

- **Visualizing Categorical Data**
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# Visualizing Categorical Data

Visualizing Categorical Data - Windows Internet Explorer

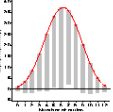
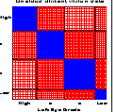
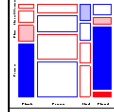
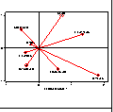
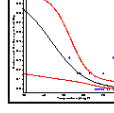
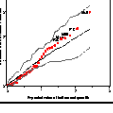
http://www.math.yorku.ca/SCS/vcd/

Visualizing Categorical Data

## Visualizing Categorical Data

by [Michael Friendly](#)

SAS Institute (Dec, 2000), [Order code 56571](#), ISBN 1-58025-660-0

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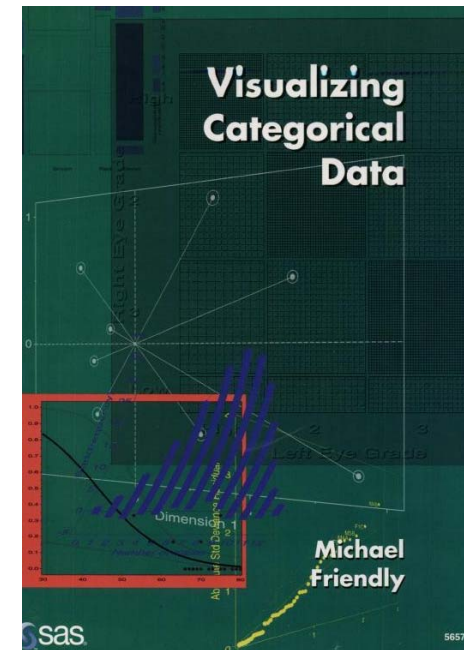
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See also:

- Reviews of [Visualizing Categorical Data](#)
- [Reader's Guide to Visualizing Categorical Data](#) (SUGI 26 paper, PDF [137k])
- VCD Sampler: [Visualizing Categorical Data: Data, Stories, and Pictures](#) (SUGI 25 paper, PDF [177k])
- [VCD Source Online](#) [550k] (Source code for datasets and macros from the initial release, all in one big file, but no longer maintained)
- [VCD Archive](#) (VCD archive, vcdprog.zip, for purchasers of the book)
- [Mosaic displays web applet](#)
- [Mosaic displays User's Guide](#) (.pdf [318k])
- [Sieve diagrams web applet](#)
- [Gallery of Data Visualization](#)

Next



```
> library(vcd)
```

vcd: Visualizing Categorical Data

<http://cran.r-project.org/web/packages/vcd/index.html>

# Berkeley admission data as in Friendly (1995).

```
> UCBAmissions
, , Dept = A
      Gender
Admit  Male Female
Admitted  512   89
Rejected  313   19

, , Dept = B
      Gender
Admit  Male Female
Admitted  353   17
Rejected  207    8

, , Dept = C
      Gender
Admit  Male Female
Admitted  120  202
Rejected  205  391

, , Dept = D
      Gender
Admit  Male Female
Admitted  138  131
Rejected  279  244

, , Dept = E
      Gender
Admit  Male Female
Admitted   53   94
Rejected  138  299

, , Dept = F
      Gender
Admit  Male Female
Admitted   22   24
Rejected  351  317
```

```
> (BerkeleyAd.array <- aperm(UCBAmissions, c(2, 1, 3)))
, , Dept = A
      Admit
Gender  Admitted Rejected
Male    512     313
Female  89      19

, , Dept = B
      Admit
Gender  Admitted Rejected
Male    353     207
Female  17      8

, , Dept = C
      Admit
Gender  Admitted Rejected
Male    120     205
Female  202     391

, , Dept = D
      Admit
Gender  Admitted Rejected
Male    138     279
Female  131     244

, , Dept = E
      Admit
Gender  Admitted Rejected
Male    53      138
Female  94      299

, , Dept = F
      Admit
Gender  Admitted Rejected
Male    22      351
Female  24      317
```

# Data: Adminnsion to Berkeley Graduate Programs

```
> dimnames(BerkeleyAd.array)[[2]] <- c("Yes", "No")
> names(dimnames(BerkeleyAd.array)) <- c("Sex", "Admit?", "Department")
> ##ftable: Flat Contingency Tables
> ftable(BerkeleyAd.array)
```

		Department					
		A	B	C	D	E	F
Sex	Admit?						
	Yes						
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

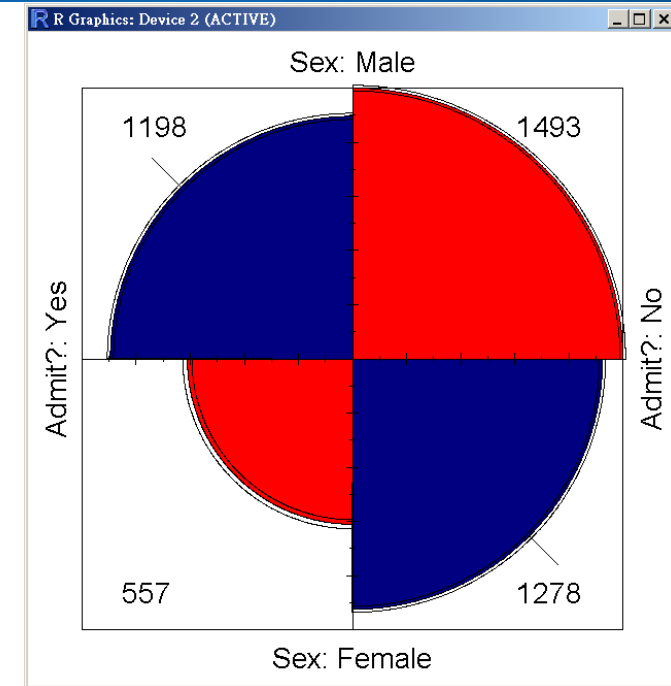
```
> margin.table(BerkeleyAd.array, 1)
Sex
  Male Female
 2691  1835
> margin.table(BerkeleyAd.array, 2)
Admit?
  Yes  No
1755 2771
> (BerkeleyAd.mdata <- margin.table(BerkeleyAd.array, c(1, 2)))
      Admit?
Sex    Yes  No
Male  1198 1493
Female 557 1278
```

# Fourfold Display

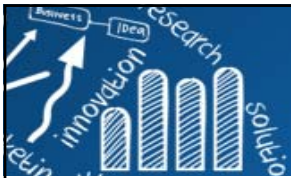
**Table:** Adminnasion to Berkeley Graduate Programs.

Gender	Adminnasion		Row Total
	Admitted	Rejected	
Males	1198	1493	2691
Females	557	1278	1835
Column Total	1755	2771	4526

- **Fourfold Display:** display for 2x2 (and 2x2xk) tables which focus on the odds ratio as a measure of association, indicating the direction and significance of associations.
- Each cell is shown by a quarter circle, whose area is proportional to the cell count, in a way that depicts the odds ratio in each of K strata.
- **Confidence rings:** for the odds ratio can be superimposed to provide a visual test of the hypothesis of no association in each stratum.
- The rings for adjacent segments are overlapped when no significant association is shown.



```
> fourfold(BerkeleyAd.mdata, std="all.max")
```



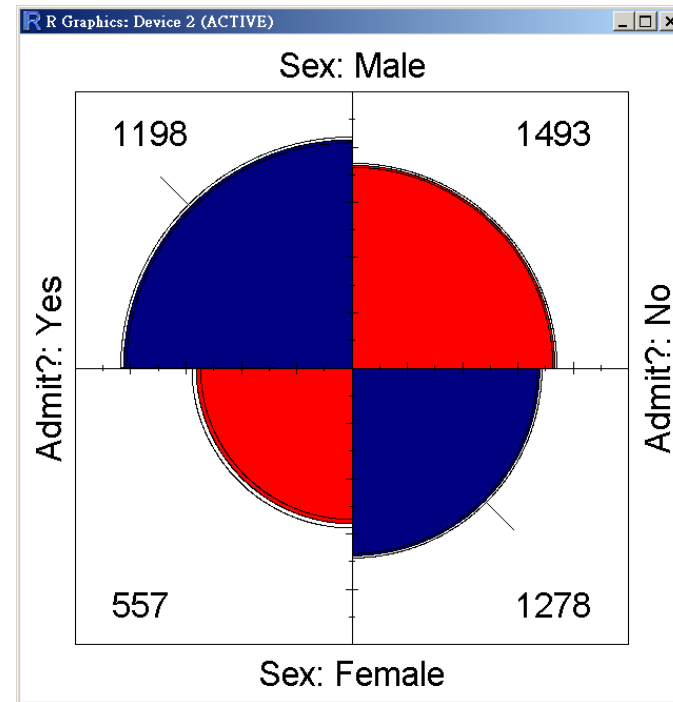
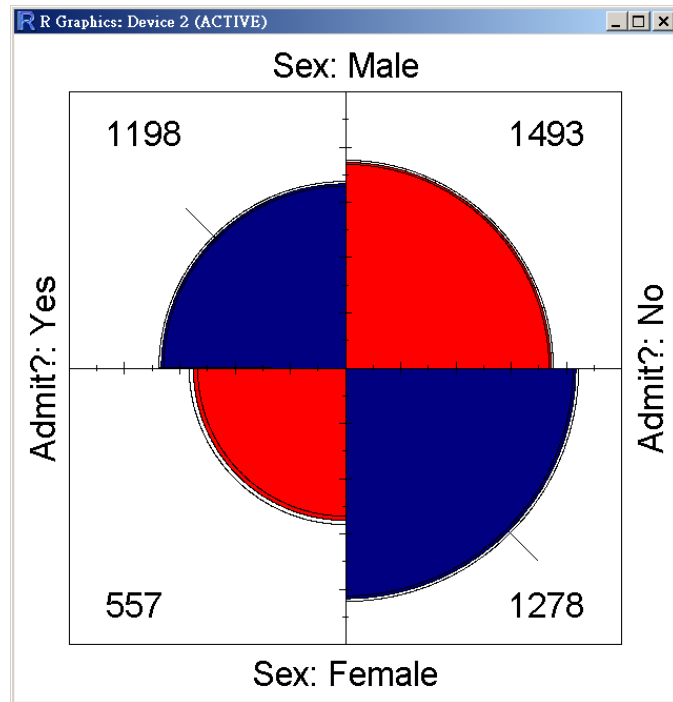
```
> fourfold(BerkeleyAd.mdata, margin = 1)
> fourfold(BerkeleyAd.mdata, margin = 2)
```

Table: UCBA admissions: gender equated.

