

Tutorial: Working with categorical data with R and the vcd package

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Abstract

This tutorial describes the creation 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.

Keywords: contingency tables, mosaic plots, sieve plots, categorical data, independence, conditional independence, R.

1. Introduction

This tutorial, part of the **vcdExtra** package, describes the creation of frequency and contingency tables from categorical variables, along with tests of independence, measures of association, and methods for graphically displaying results. It borrows structure and some ideas from Robert Kabacoff's *Quick-R* web page, <http://www.statmethods.net/stats/frequencies.html>.

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 my book, *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.

A more complete theoretical description of these statistical methods is provided in Agresti's (2002) *Categorical Data Analysis*. For this, see the Splus/R companion by Laura Thompson, <https://home.comcast.net/~lthompson221/Splusdiscrete2.pdf>.

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 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 [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 [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)

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 5) 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.

¹In 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.

```
> 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.

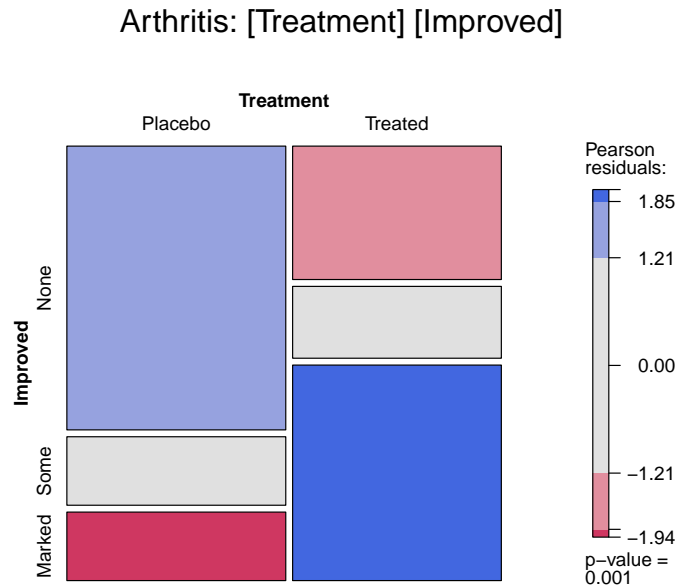


Figure 1: Mosaic plot for the `Arthritis` data, showing the marginal model of independence for `Treatment` and `Improved`. Age, a covariate, and Sex are ignored here.

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

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.

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()` function to print the results more attractively.

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

Table ignores missing values. 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 crosstabulations using formula style input.

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

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).

```
> (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. 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.

A contingency table in table form (an object of `class(table)`) can be converted to a data.frame with `as.data.frame()`.³ The resulting `data.frame` contains columns representing the classifying

³ Because R is object-oriented, this is actually a short-hand for the function `as.data.frame.table()`.

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

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

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` \times `Sex` \times `Improved`.⁴

```
> 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
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

⁴ `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.

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**, \times **Sex** and **Improved**.

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

'data.frame':      84 obs. of  3 variables:
 $ Treatment: Factor w/ 2 levels "Placebo","Treated": 1 1 1 1 1 1 1 1 1 1 ...
 $ Sex      : Factor w/ 2 levels "Female","Male": 1 1 1 1 1 1 1 1 1 1 ...
 $ Improved : Factor w/ 3 levels "Marked","None",...: 2 2 2 2 2 2 2 2 2 2 ...
```

2.6. 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 `data/` directory of **vcdExtra**, can be read as follows:

```
> tv.data<-read.table(system.file("data","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 Nielsen 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")
```

But this 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.

```
> 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.

```
> 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!

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

	sex	party	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 = 138.2898, 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:  UCBAmissions
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(UCBAmissions, log=FALSE)

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

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

Log Odds Ratio Std. Error z value Pr(>|z|)
A      -1.052076   0.259993 -4.0466 2.599e-05 ***
B      -0.220023   0.427128 -0.5151  0.3032
C       0.124922   0.143727  0.8692  0.1924
D      -0.081987   0.149975 -0.5467  0.2923
E       0.200187   0.199581  1.0030  0.1579
F      -0.188896   0.302085 -0.6253  0.2659
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> woolf_test(UCBAmissions)
```

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

```
data:  UCBAmissions
X-squared = 17.9017, 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 2.⁵

