting this mosaic and other plots, it is important to understand that associations included in the model—here, that between day and time—are *not* shown in the shading of the cells, because they have been fitted (taken into account) in the loglinear model.

For comparison, you might want to try fitting the model of homogeneous association. This allows all pairs of factors to be associated, but asserts that each pairwise association is the same across the levels of the remaining factor. The resulting plot displays the contributions to a 3-way association, but is not shown here.

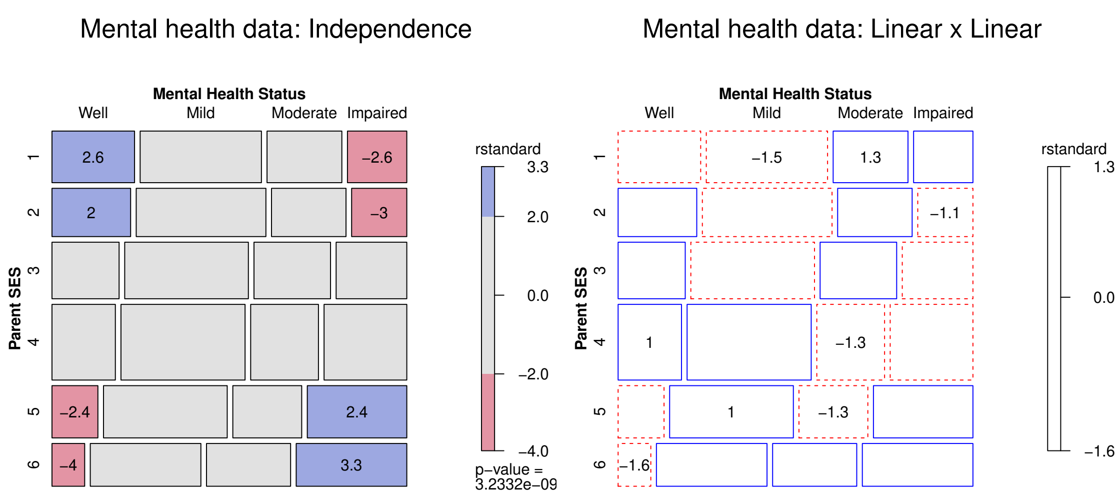
```
> mosaic(~ Day + Network + Time, data=TV2,
+           expected=~Day:Time + Day:Network + Time:Network,
+           legend=FALSE, gp=shading_Friendly)
```

5.2 Mosaics for `glm()` and `gnm()` models

The **vcdExtra** package provides an additional method, `mosaic.glm()` for models fit with `glm()` and `gnm()`.[12] These are not restricted to the Poisson family, but only apply to cases where the response variable is non-negative.

$\boxed{\textbf{\textit{Example}}:}$ Here, we plot the independence and the linear-by-linear association model for the Mental health data from Section 4.2. These examples illustrate some of the options for labeling (variable names and residuals printed in cells). Note that the `formula` supplied to `mosaic()` for "glm" objects refers to the order of factors displayed in the plot, not the model.

```
> long.labels <- list(set_varnames = c(mental="Mental Health Status", ses="Parent SES"))
> mosaic(indep, ~ses+mental, residuals_type="rstandard",
+       labeling_args = long.labels, labeling=labeling_residuals,
+       main="Mental health data: Independence")
> mosaic(linlin, ~ses+mental, residuals_type="rstandard",
+       labeling_args = long.labels, labeling=labeling_residuals, suppress=1,
+       gp=shading_Friendly, main="Mental health data: Linear x Linear")
```



The **gnm** package also fits a wide variety of models with nonlinear terms or terms for structured associations of table variables. In the following, we fit the RC(1) model

$$\log(m_{ij}) = \mu + \lambda_i^A + \lambda_j^B + \phi\mu_i\nu_j$$

This is similar to the linear by linear model, except that the row effect parameters (μ_i) and column parameters (ν_j) are estimated from the data rather than given assigned equally-spaced values. The multiplicative terms are specified by the `Mult()`.

[12] Models fit with `gnm()` are of `class = c("gnm", "glm", "lm")`, so all `*.glm` methods apply, unless overridden in the **gnm** package.

```
> Mental$mental <- C(Mental$mental, treatment)
> Mental$ses <- C(Mental$ses, treatment)
> RC1model <- gnm(Freq ~ mental + ses + Mult(mental, ses),
+                 family = poisson, data = Mental)
> mosaic(RC1model, residuals_type="rstandard", labeling_args = long.labels,
+        labeling=labeling_residuals, suppress=1, gp=shading_Friendly,
+        main="Mental health data: RC(1) model")
```

Other forms of nonlinear terms are provided for the inverse of a predictor (`Inv()`) and the exponential of a predictor (`Exp()`). You should read `vignette("gnmOverview", package="gnm")` for further details.