Gender	Row Percents (%)		Row Total
	Admitted	Rejected	
Males	44.52	55.48	100
Females	30.35	69.65	100

Table: UCBA admissions: admission equated

Column Percents (%)	Admissions	
	Admitted	Rejected
Males	68.26	53.88
Females	31.14	46.12
Column Total	100	100

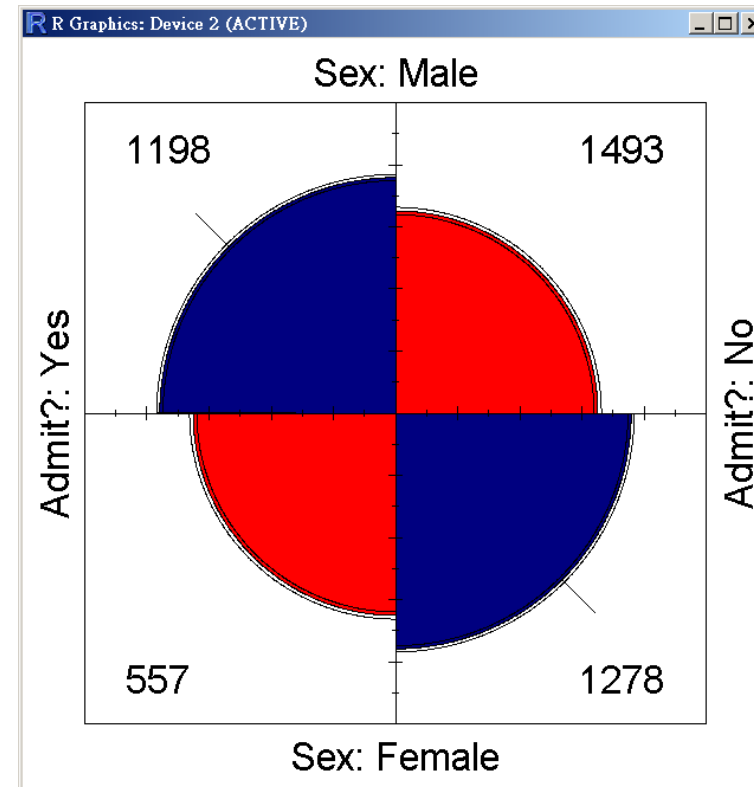


```
> fourfold(BerkeleyAd.mdata, margin = c(1, 2))
```

**Table:** UCBA admissions: gender and admission equated

Column Percents (%)	Admissions	
	Admitted	Rejected
Males	55.89	44.11
Females	40.31	59.69
Column Total	100	

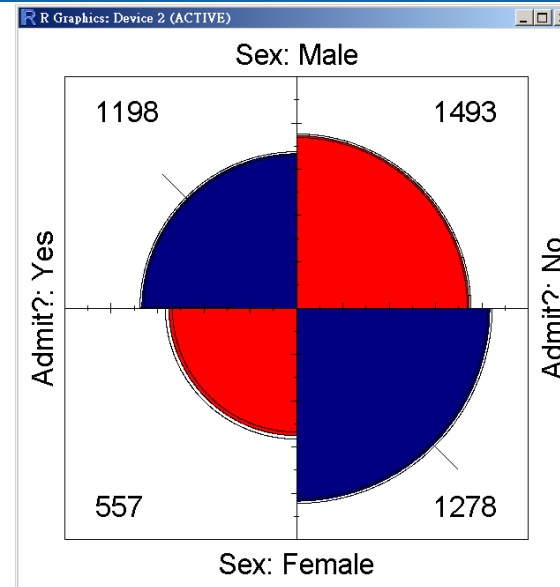
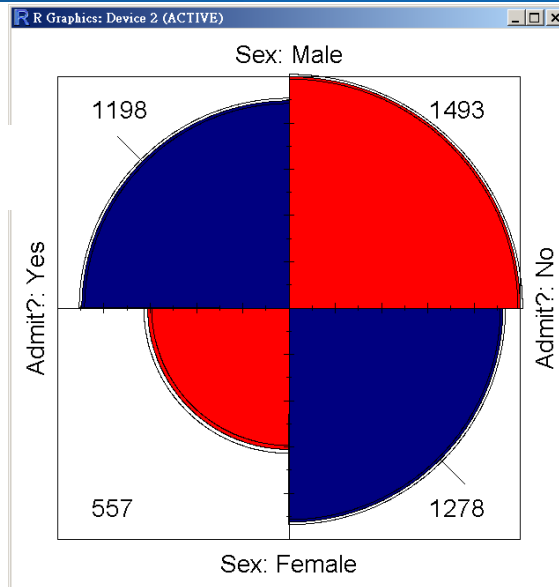
Column Percents (%)	Admissions		Row Total
	Admitted	Rejected	
Males	68.26	53.88	122.14
Females	31.14	46.12	77.26
Column Total	100	100	





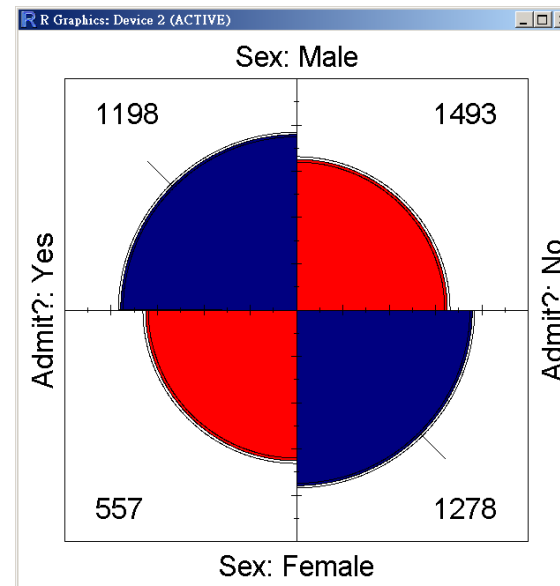
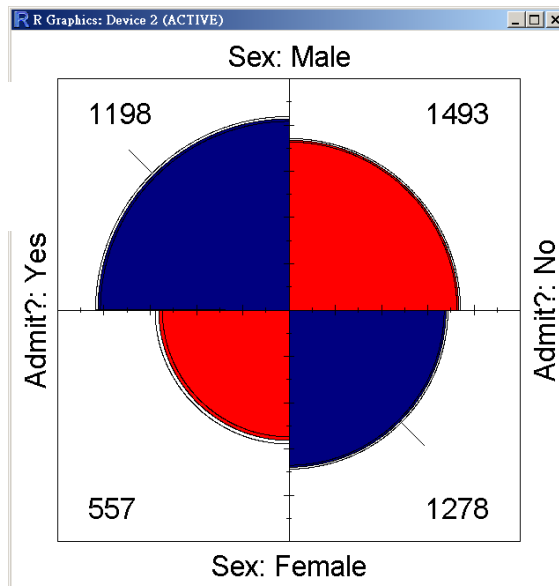
# Comparison

std="all.max"



gender equated

admission equated

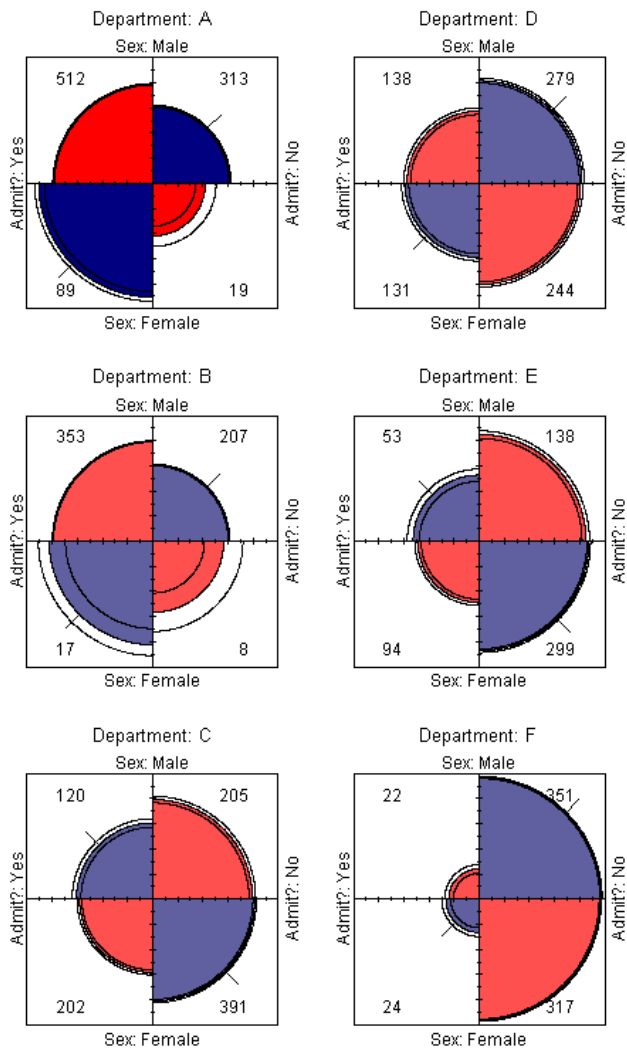


gender and admission equated

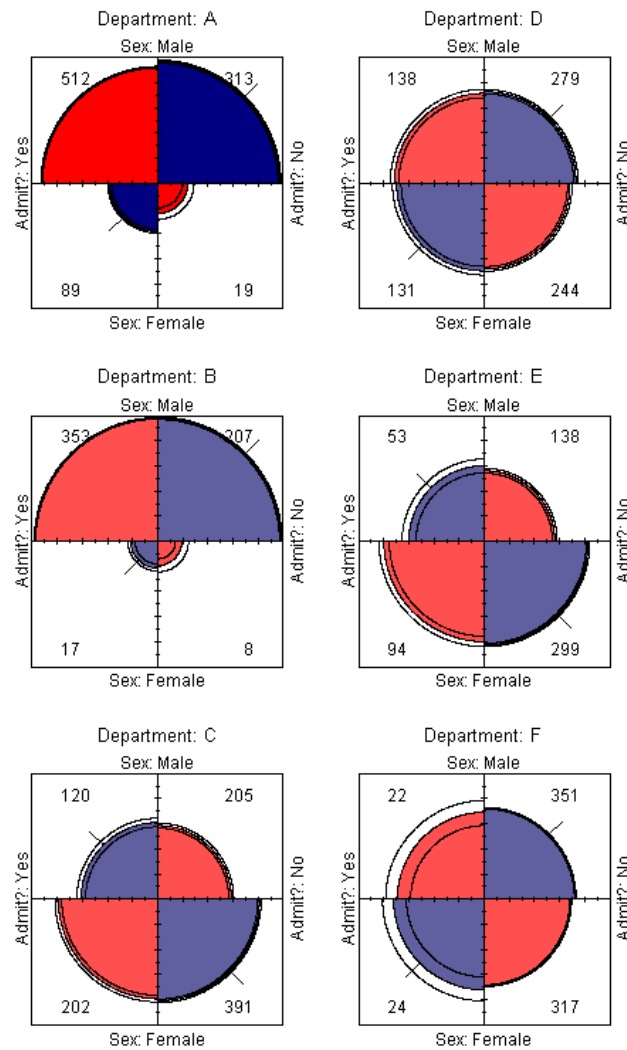


- > fourfold(BerkeleyAd.array, margin = 1)
- > fourfold(BerkeleyAd.array, margin = 2)