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

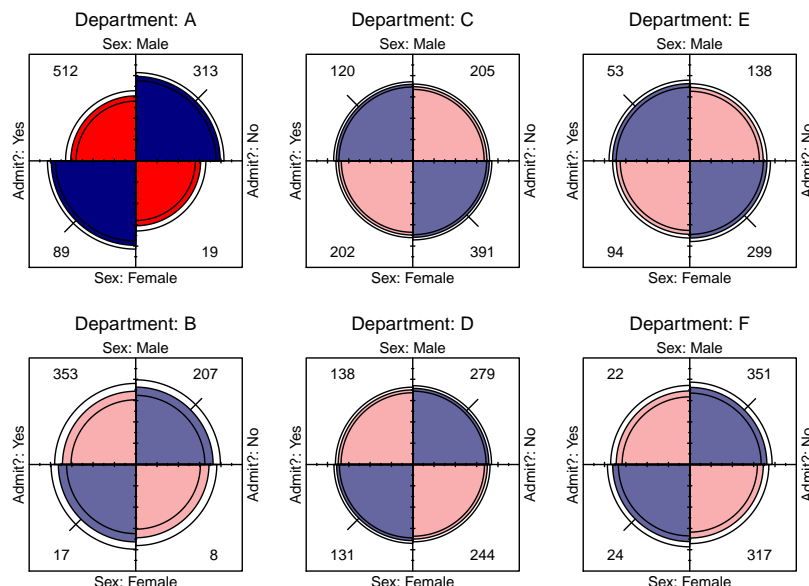


Figure 2: Fourfold display for the UCBAmissions data. Where the odds ratio differs significantly from 1.0, the confidence bands do not overlap, and the circle quadrants are shaded more intensely.

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)
```

Finally, there is a `plot()` method for `oddsratio` objects. By default, it shows the 95% confidence interval for the log odds ratio. Figure 3 is produced by:

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

3.5. 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(GSSstab)
```

⁵The color values `col[3:4]` were modified from their default values to show a greater contrast between significant and insignificant associations here.

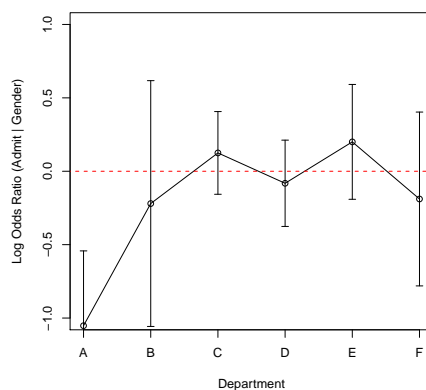


Figure 3: Log odds ratio plot for the UCBA admissions data.

```

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

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

```

For tables with ordinal variables, like `JobSat`, some people prefer the Goodman-Kruskal γ statistic (see §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.

3.6. 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).⁶ 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))
```

⁶ Don't confuse this with `kappa()` in base R that computes something entirely different (the condition number of a matrix).

```

              value      ASE      z
Unweighted 0.1293303 0.06884553 1.878557
Weighted   0.2373806 0.12646539 1.877040

```

```
> confint(K)
```

```

Kappa      lwr      upr
Unweighted -0.00560450 0.2642650
Weighted   -0.01048698 0.4852482

```

A visualization of agreement, both unweighted and weighted for degree of departure from exact agreement is provided by the `agreementplot()` function. Figure 4 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

```

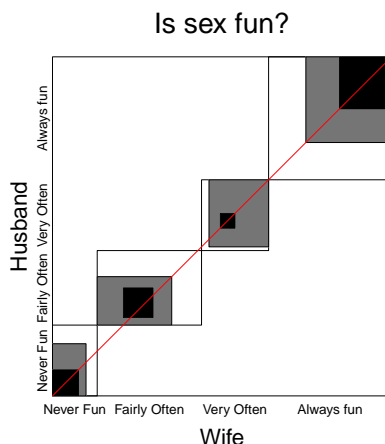


Figure 4: Agreement plot for the `SexualFun` data.

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*.

3.7. 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.