5.3 Mosaic tips and techniques

The **vcd** package implements an extremely general collection of graphical methods for n-way frequency tables within the strucplot framework, which includes mosaic plots (`mosaic()`), as well as association plots (`assoc()`), sieve diagrams (`sieve()`), as well as tabular displays (`structable()`).

The graphical methods in **vcd** support a wide of options that control almost all of the details of the plots, but it is often difficult to determine what arguments you need to supply to achieve a given effect from the `help()`. As a first step, you should read the `vignette("strucplot")` in **vcd** to understand the overall structure of these plot methods. The notes below describe a few useful things that may not be obvious, or can be done in different ways.

5.3.1 Changing the labels for variables and levels

With data in contingency table form or as a frequency data frame, it often happens that the variable names and/or the level values of the factors, while suitable for analysis, are less than adequate when used in mosaic plots and other strucplot displays.

For example, we might prefer that a variable named `ses` appear as `"Socioeconomic Status"`, or a factor with levels `c("M", "F")` be labeled using `c("Male", "Female")` in a plot. Or, sometimes we start with a factor whose levels are fully spelled out (e.g., `c("strongly disagree", "disagree", "neutral", "agree", "strongly agree")`), only to find that the level labels overlap in graphic displays.

The strucplot framework in **vcd** provides an extremely large variety of functions and options for controlling almost all details of text labels in mosaics and other plots. See `help(labelings)` for an overview.

For example, in Section 2.1 we showed how to rearrange the dimensions of the `UCBAdmissions` table, change the names of the table variables, and relabel the levels of one of the table variables. The code below changes the actual table for plotting purposes, but we pointed out that these changes can create other problems in analysis.

```
> UCB <- aperm(UCBAdmissions, c(2, 1, 3))
> names(dimnames(UCB)) <- c("Sex", "Admit?", "Department")
> dimnames(UCB)[[2]] <- c("Yes", "No")
```

The same effects can be achieved *without* modifying the data using the `set_varnames` and `set_labels` options in `mosaic()` as follows:

```
> vnames <- list(set_varnames = c(Admit="Admission", Gender="Sex", Dept="Department"))
> lnames <- list(Admit = c("Yes", "No"),
+               Gender = c("Males", "Females"),
+               Dept = LETTERS[1:6])
> mosaic(UCBAdmissions, labeling_args=vnames, set_labels=lnames)
```

In some cases, it may be sufficient to abbreviate (or clip, or rotate) level names to avoid overlap. For example, the statements below produce another version of Figure 7 with days of the week abbreviated to their first three letters. Section 4 in the `vignette("strucplot")` provides many other examples.

```
> dimnames(TV2)$Time <- c("8", "9", "10")      # re-level for mosaic display
> mosaic(~ Day + Network + Time, data=TV2, expected=~Day:Time + Network,
+          legend=FALSE, gp=shading_Friendly,
+          labeling_args=list(abbreviate=c(Day=3)) )
```

6 Continuous predictors

When continuous predictors are available—and potentially important— in explaining a categorical outcome, models for that outcome include: logistic regression (binary response), the proportional odds model (ordered polytomous response), multinomial (generalized) logistic regression. Many of these are special cases of the generalized linear model using the `"poisson"` or `"binomial"` family and their relatives.

6.1 Spine and conditional density plots

I don't go into fitting such models here, but I would be remiss not to illustrate some visualizations in **vcd** that are helpful here. The first of these is the spine plot or spinogram (Hummel 1996) (produced with `spine()`). These are special cases of mosaic plots with specific spacing and shading to show how a categorical response varies with a continuous or categorical predictor.

They are also a generalization of stacked bar plots where not the heights but the *widths* of the bars corresponds to the relative frequencies of `x`. The heights of the bars then correspond to the conditional relative frequencies of y in every `x` group.