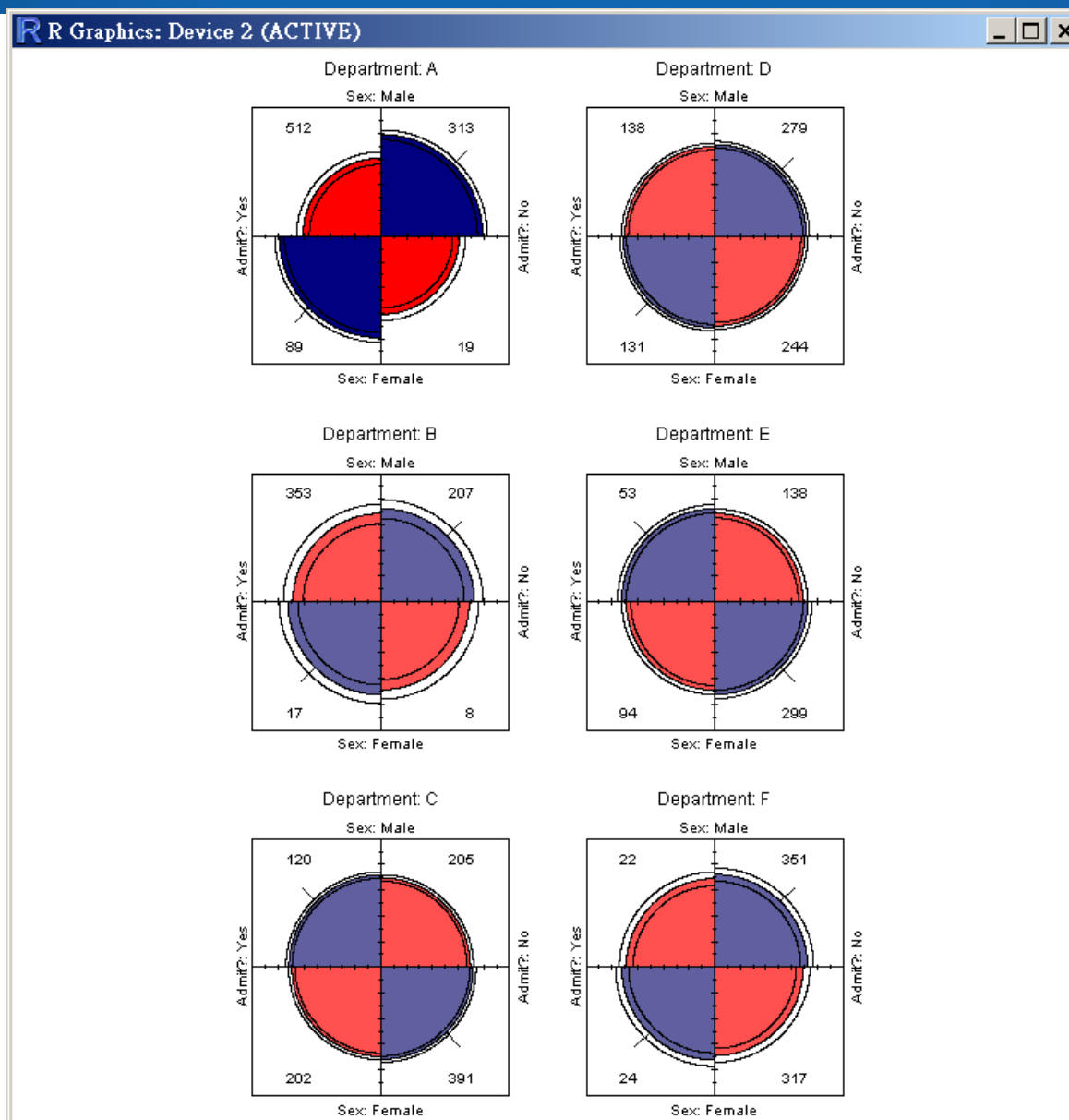
R Graphics: Device 2 (ACTIVE)



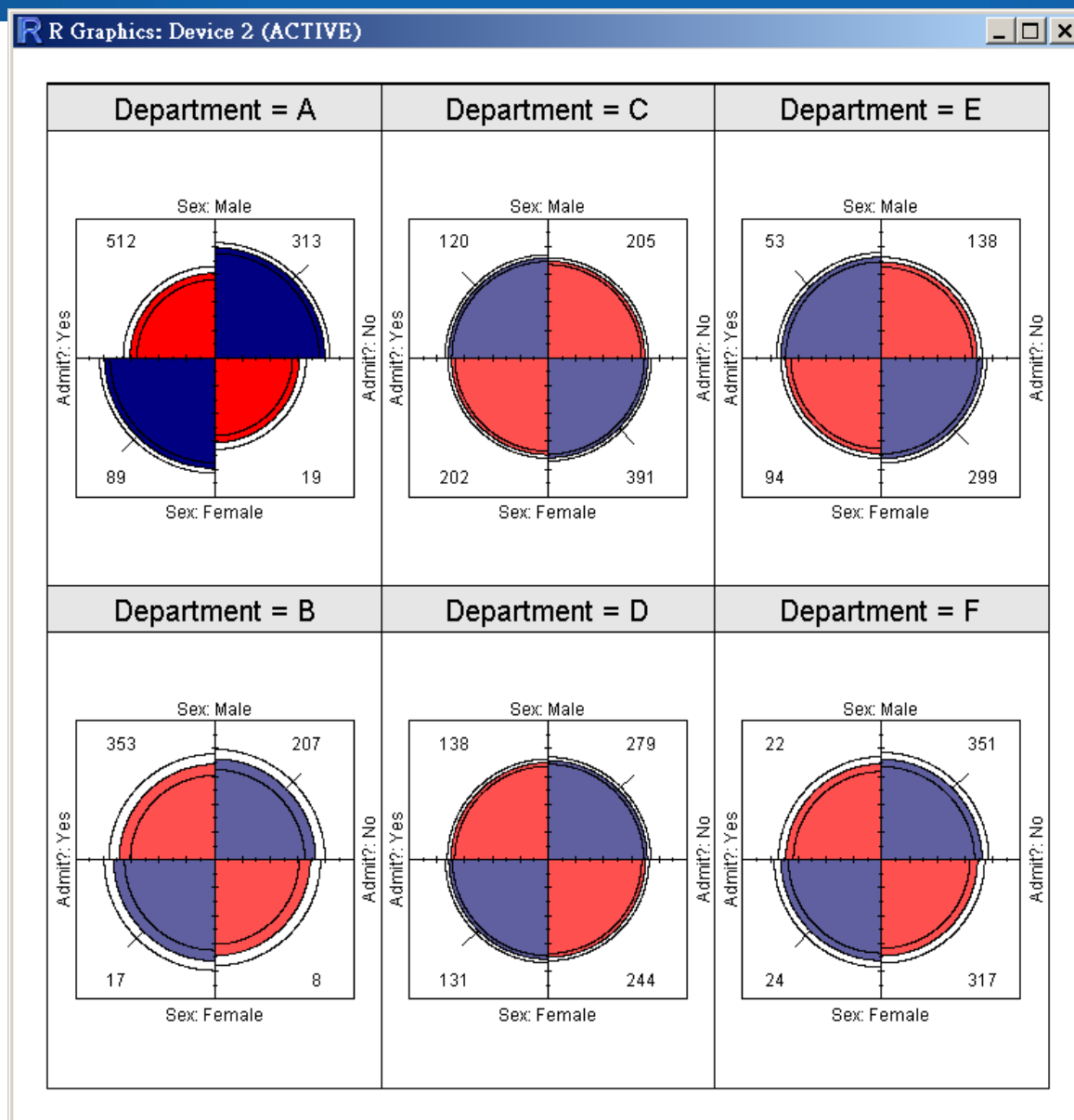
R Graphics: Device 2 (ACTIVE)



# > fourfold(BerkeleyAd.array)



```
cotabplot(BerkeleyAd.array, panel = cotab_fourfold)
```



# Make a Contingency Table

```
> score <- as.factor(sample(c("High","Low"), 20, replace=TRUE))
> gender <- as.factor(sample(c("F","M"), 20, replace=TRUE))
> my.data <- data.frame(gender=gender, score=score)
```

```
> my.data
  gender score
1      M  High
2      F  High
3      F   Low
4      M  High
5      F   Low
...
19     F   Low
20     F   Low
```

```
> table(my.data)
      score
gender High Low
   F      1   9
   M      8   2
```

```
> my.table <- table(my.data)
> str(my.table)
'table' int [1:2, 1:2] 1 8 9 2
- attr(*, "dimnames")=List of 2
 ..$ gender: chr [1:2] "F" "M"
 ..$ score : chr [1:2] "High" "Low"
> class(my.table)
[1] "table"
```

# Data: Hair and Eye Color and Gender in 592 statistics students.

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

```
> str(HairEyeColor)
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"
> class(HairEyeColor)
[1] "table"
```

# Make a Contingency Table

```
> (HEC <- structable(Eye ~ Sex + Hair,
                     data = HairEyeColor))
```

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

```
> (HEC1 <- structable(Hair ~ Eye + Sex,
                      data = HairEyeColor))
```

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

```
> (HEC2 <- structable(~Eye + Sex +
                      Hair, data = HairEyeColor))
```

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

# Association Plots

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

```
      Eye
```

```
Hair   Brown Blue Hazel Green
```

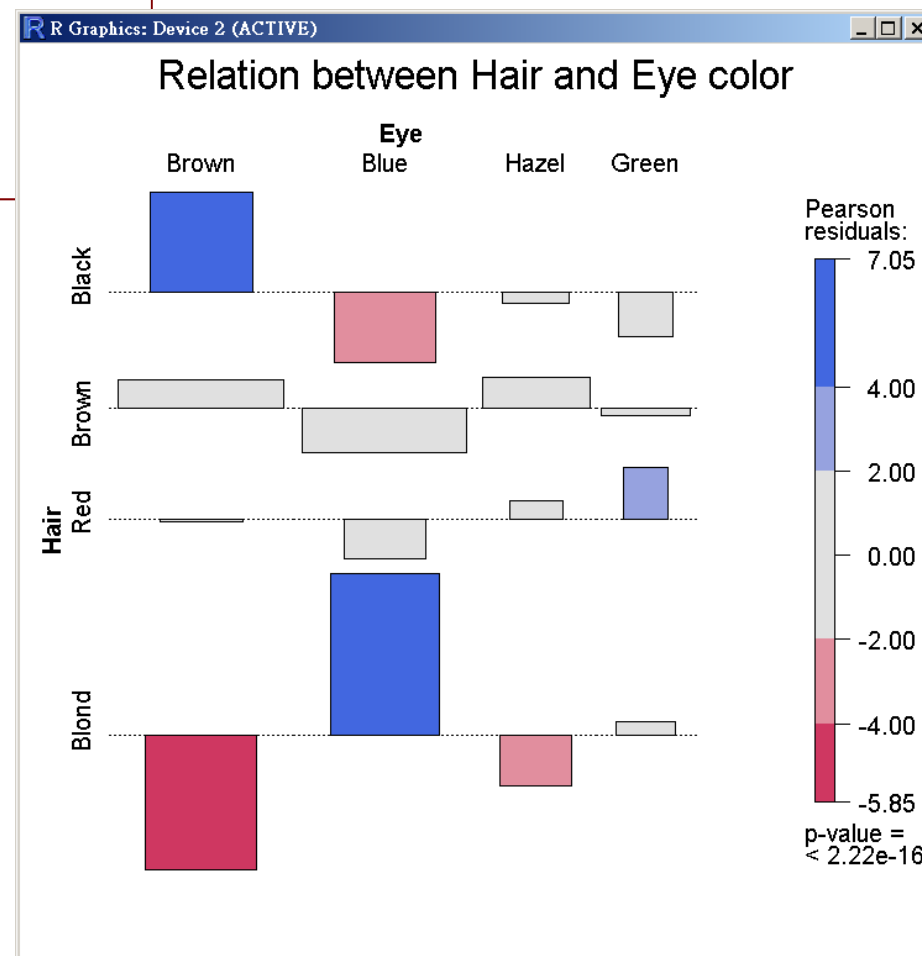
```
Black   68   20   15    5
```

```
Brown  119   84   54   29
```

```
Red     26   17   14   14
```

```
Blond    7   94   10   16
```