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.

```
> 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 5. `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 are most advanced 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.

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

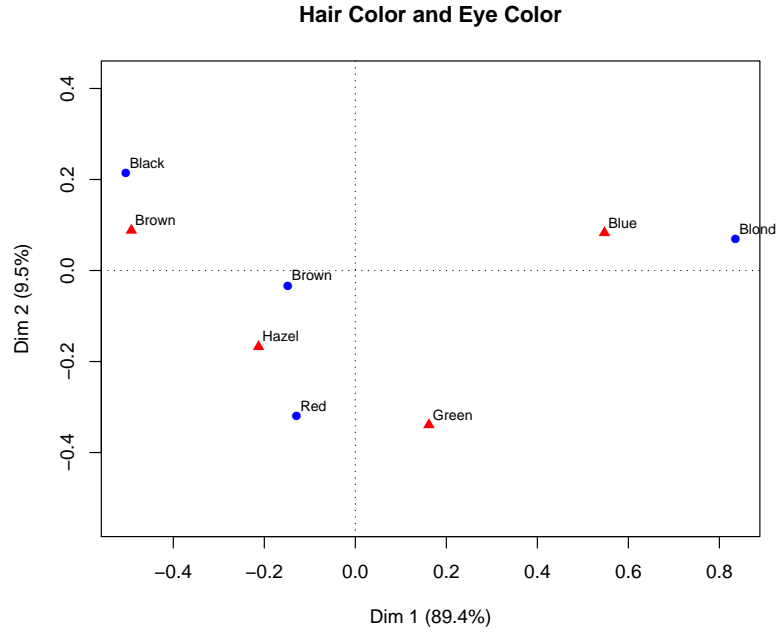


Figure 5: Correspondence analysis plot for the HairEye data.

shows how to express each model for `loglm()` in R.⁷ 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”.

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

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

For example, the formula $\sim A + B + C$ 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

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

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.

⁷ 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")`.

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

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

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.

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()`.

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)
> # compare models using AIC
> AIC(indep, roweff, coleff, linlin)
```

	df	AIC
indep	9	209.5908
roweff	12	174.4537
coleff	14	179.0023
linlin	10	174.0681

In model comparisons, we can 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 P(>|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 P(>|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.

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 $\sim A+B$ 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 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)

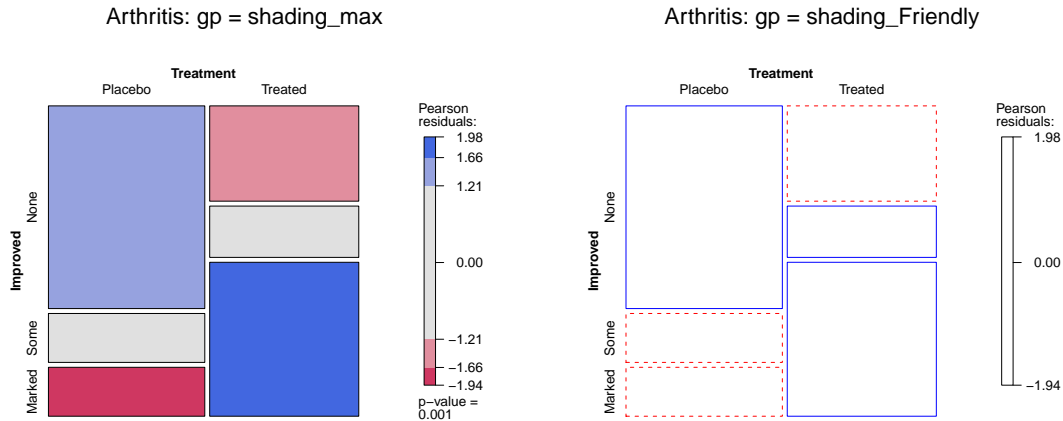
```

```

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

```

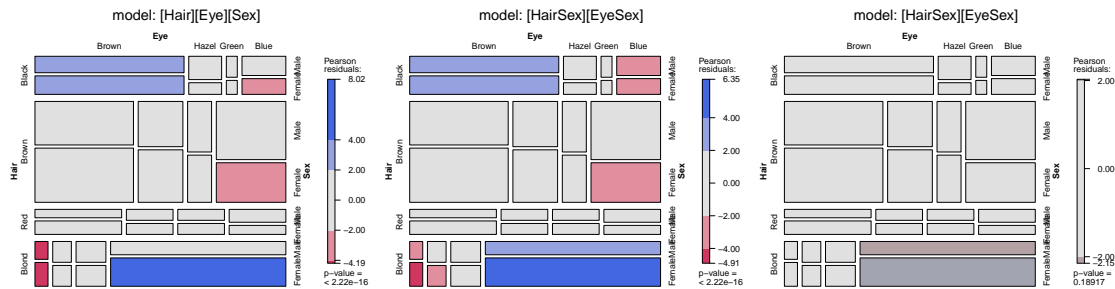
In contrast, one of the other shading schemes, from [Friendly \(1994\)](#) (use: `gp = shading_Friendly`), uses fixed cutoffs of $\pm 2, \pm 4$, to shade cells which are *individually* significant at approximately $\alpha = 0.05$ and $\alpha = 0.001$ levels, respectively. The right panel below uses `gp = 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 2.6 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 6