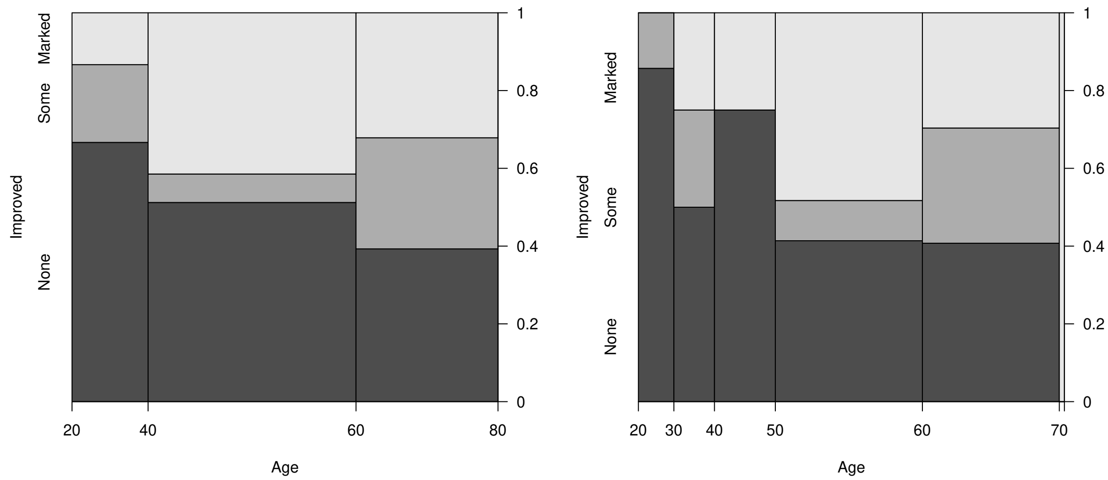
Example: For the `Arthritis` data, we can see how `Improved` varies with `Age` as follows. `spine()` takes a formula of the form `y ~ x` with a single dependent factor and a single explanatory variable `x` (a numeric variable or a factor). The range of a numeric variable`x` is divided into intervals based on the `breaks` argument, and stacked bars are drawn to show the distribution of `y` as `x` varies. As shown below, the discrete table that is visualized is returned by the function.

```
> (spine(Improved ~ Age, data = Arthritis, breaks = 3))

         Improved
Age        None Some Marked
  [20,40]    10    3      2
  (40,60]    21    3     17
  (60,80]    11    8      9

> (spine(Improved ~ Age, data = Arthritis, breaks = "Scott"))

         Improved
Age        None Some Marked
  [20,30]     6    1      0
  (30,40]     4    2      2
  (40,50]     9    0      3
  (50,60]    12    3     14
  (60,70]    11    8      8
  (70,80]     0    0      1
```



The conditional density plot (Hofmann and Theus 2005) is a further generalization. This visualization technique is similar to spinograms, but uses a smoothing approach rather than discretizing the explanatory variable. As well, it uses the original x axis and not a distorted one.

```
> cdplot(Improved ~ Age, data = Arthritis)
> with(Arthritis, rug(jitter(Age), col="white", quiet=TRUE))
```

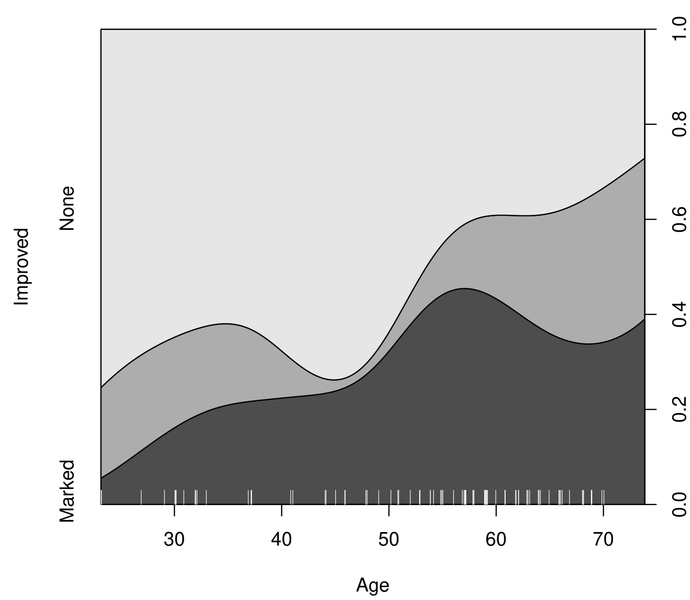


Figure 8: Conditional density plot for the Arthritis data showing the variation of Improved with Age.

In such plots, it is useful to also see the distribution of the observations across the horizontal axis, e.g., with a `rug()` plot. Figure 8 uses `cdplot()` from the **graphics** package rather than `cd_plot()` from **vcd**, and is produced with

```
> cdplot(Improved ~ Age, data = Arthritis)
> with(Arthritis, rug(jitter(Age), col="white", quiet=TRUE))
```

From Figure 8 it can be easily seen that the proportion of patients reporting Some or Marked improvement increases with Age, but there are some peculiar bumps in the distribution. These may be real or artifactual, but they would be hard to see with most other visualization methods. When we switch from non-parametric data exploration to parametric statistical models, such effects are easily missed.

6.2 Model-based plots: effect plots and ggplot2 plots

The nonparametric conditional density plot uses smoothing methods to convey the distributions of the response variable, but displays that are simpler to interpret can often be obtained by plotting the predicted response from a parametric model.