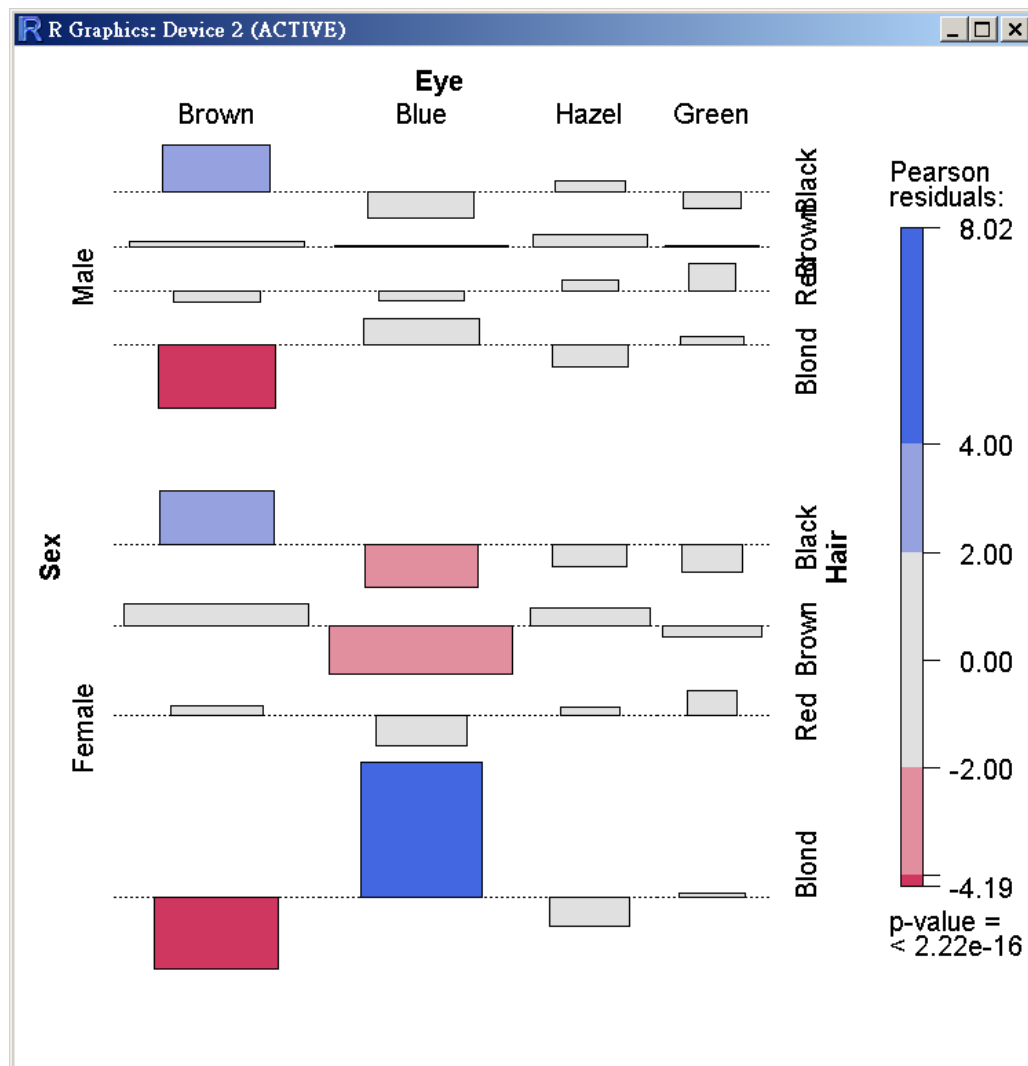
```
> assoc(x, main = "...", shade = TRUE)
```





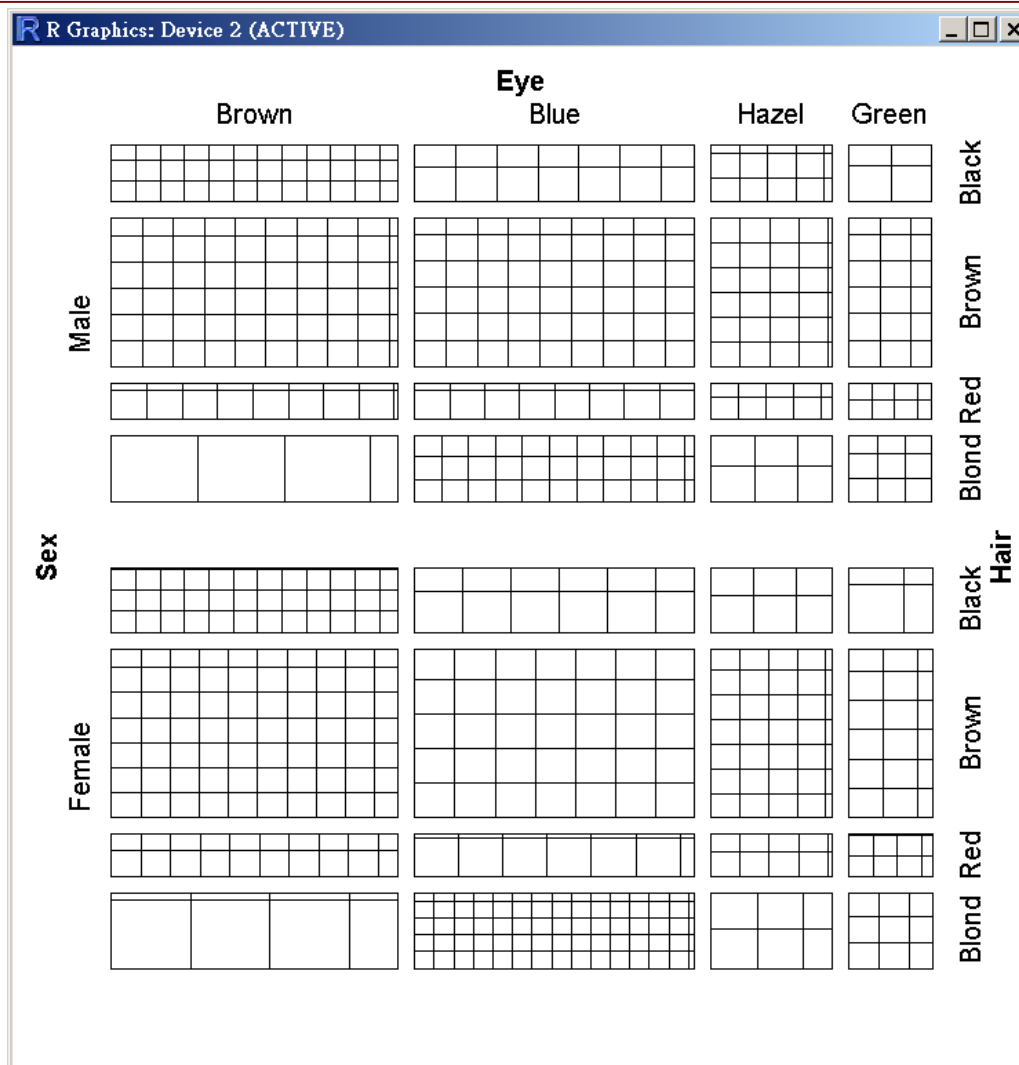
# Association Plots

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



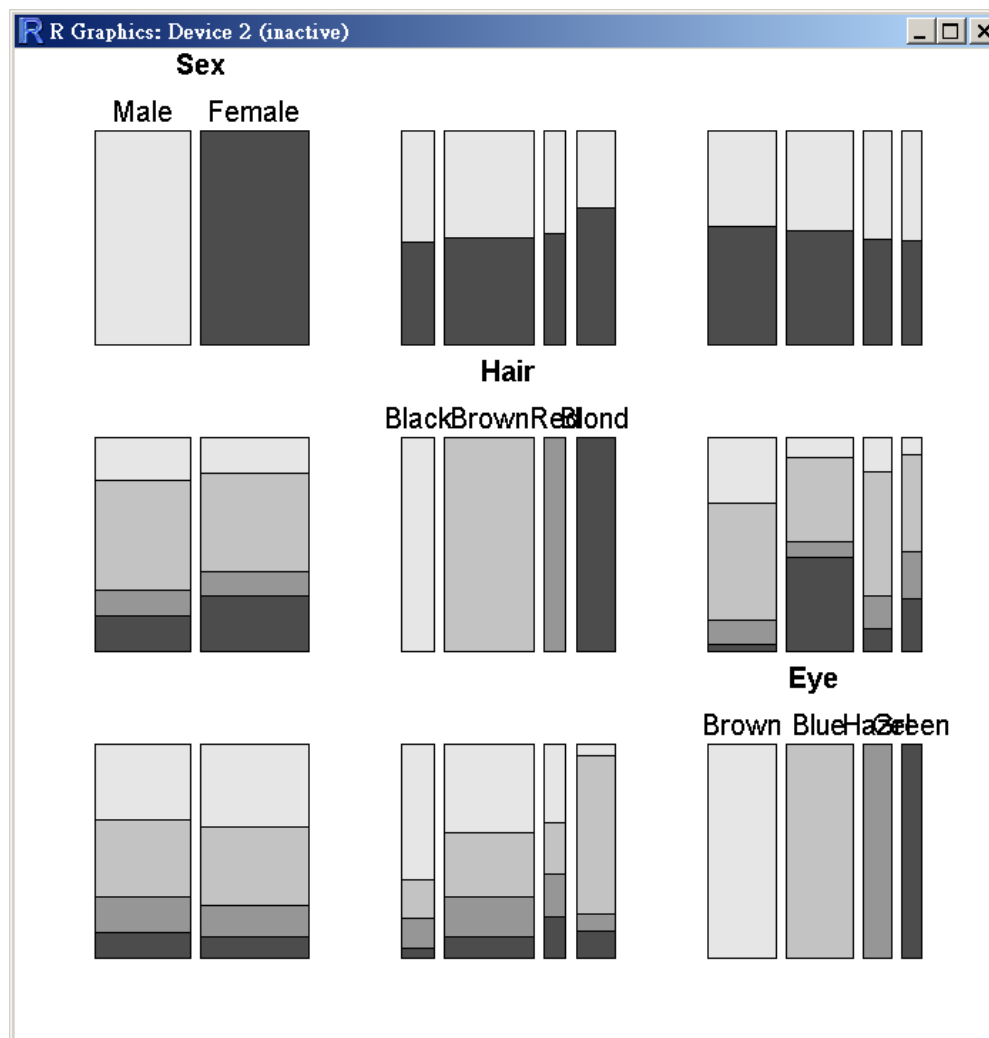
# Sieve Plots

```
> sieve(~Sex + Eye + Hair, data=HEC,
        spacing = spacing_dimequal(c(2,0.5,0.5)))
```



# Scatterplot Matrices

```
> pairs(HEC, highlighting = 1, diag_panel = pairs_diagonal_mosaic,
diag_panel_args = list(fill = grey.colors))
```



# Mosaic Displays for Two-way Tables

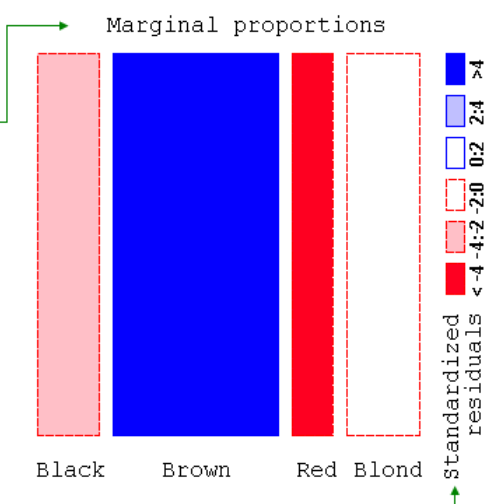
- Proposed by Hartigan & Kleiner (1981) and extended in Friendly (1994a), represents the counts in a contingency table directly by tiles.
- Tiles size is proportional to the cell frequency.

		Hair Color				Total
		BLACK	BROWN	RED	BLOND	
Eye Color	Brown	68	119	26	7	220
	Blue	20	84	17	94	215
	Hazel	15	54	14	10	93
	Green	5	29	14	16	64
Total	O	108	286	71	127	n 592

**Question:**  
how to understand the nature of the association between hair and eye color.

The Pearson  $\chi^2$  for these data is 138.3 with 9 degrees of freedom, indicating substantial departure from independence.