```
> 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)
```

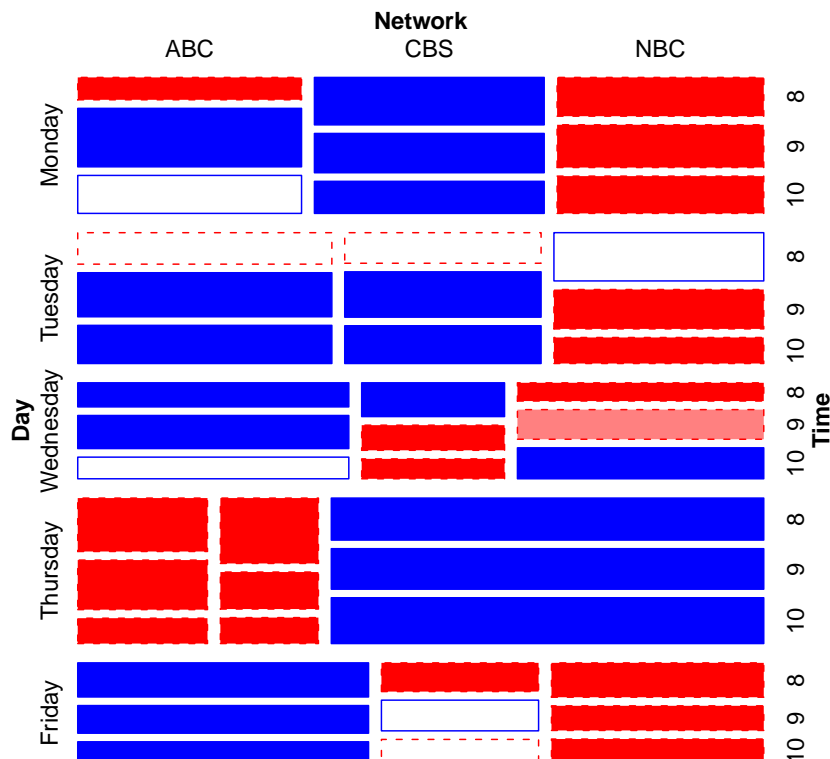


Figure 6: Mosaic plot for the TV data showing model of joint independence, $\text{Day:Time} + \text{Network}$.

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.

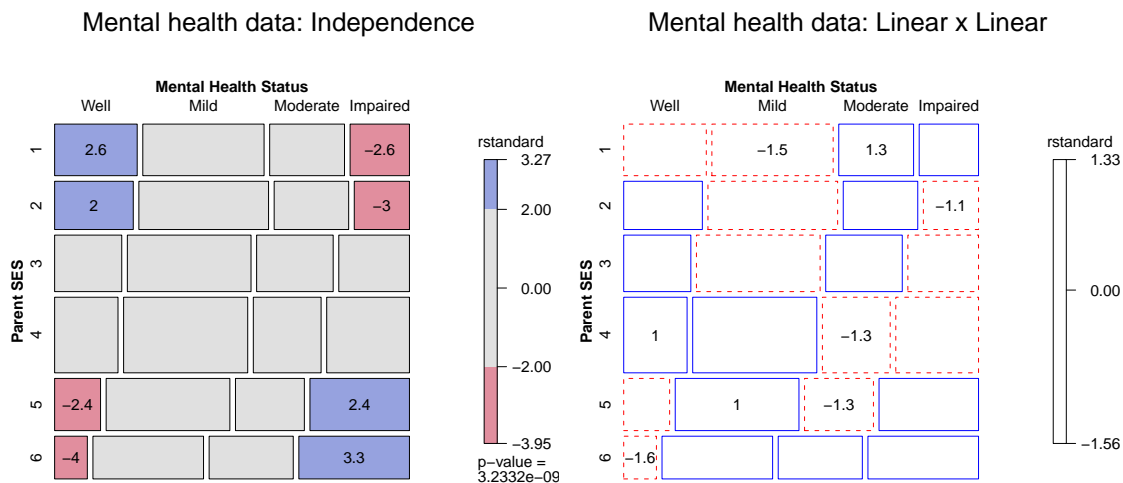

