

Correspondence Analysis & Related Methods

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SESSION 11: CORRESPONDENCE ANALYSIS: theory implemented in R

Correspondence analysis (repeat)

- Table of nonnegative data N
- Divide N by its grand total n to obtain the so-called *correspondence matrix* $P = (1/n)N$
- Let the row and column marginal totals of P be the vectors r and c respectively, that is the vectors of row and column *masses*, and D_r and D_c be the diagonal matrices of these masses

$$S = D_r^{-1/2} (P - rc^T) D_c^{-1/2} = D_r^{1/2} (D_r^{-1} P D_c^{-1} - 11^T) D_c^{1/2}$$

$$\frac{P_{ij} - r_i c_j}{\sqrt{r_i c_j}} \quad \sqrt{r_i} \left(\frac{P_{ij}}{r_i c_j} - 1 \right) \sqrt{c_j}$$

$$S = U D_\alpha V^T$$

Principal coordinates $F = D_r^{-1/2} U D_\alpha$
 coordinates $G = D_c^{-1/2} V D_\alpha$

Standard coordinates $\Phi = D_r^{-1/2} U$
 coordinates $\Gamma = D_c^{-1/2} V$

Parts of inertia $\alpha_k^2 \quad k=1,2,\dots$

R implementation

```
# read in data into data-frame data_set
# the next 14 commands are all you need to compute CA results
data.P <- data_set/sum(data_set)
data.r <- apply(data.P,1,sum)
data.c <- apply(data.P,2,sum)
data.Dr <- diag(data.r)
data.Dc <- diag(data.c)
data.Drmh <- diag(1/sqrt(data.r))
data.Dcmh <- diag(1/sqrt(data.c))
data.P <- as.matrix(data.P)
data.S <- data.Drmh %**% (data.P-data.r%o%data.c) %**% data.Dcmh
data.svd <- svd(data.S)
data.rsc <- data.Drmh%**data.svd$u
data.csc <- data.Dcmh%**data.svd$v
data.rpc <- data.rsc%**diag(data.svd$d)
data.cpc <- data.csc%**diag(data.svd$d)
# the symmetric map
plot(data.rpc[,1],data.rpc[,2],type="n",pty="s")
text(data.rpc[,1],data.rpc[,2],label=rownames(data))
# now do it in one shot using ca package (first install from CRAN)
library(ca)
plot(ca(data_set))
```

"Salud" data (from Encuesta Nacional de Salud, España)

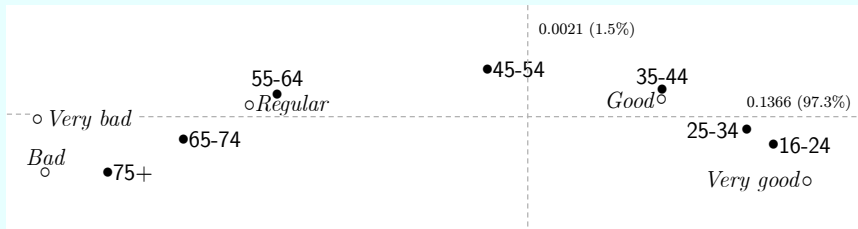
Table 1: Crosstabulation of age groups by perceived health status

AGE GROUP	Very Good	Good	Regular	Bad	Very Bad	SUM
16-24	243	789	167	18	6	1223
25-34	220	809	164	35	6	1234
35-44	147	658	181	41	8	1035
45-54	90	469	236	50	16	861
55-64	53	414	306	106	30	909
65-74	44	267	284	98	20	713
75+	20	136	157	66	17	396
SUM	817	3542	1495	414	103	6371

Table 2: Row percentages calculated from Table 1

AGE GROUP	Very Good	Good	Regular	Bad	Very Bad	SUM
16-24	19.9	64.5	13.7	1.5	0.5	100.0
25-34	17.8	65.6	13.3	2.8	0.5	100.0
35-44	14.2	63.6	17.5	4.0	0.8	100.0
45-54	10.5	54.5	27.4	5.8	1.9	100.0
55-64	5.8	45.5	33.7	11.7	3.3	100.0
65-74	6.2	37.4	39.8	13.7	2.8	100.0
75+	5.1	34.3	39.6	16.7	4.3	100.0
AVERAGE	12.8	55.6	23.5	6.5	1.6	100.0

Symmetric CA map



Numerical scale from CA solution (principal coordinates)

	very bad	bad	regular	good	very good
original scale:	-0.767	-0.755	-0.439	0.198	0.423

Any linear transformation still retains optimality of results.

So to convert to 0 to 100 scale (for example):

- **first add 0.767** to all values so the scale runs from 0 to $0.423+0.767= 1.190$
- **multiply by 100/1.190** so the scale runs from 0 to 100

CA of perceived health status - optimal scale



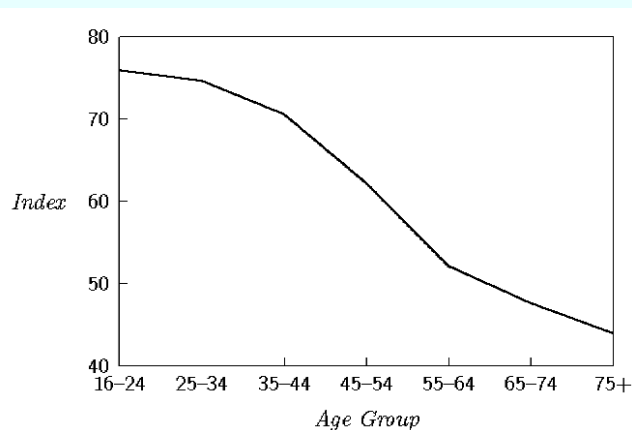
Redefining the optimal scale

	very bad	bad	regular	good	very good
original scale:	-0.767	-0.755	-0.439	0.198	0.423
new scale:	0.0	1.0	27.6	81.1	100.00