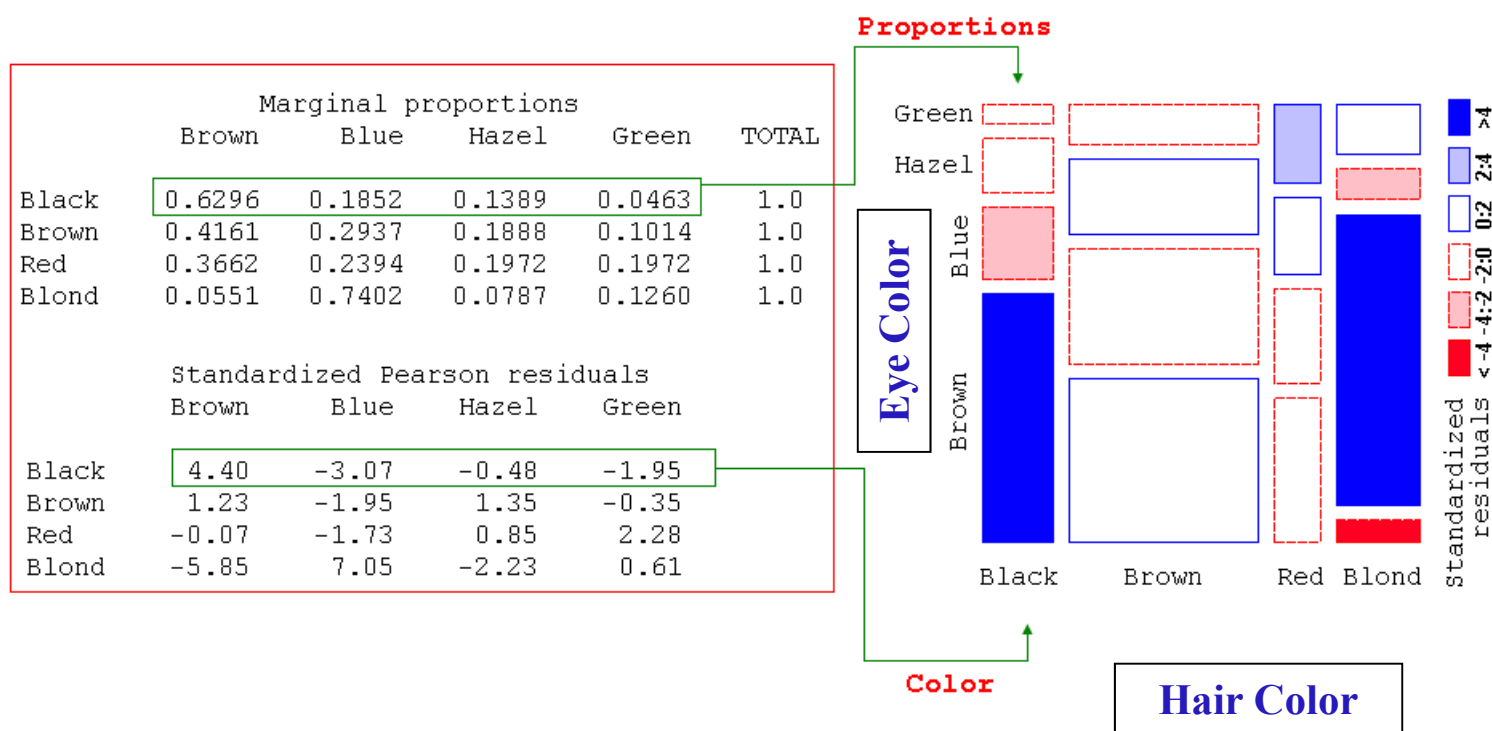
$p = \frac{O}{n}$	Marginal proportions			
	Black	Brown	Red	Blond
	0.1824	0.4831	0.1199	0.2145
$E = \frac{n}{4}$	Fitted frequencies			
	Black	Brown	Red	Blond
	148.00	148.00	148.00	148.00
$d = \frac{O - E}{\sqrt{E}}$	Standardized Pearson residuals			
	Black	Brown	Red	Blond
	-3.29	11.34	-6.33	-1.73



Hair Color

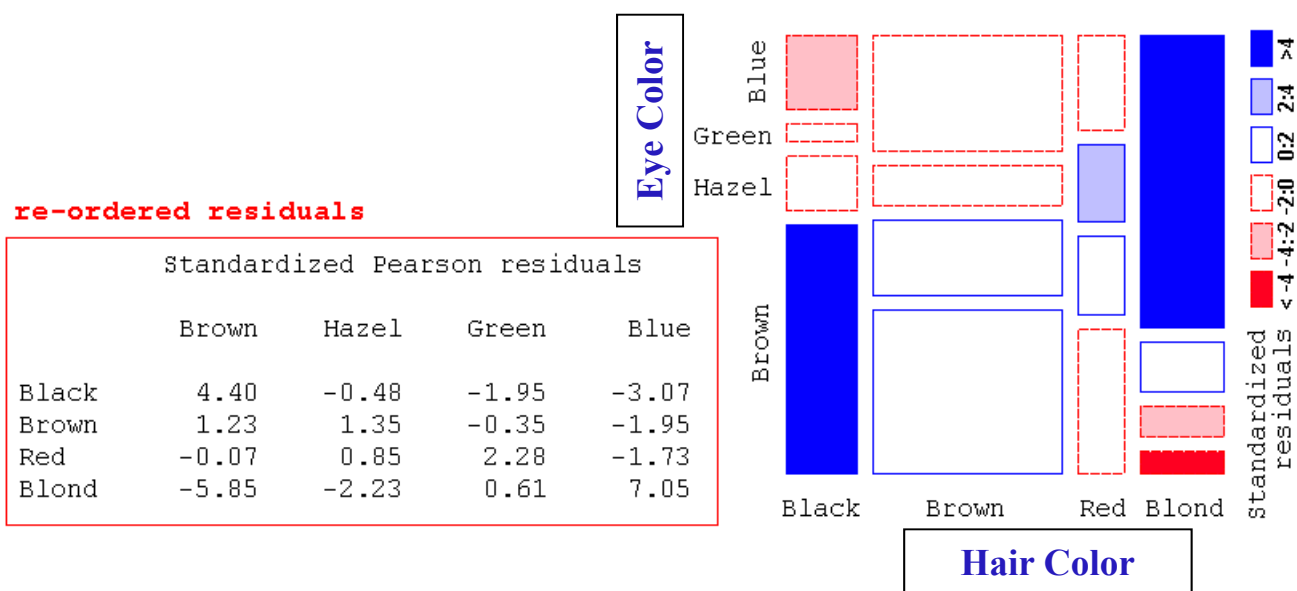
# Mosaic Displays: interpretation

- The association between Hair Color and Eye Color:
  - **Positive values (Blue):** cells whose observed frequency is substantially greater than would be found under independence;
  - **Negative values (Red):** indicate cells which occur less often than under independence.



# Mosaic Displays: reordering

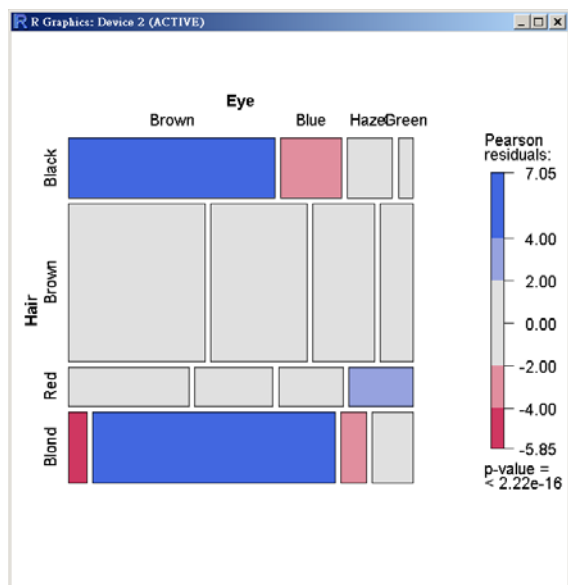
- Reordering the rows or columns of the two-way table so that the residuals have an opposite corner pattern of signs.
- The association between Hair and Eye color is that
  - people with **dark hair** tend to have **dark eyes**,
  - those with **light hair** tend to have **light eyes**,
  - people with **red hair** do not quite fit this pattern



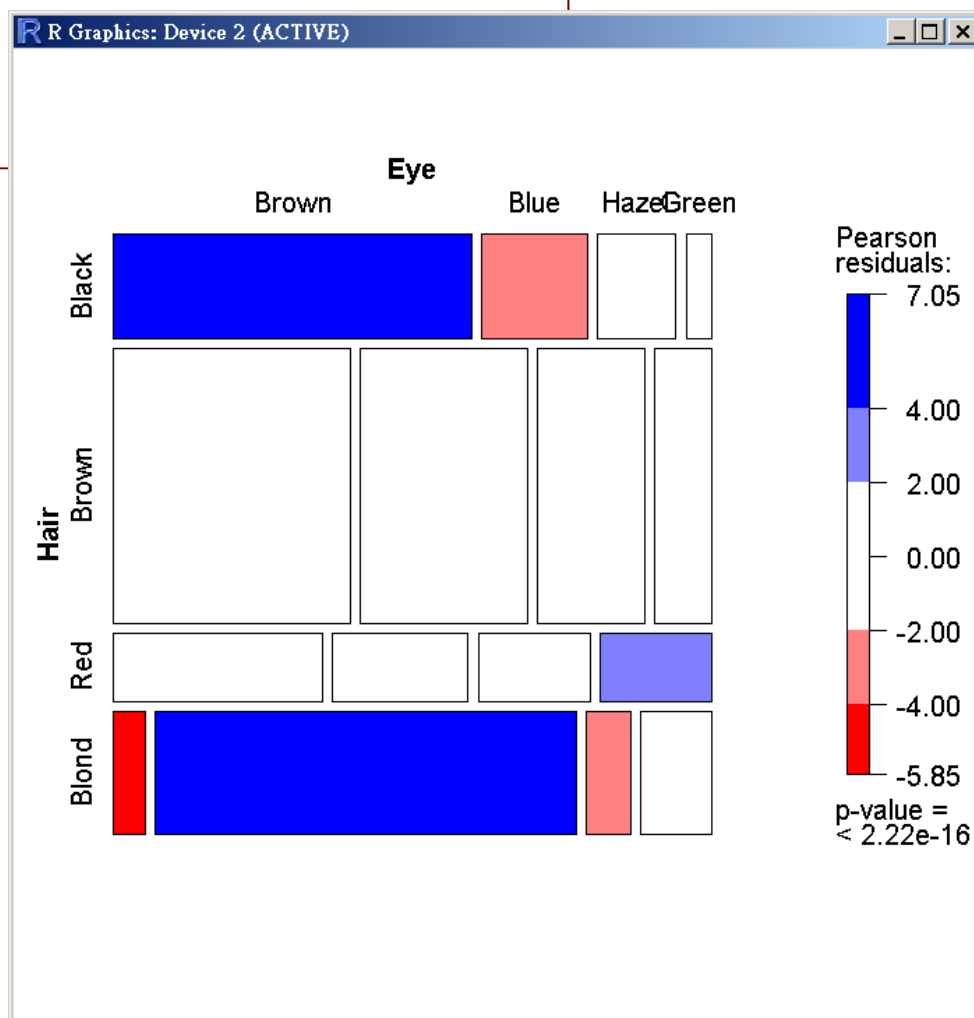
```
> mosaic(haireye, gp = shading_hsv)
```