```
> mosaic(~ Day + Network + Time, data=TV2,
+         expected=~Day:Time + Day:Network + Time:Network,
+         legend=FALSE, gp=shading_Friendly)
```

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

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

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).

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



6. Continuous predictors: spine and conditional density plots

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.

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.

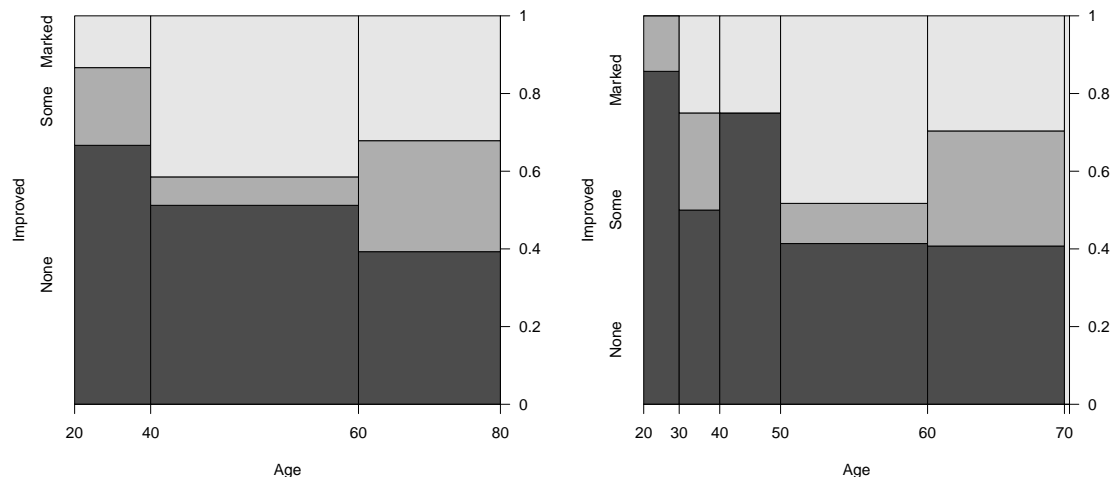
For the `Arthritis` data, we can see how `Improved` varies with `Age` as follows. `spine()` takes a formula of the form `y ~ x` with a single dependent factor and a single explanatory variable **x** (a numeric variable or a factor). The range of a numeric variable **x** is divided into intervals based 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))
```

Age	Improved		
	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"))
```

Age	Improved		
	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))
```

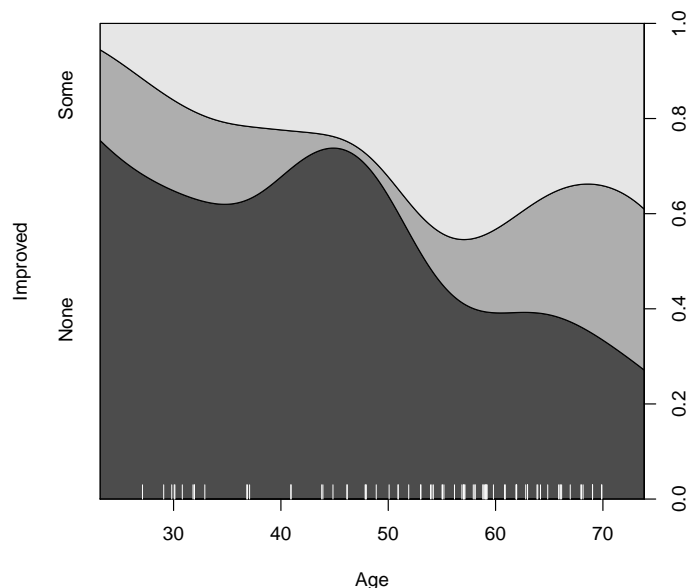


Figure 7: Conditional density plot for the `Arthritis` data showing the variation of `Improved` with `Age`.

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 7 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 7 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.

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