Calculating averages for the age groups

	16-24	25-34	35-44	45-54	55-64	65-74	75+
	75.97	74.69	70.63	62.25	52.17	47.67	44.01

CA of perceived health status - optimal scale



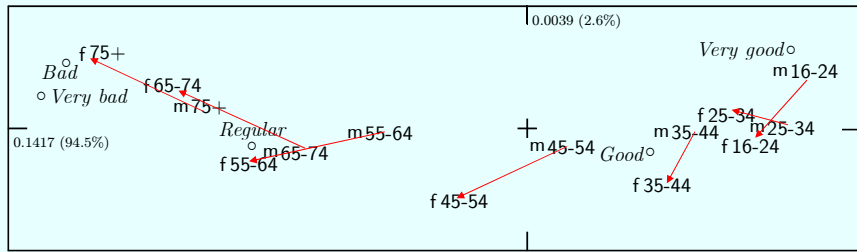
```
# rescaling the optimal scale
data.range <- max(data.csc[,1])-min(data.csc[,1])
data.scale <- (data.csc[,1]-min(data.csc[,1]))*100/data.range
```

Perceived health status: male - female

Table 3: Age group and sex interactively crosstabulated with health status

AGE GROUP	Very Good	Good	Regular	Bad	Very Bad	SUM
MALES						
16-24	145	402	84	5	3	639
25-34	112	414	74	13	2	615
35-44	80	331	82	24	4	521
45-54	54	231	102	22	6	415
55-64	30	219	119	53	12	433
65-74	18	125	110	35	4	292
75+	9	67	65	25	8	174
FEMALES						
16-24	98	387	83	13	3	584
25-34	108	395	90	22	4	619
35-44	67	327	99	17	4	514
45-54	36	238	134	28	10	446
55-64	23	195	187	53	18	476
65-74	26	142	174	63	16	421
75+	11	69	92	41	9	222
SUM	817	3542	1495	414	103	6371

Perceived health status: male - female



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SESSION 12: CORRESPONDENCE ANALYSIS: three examples, using R package ca

R package ca

The **ca** package (downloadable from CRAN) consists of two main functions **ca** (simple CA) and **mjca** (multiple and joint CA), as well as two- and three-dimensional plotting routines (the package **rgl** needs to be installed as well for the 3-d graphics)

```
ca(ca)
```

The function **ca** computes a simple correspondence analysis based on the singular value decomposition.

The options **suprow** and **supcol** allow supplementary (passive) rows and columns to be specified. Using the options **subsetrow** and/or **subsetcol** result in a subset CA being performed.

Usage

```
ca(obj, nd = NA, suprow = NA, supcol = NA, subsetrow = NA, subsetcol = NA, swisign = NA)
```

Arguments

obj A two-way table of non-negative data, usually frequencies.
nd Number of dimensions to be included in the output; if NA the maximum possible dimensions are included.
suprow Indices of supplementary rows.
supcol Indices of supplementary columns.
subsetrow Row indices of subset.
subsetcol Column indices of subset.
swisign A vector of 1's and -1's indicating for which dimension to switch the coordinates.

Value of ca object

Value

sv	Singular values
nd	Dimension of the solution
rownames	Row names
rowmass	Row masses
rowdist	Row chi-square distances to centroid
rowinertia	Row inertias
rowcoord	Row standard coordinates
rowsup	Indices of row supplementary points
colnames	Column names
colmass	Column masses
coldist	Column chi-square distances to centroid
colinertia	Column inertias
colcoord	Column standard coordinates
colsup	Indices of column supplementary points

Options for plotting used so far

```
plot(x, dim = c(1,2), map = "symmetric", what = c("all", "all"), mass = c(FALSE, FALSE),  
      contrib = c("none", "none"), col = c("#000000", "#FF0000"), pch = c(16, 1, 17, 24),  
      labels = c(2, 2), arrows = c(FALSE, FALSE), ...)
```

Arguments

x Simple correspondence analysis object returned by **ca**
dim Numerical vector of length 2 indicating the dimensions to plot on horizontal and vertical axes respectively; default is 1st dimension horizontal and 2nd vertical
map Character string specifying the map type. Allowed options include
"symmetric" (default)
"rowprincipal"
"colprincipal"
"symbiplot"
"rowgab"
"colgab"
"rowgreen"
"colgreen"
what Vector of two character strings specifying the contents of the plot. First entry sets the rows and the second entry the columns. Allowed values are
"all" (all available points, default)
"active" (only active points are displayed)
"passive" (only supplementary points are displayed)
"none" (no points are displayed)
mass Vector of two logicals specifying if the mass should be represented by the area of the point symbols (first entry for rows, second one for columns)
labels Vector of length two specifying if the plot should contain symbols only (0), labels only (1) or both symbols and labels (2). Setting labels to 2 results in the symbols being plotted at the coordinates and the labels with an offset.
arrows Vector of two logicals specifying if the plot should contain points (FALSE, the default) or arrows (TRUE). First value sets the rows and the second value sets the columns.
... Further arguments passed to plot and points.