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

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



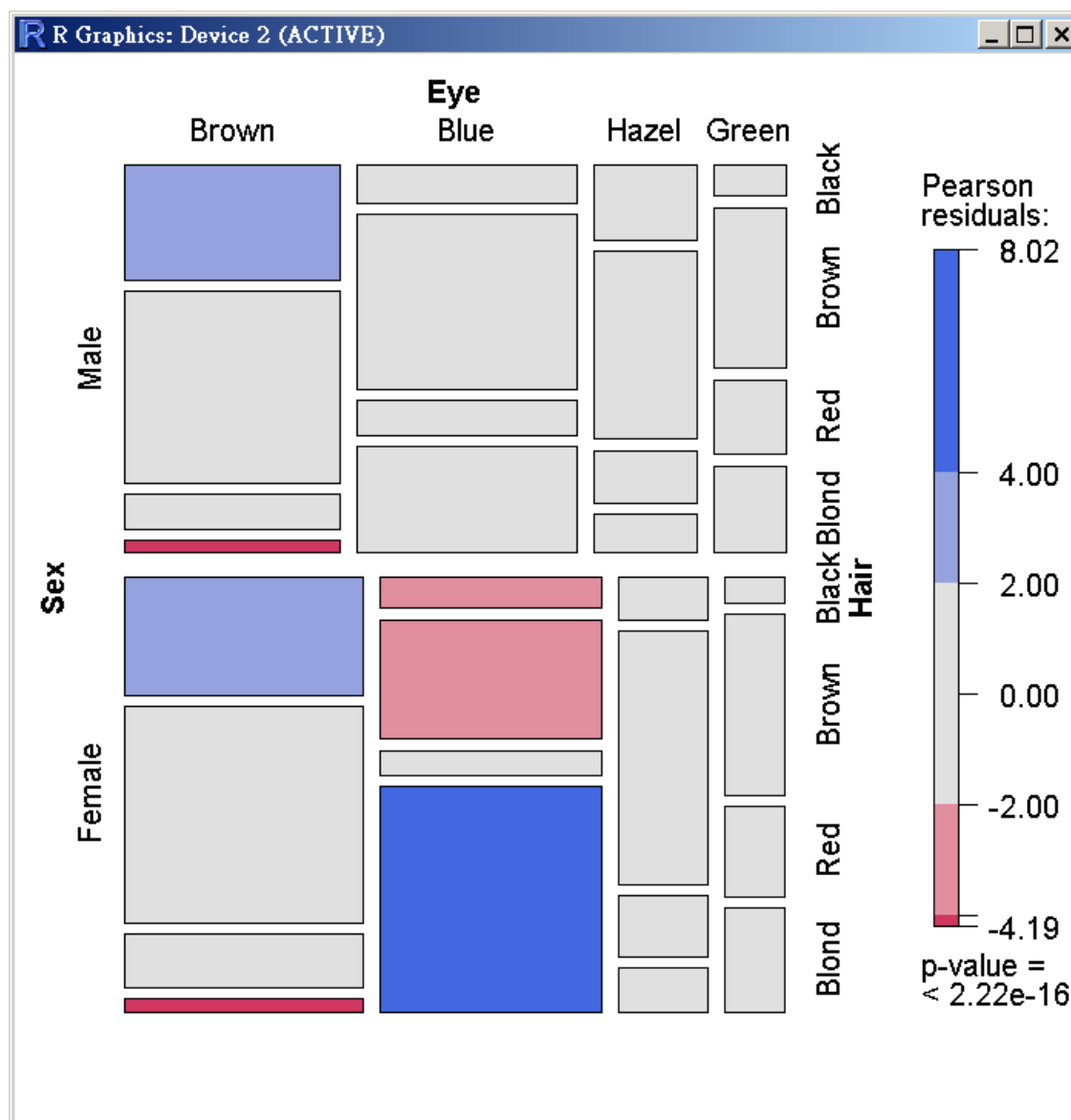
```
> mosaic(haireye, gp = shading_hcl)
```



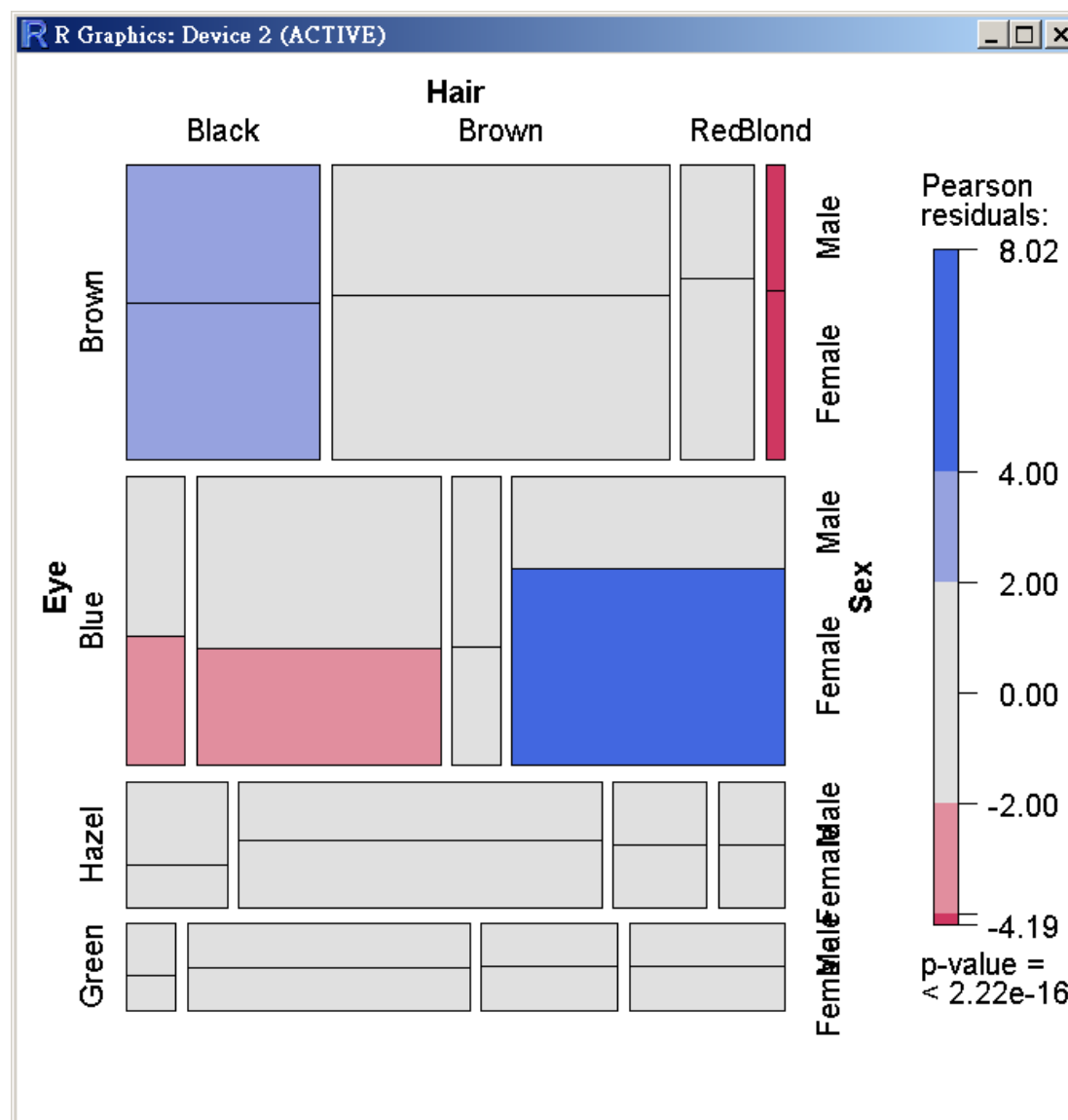




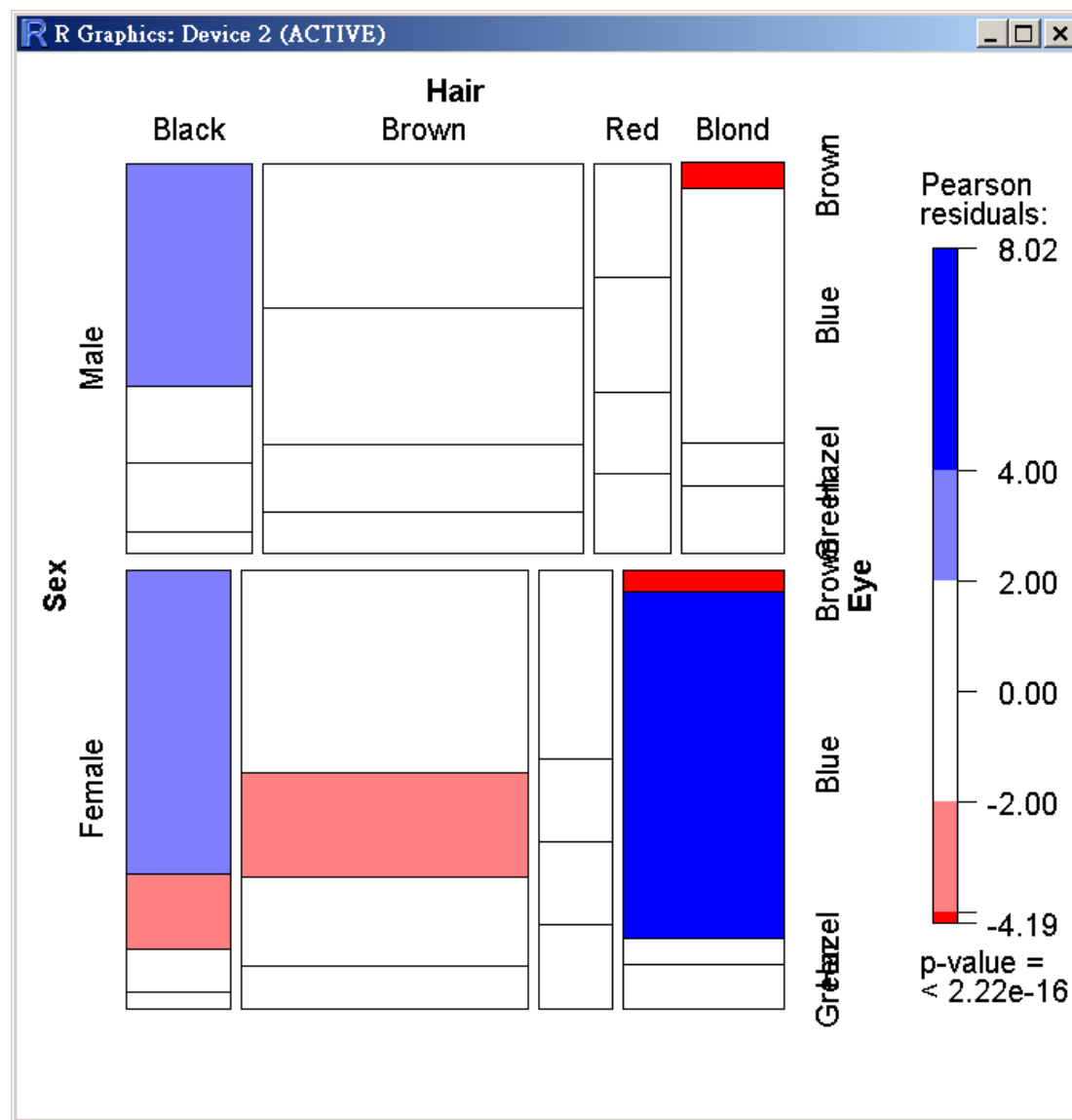
```
> mosaic(~Sex + Eye + Hair, data=HairEyeColor,
         shade=TRUE)
```



```
> mosaic(Sex ~ Eye + Hair, data=HairEyeColor,
         gp=shading_hcl)
```



```
> mosaic(Eye ~ Sex + Hair, data=HairEyeColor,
         gp=shading_hsv)
```