For complex `glm()` models with interaction effects, the **effects** package provides the most useful displays, plotting the predicted values for a given term, averaging over other predictors not included in that term. I don't illustrate this here, but see **??** and `help(package="effects")`.

Here I just briefly illustrate the capabilities of the **ggplot2** package for model-smoothed plots of categorical responses in `glm()` models.

Example: The `Donner` data frame in **vcdExtra** gives details on the survival of 90 members of the Donner party, a group of people who attempted to migrate to California in 1846. They were trapped by an early blizzard on the eastern side of the Sierra Nevada mountains, and before they could be rescued, nearly half of the party had died. What factors affected who lived and who died?

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

'data.frame':        90 obs. of  5 variables:
 $ family  : Factor w/ 10 levels "Breen","Donner",..: 9 1 1 1 1 1 1 1 1 1 ...
 $ age     : int  23 13 1 5 14 40 51 9 3 8 ...
 $ sex     : Factor w/ 2 levels "Female","Male": 2 2 1 2 2 1 2 2 2 2 ...
 $ survived: int  0 1 1 1 1 1 1 1 1 1 ...
 $ death   : POSIXct, format: "1846-12-29" NA ...
```

A potential model of interest is the logistic regression model for $Pr(survived)$, allowing separate fits for males and females as a function of `age`. The key to this is the `stat_smooth()` function, using `method = "glm", method.args = list(family = binomial)`. The `formula = y ~ x` specifies a linear fit on the logit scale (Figure 9, left)

```
> # separate linear fits on age for M/F
> ggplot(Donner, aes(age, survived, color = sex)) +
+   geom_point(position = position_jitter(height = 0.02, width = 0)) +
+   stat_smooth(method = "glm", method.args = list(family = binomial), formula = y ~ x,
+             alpha = 0.2, size=2, aes(fill = sex))
```

Alternatively, we can allow a quadratic relation with `age` by specifying `formula = y ~ poly(x,2)` (Figure 9, right).

```
> # separate quadratics
> ggplot(Donner, aes(age, survived, color = sex)) +
+   geom_point(position = position_jitter(height = 0.02, width = 0)) +
+   stat_smooth(method = "glm", method.args = list(family = binomial), formula = y ~ poly(x,2),
+              alpha = 0.2, size=2, aes(fill = sex))
```

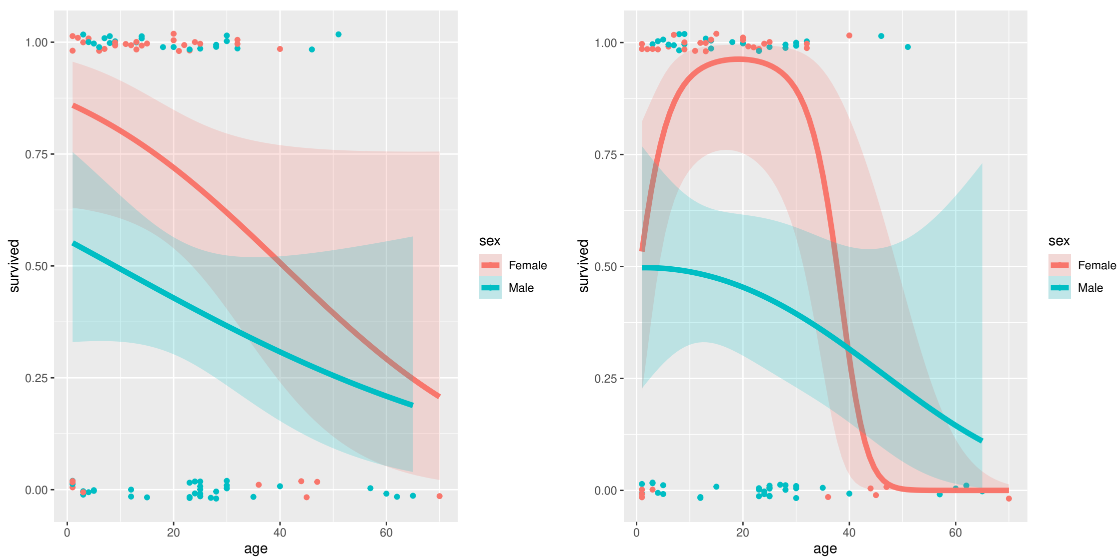


Figure 9: Logistic regression plots for the `Donner` data showing survival vs. age, by sex. Left: linear logistic model; right: quadratic model

These plots very nicely show (a) the fitted $Pr(survived)$ for males and females; (b) confidence bands around the smoothed model fits and (c) the individual observations by jittered points at 0 and 1 for those who died and survived, respectively.

References

Agresti A (2002). *Categorical Data Analysis*. 2nd edition. John Wiley & Sons, Hoboken, New Jersey.

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