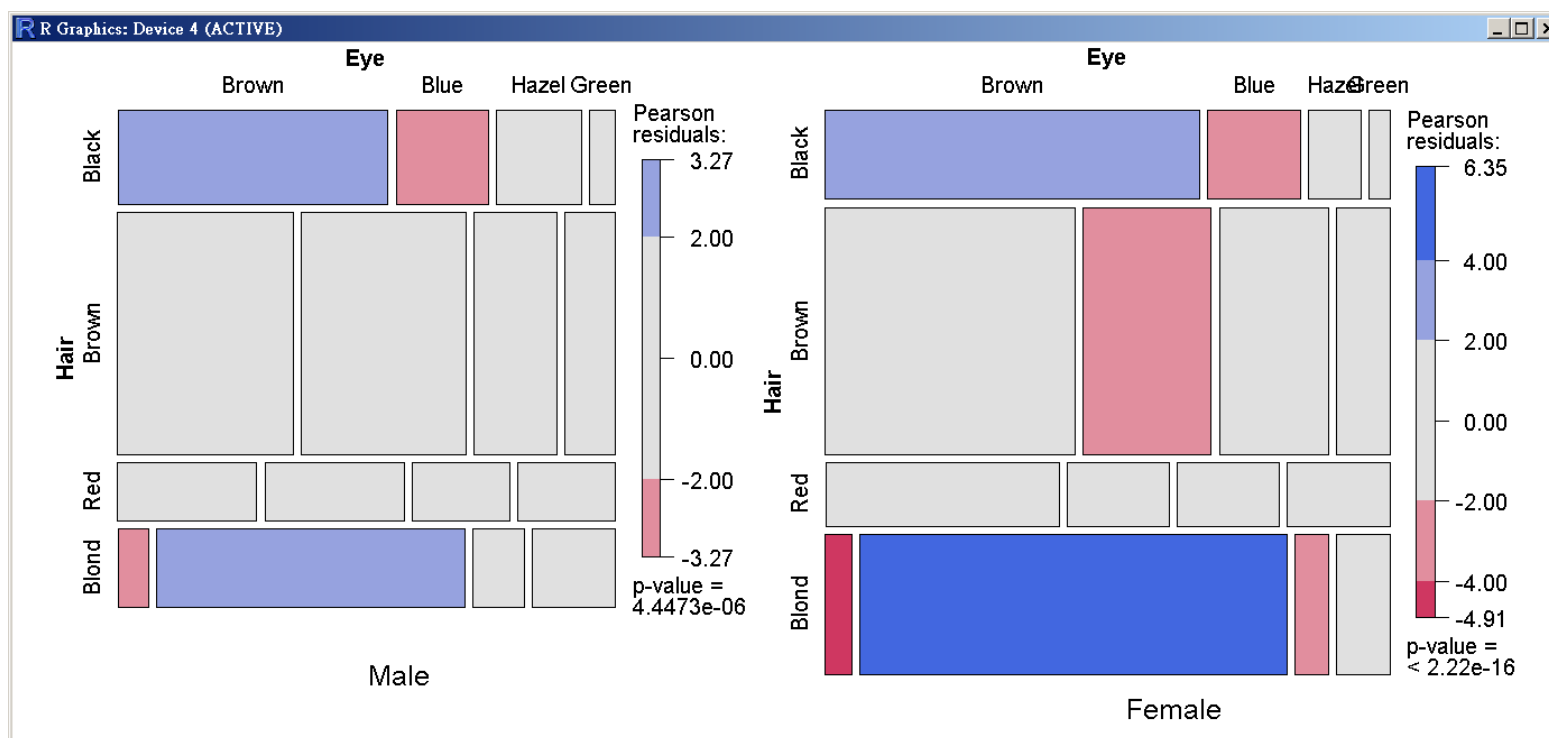


# Viewport

```

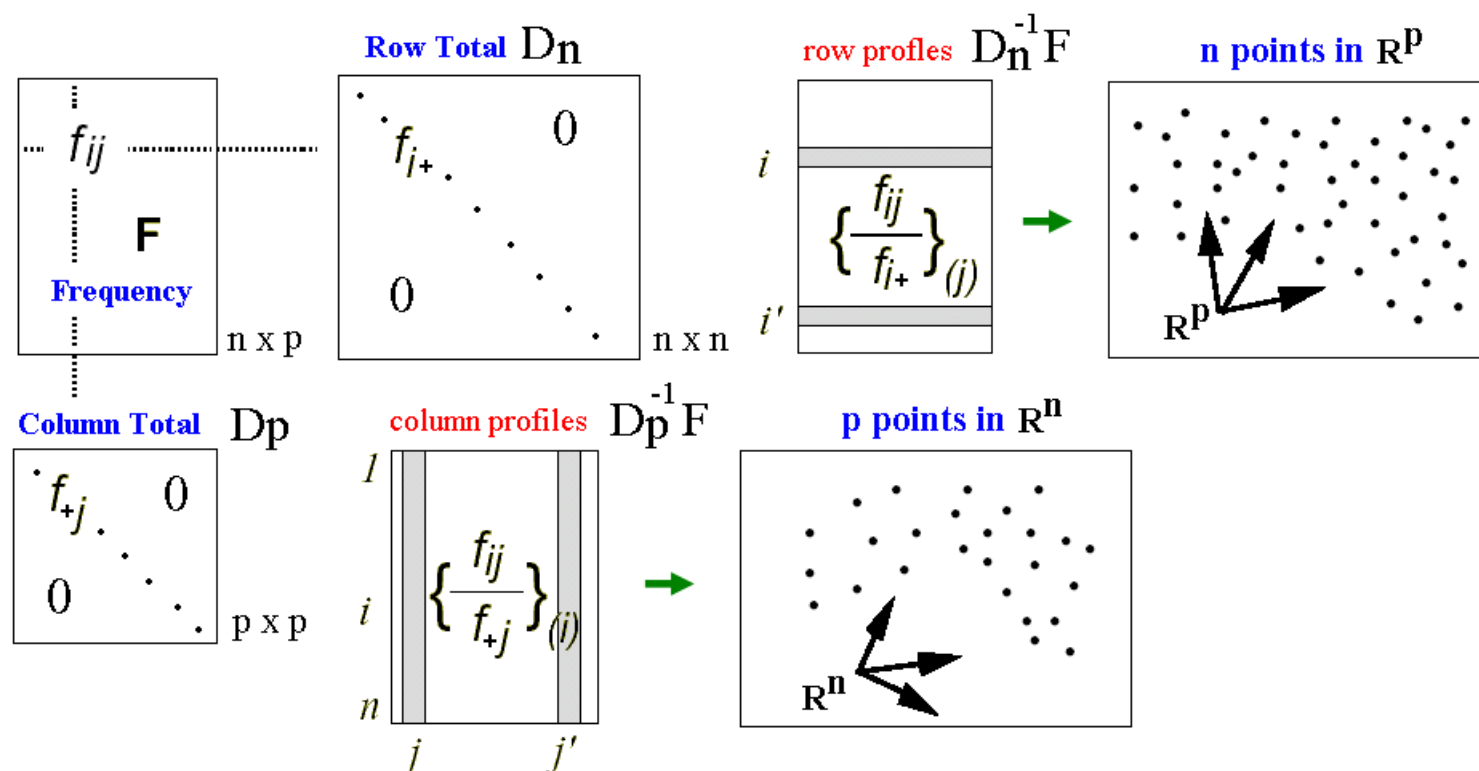
> pushViewport(viewport(layout = grid.layout(ncol = 2)))
> pushViewport(viewport(layout.pos.col = 1))
> mosaic(HEC[["Male"]], margins = c(left = 2.5, top = 2.5, 0), sub="Male",
newpage = FALSE, gp = shading_hcl)
> popViewport()
> pushViewport(viewport(layout.pos.col = 2))
> mosaic(HEC[["Female"]], margins = c(top = 2.5, 0), sub="Female", newpage =
FALSE, gp = shading_hcl)
> popViewport(2)

```



# Simple Correspondance Analysis (CA)

- Correspondence Analysis = PCA for categorical variables.
- Correspondence analysis is designed to analyze **simple two-way** and **multi-way tables** containing some measure of correspondence between the rows and columns.
- CA finds scores for the row and column categories on a small number of dimensions which account for the greatest proportion of the  $\chi^2$  for association between the row and column categories, just as principal components account for maximum variance.



# Correspondance Analysis (conti.)

$n$  row points in  $\mathbb{R}^p$  space

$p$  column points in  $\mathbb{R}^n$  space

Analysis of Table X

$$\mathbf{X} = \mathbf{D}_n^{-1}\mathbf{F}$$

$p$  coordinates

$$\frac{f_{ij}}{f_i}, \text{ for } j=1, 2, \dots, p.$$

$$\mathbf{X} = \mathbf{D}_p^{-1}\mathbf{F}'$$

$n$  coordinates

$$\frac{f_{ij}}{f_j}, \text{ for } i=1, 2, \dots, n.$$

with Metric M

$$\mathbf{M} = \mathbf{D}_p^{-1}$$

Chi-square distances

$$\mathbf{M} = \mathbf{D}_n^{-1}$$

$$d^2(i, i') = \sum_{j=1}^p \frac{1}{f_j} \left( \frac{f_{ij}}{f_i} - \frac{f_{i'j}}{f_{i'}} \right)^2$$

$$d^2(j, j') = \sum_{i=1}^n \frac{1}{f_i} \left( \frac{f_{ij}}{f_j} - \frac{f_{ij'}}{f_{j'}} \right)^2$$

Criterion N

$$\mathbf{N} = \mathbf{D}_n$$

mass of point  $i$ :  $f_i$

$$\mathbf{N} = \mathbf{D}_p$$

mass of point  $j$ :  $f_j$

**2.** If two rows having identical distribution profiles are aggregated, then the distances between columns remain unchanged.

Matrix to diagonalize

Principal axes

The property is important, because it guarantees a satisfactory invariance of the results irrespective of how the variables were originally coded.

Coordinates of points on the axes

**The reason for choosing the chi-square distance is:** it verifies the property of distributional equivalency:

**1.** If two columns having identical profiles are aggregated, then the distances between rows remain unchanged.

In  $\mathbb{R}^p$

$$\mathbf{S} = \mathbf{F}'\mathbf{D}_n^{-1}\mathbf{F}\mathbf{D}_p^{-1}$$

$$\mathbf{S}\mathbf{u}_\alpha = \lambda_\alpha \mathbf{u}_\alpha$$

$$\boldsymbol{\psi}_\alpha = \mathbf{D}_n^{-1}\mathbf{F}\mathbf{D}_p^{-1}\mathbf{u}_\alpha$$

$$\psi_{\alpha i} = \sum_{j=1}^p \frac{f_{ij}}{f_i \cdot f_j} u_{\alpha j}$$

In  $\mathbb{R}^n$

$$\mathbf{T} = \mathbf{F}\mathbf{D}_p^{-1}\mathbf{F}'\mathbf{D}_n^{-1}$$

$$\mathbf{T}\mathbf{v}_\alpha = \lambda_\alpha \mathbf{v}_\alpha$$

$$\boldsymbol{\varphi}_\alpha = \mathbf{D}_p^{-1}\mathbf{F}'\mathbf{D}_n^{-1}\mathbf{v}_\alpha$$

$$\varphi_{\alpha j} = \sum_{i=1}^n \frac{f_{ij}}{f_i \cdot f_j} v_{\alpha i}$$

# Correspondance Analysis (conti.)

- Row points for the disciplines, Column points for the years.
- The anthropology degree and the engineering degree are far from each other because their profiles are different, mathematics degree is near the engineering degree because their profiles are similar.
- Each year point represents the profile of that year across the various disciplines.

Science Doctorates in the USA, 1960-1975

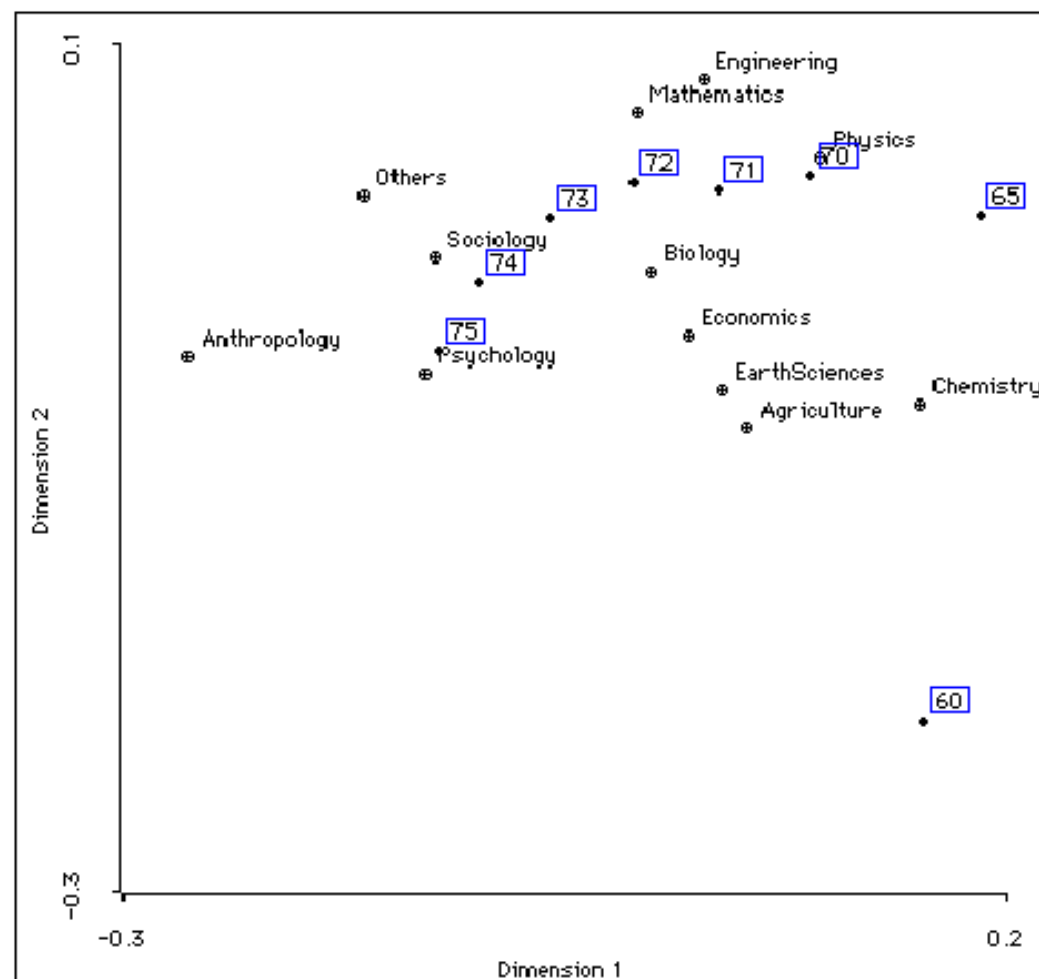
Discipline/Year	1960	1965	1970	1971	1972	1973	1974	1975
Engineering	794	2073	3432	3495	3475	3338	3144	2959
Mathematics	291	685	1222	1236	1281	1222	1196	1149
Physics	530	1046	1655	1740	1635	1590	134	1293
Chemistry	1078	1444	2234	2204	2011	1849	1792	1762
Earth Sciences	253	375	511	550	580	577	570	556
Biology	1245	1963	3360	3633	3580	3636	3473	3498
Agriculture	414	576	803	900	855	853	830	904
Psychology	772	954	1888	2116	2262	2444	2587	2749
Sociology	162	239	504	583	638	599	645	680
Economics	341	538	826	791	863	907	833	867
Anthropology	69	82	217	240	260	324	381	385
Others	314	502	1079	1392	1500	1609	1531	1550

The multidimensional time series on the number of science doctorates conferred in the USA from 1960 to 1975 (Greenacre, 1984).

# Correspondance Analysis (conti.)

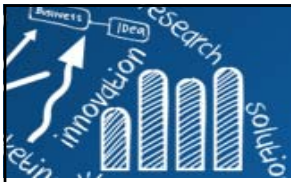
## Interpretation

- Each discipline point will lie in the neighborhood of the year in which the discipline's profile is prominent.
- There are relatively more agriculture, earth science and chemistry degrees in 1960, while the trend from 1965 to 1975 appears to be away from the physical sciences towards the social sciences.
- The points such as earth sciences and economics lie within the parabolic configuration of the years points; this implies that the profiles of these disciplines are higher than average in the early and later years.



**Note that** the positions of two sets of points with respect to each other are not directly comparable and should be interpreted with caution.





# Multiple Correspondance Analysis (Homogeneity Analysis)

- Multiple Correspondence Analysis (MCA) is known as homogeneity analysis, or dual scaling, or reciprocal averaging.
- The general idea of homogeneity analysis is to make a joint plot in  $p$ -space of all objects (or individuals) and the categories of all variables.
- Objects close to the categories they fall in and categories close to objects belonging in them

	1, 2, . . . , J	# variables
	$k_1, k_2, . . . , k_J$	# categories
i = 1		$G_j(i, t) = \begin{cases} 0, & \text{o.w.} \\ 1, & i \in t = 1, \dots, k_j \end{cases}$
.		
.		
.		
N		

$G = [ G1 \mid G2 \mid \dots \mid GJ ]$

do PCA to the  $G$  matrix

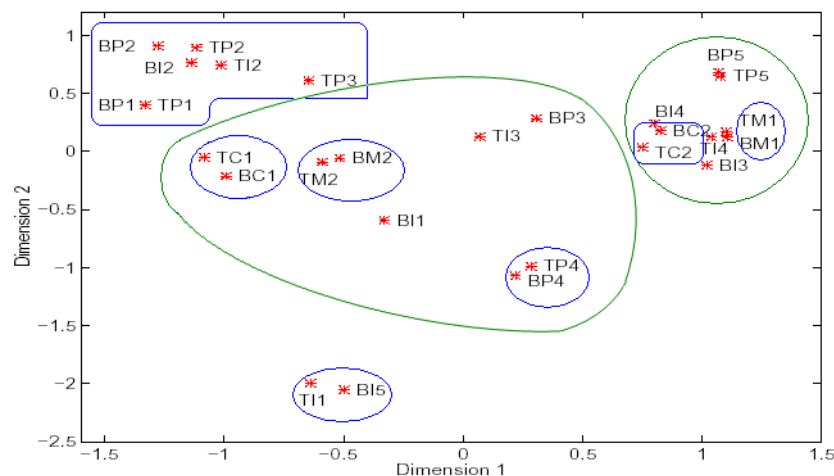
→  $X$  be a  $N \times p$  matrix containing the coordinates of the objects.

$Y$  be a  $\sum_j k_j \times p$  matrix containing the coordinates of the category points.

# Homogeneity Analysis (conti.)

## Mammals Dentition Example

The data for this example are taken from Hartigan (1975) (also discussed in Michailidis and De Leeuw, 1999). Dental characteristics are used in the classification of 66 different kinds of mammals. Mammals' teeth are divided into four groups: incisors, canines, premolars, and molars.



Category quantifications of the variables in the mammals dentition example

### Description for Variables

- TI: Top incisors;  
 1: 0 incisors, 2: 1 incisors,  
 3: 2 incisors, 4: 3 or more incisors
- BI: Bottom incisors;  
 1: 0 incisors, 2: 1 incisors,  
 3: 2 incisors, 4: 3 incisors,  
 5: 4 incisors
- TC: Top canine;  
 1: 0 canines, 2: 1 canines,
- BC: Bottom canine;  
 1: 0 canines, 2: 1 canines,
- TP: Top premolar;  
 1: 0 premolars, 2: 1 premolars,  
 3: 2 premolars, 4: 3 premolars  
 5: 4 premolars
- BP: Bottom premolar;  
 1: 0 premolars, 2: 1 premolars,  
 3: 2 premolars, 4: 3 premolars  
 5: 4 premolars
- TM: Top molar;  
 1: 0-2 molars, 2: 3 or more molars,
- BM: Bottom molar;  
 1: 0-2 molars, 2: 3 or more molars

TB T B T B T B  
 I I C C P P M M

4	5	2	2	4	4	2	2	Opposum
4	4	2	2	4	5	2	2	Hairy-Tail-Mole
4	3	2	2	4	4	2	2	Common-Mole
4	4	2	2	5	2	2	2	Star-Nose-Mole
3	4	2	2	4	4	2	2	Brown-Bat
3	4	2	2	3	4	2	2	Silver-Hair-Bat
3	4	2	2	3	4	2	2	Pigmy-Bat
3	4	2	2	3	4	2	2	House-Bat
2	4	2	2	3	4	2	2	Red-Bat
2	4	2	2	3	4	2	2	Hoary-Bat
3	4	2	2	3	4	2	2	Lump-Nose-Bat
1	4	2	2	3	4	2	2	Armadillo
3	2	1	3	3	3	3	3	Fika
3	3	1	3	1	4	3	3	Snowshoe-Rabbit
3	3	1	3	1	3	3	3	Beaver
3	3	1	3	1	3	3	3	Marmot
3	3	1	3	1	3	3	3	Groundhog
3	3	1	3	1	3	3	3	Prairie-Dog
3	3	1	3	1	3	3	3	Ground-Squirrel
3	3	1	3	1	3	3	3	Chipmunk
2	2	1	2	2	2	2	2	Gray-Squirrel
2	2	1	2	2	2	2	2	Fox-Squirrel
2	2	1	2	2	2	2	2	Pocket-Gopher
2	2	1	2	2	2	2	2	Kangaroo-Rat
2	2	1	1	1	2	2	2	Pack-Rat
2	2	1	1	1	2	2	2	Field-Mouse
2	2	1	1	1	2	2	2	Muskrat
2	2	1	1	1	2	2	2	Black-Rat
2	2	1	1	1	2	2	2	House-Mouse
2	2	1	2	2	2	2	2	Porcupine
2	2	1	2	2	2	2	2	Guinea-Pig
2	4	2	2	2	2	2	2	Coyote
4	4	2	2	2	2	2	2	Wolf
4	4	2	2	2	2	2	2	Fox
4	4	2	2	2	2	2	2	Bear
4	4	2	2	2	2	2	2	Civet-Cat
4	4	2	2	2	2	2	2	Raccoon
4	4	2	2	2	2	2	2	Marten
4	4	2	2	2	2	2	2	Risher
4	4	2	2	2	2	2	2	Weasel
4	4	2	2	2	2	2	2	Mink
4	4	2	2	2	2	2	2	Ferrer
4	4	2	2	2	2	2	2	Wolverine
4	4	2	2	2	2	2	2	Badger
4	4	2	2	2	2	2	2	Skunk
4	4	2	2	2	2	2	2	River-Otter
4	4	2	2	2	2	2	2	Sea-Otter
4	4	2	2	2	2	2	2	Jaguar
4	4	2	2	2	2	2	2	Ocelot
4	4	2	2	2	2	2	2	Cougar
4	4	2	2	2	2	2	2	Lynx
4	3	2	2	2	2	2	2	Fur-Seal
4	3	2	2	2	2	2	2	Sea-Lion
2	1	2	2	2	4	4	1	Walrus
4	3	2	2	2	4	4	1	Grey-Seal
3	2	2	2	5	5	5	1	Blephant-Seal
3	4	2	2	4	4	2	2	Peccary
1	5	1	4	4	2	2	2	Elk
1	5	1	4	4	2	2	2	Deer
1	5	1	4	4	2	2	2	Moose
1	5	1	4	4	2	2	2	Reindeer
1	5	1	4	4	2	2	2	Antelope
1	5	1	4	4	2	2	2	Bison
1	5	1	4	4	2	2	2	Mountain-Goat
1	5	1	4	4	2	2	2	Muskox
1	5	1	4	4	2	2	2	Mountain-Sheep