Correspondence analysis

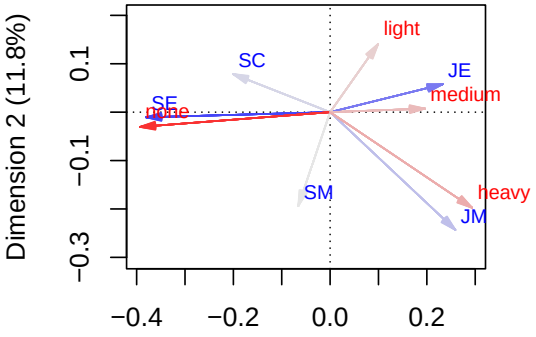
Introduction to correspondence analysis (CA)

- Context: $\mathbf{Y}$ (abundance)
  - Goal: Graphically display the relationships between and/or within the rows and columns

We go from this dataset:

	none	light	medium	heavy
SM	4	2	3	2
JM	4	3	7	4
SE	25	10	12	4
JE	18	24	33	13
SC	10	6	7	2

to this plot:



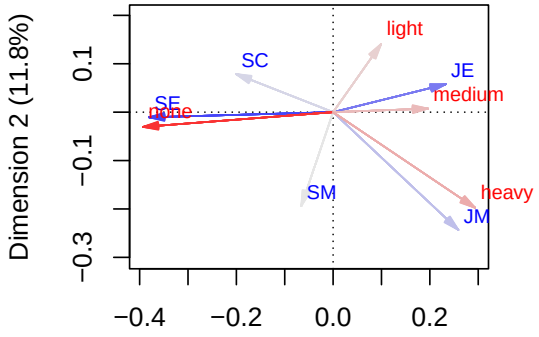
Introduction to correspondence analysis (CA)

- Context: $\mathbf{Y}$ (abundance)
  - Goal: Graphically display the relationships between and/or within the rows and columns

We go from this dataset:

	none	light	medium	heavy
SM	0.36	0.18	0.27	0.18
JM	0.22	0.17	0.39	0.22
SE	0.49	0.20	0.24	0.08
JE	0.20	0.27	0.38	0.15
SC	0.40	0.24	0.28	0.08

to this plot:



Example applications

Datasets

- Rows are various dams, and columns are counts of waterbird species
- Rows are various immune compartments (e.g. blood, spleen, lymph), and columns are frequencies of immune cell types (e.g. T cells, B cells, NK cells)
- Rows are company brands (e.g. Cadbury, Beacon, Lindt), and columns are consumer ratings on a 1-5 scale (e.g. quality, price, taste)

Key characteristics

- Non-negative
- Natural zero (i.e. zero means literally nothing and not simply that two quantities are equal, for example)
- Same units (e.g. counts all in thousands)

The key property of the data is that proportions make sense throughout.

Correspondence matrix, $\mathbf{P}$

- Suppose that we have some matrix $\mathbf{X} : I \times J$ where each element
  - Rows can be thought of as observations and columns as variables
- The correspondence matrix $\mathbf{P} : I \times J$ is the matrix of overall proportions where

$$P_{ij} = \frac{x_{ij}}{\sum_{i=1}^{I} \sum_{j=1}^{J} x_{ij}} = \frac{x_{ij}}{n}$$

We go from $\mathbf{X}$

	none	light	medium	heavy
SM	4	2	3	2
JM	4	3	7	4
SE	25	10	12	4
JE	18	24	33	13
SC	10	6	7	2

to $\mathbf{P}$

	none	light	medium	heavy
SM	0.02	0.01	0.02	0.01
JM	0.02	0.02	0.04	0.02
SE	0.13	0.05	0.06	0.02
JE	0.09	0.12	0.17	0.07
SC	0.05	0.03	0.04	0.01

Independence of rows and columns

- Let $\mathbf{r}$ be the vector of row totals, i.e. $r_i = \sum_{j=1}^{J} P_{ij} = \mathbf{P1}$
- Let $\mathbf{c}$ be the vector of column totals, i.e. $c_j = \sum_{i=1}^{I} P_{ij} = \mathbf{P'1}$
- Then if the rows are independent of the cells, we have that

$$p_{ij} = r_i c_j, \implies \mathbf{P}_{\text{ind}} = \mathbf{rc'}$$

	none	light	medium	heavy
SM	0.02	0.01	0.02	0.01
JM	0.03	0.02	0.03	0.01
SE	0.08	0.06	0.08	0.03
JE	0.14	0.11	0.15	0.06
SC	0.04	0.03	0.04	0.02

Matrix of residuals

- Under the assumption of independence, we can calculate residuals:

$$\mathbf{P} - \mathbf{P}_{\text{ind}} = \mathbf{P} - \mathbf{r}\mathbf{c}'.$$

- Continuing the smoking example, we then have

$\mathbf{P}$

	none	light	medium	heavy
SM	0.02	0.01	0.02	0.01
JM	0.02	0.02	0.04	0.02
SE	0.13	0.05	0.06	0.02
JE	0.09	0.12	0.17	0.07
SC	0.05	0.03	0.04	0.01

$\mathbf{P} - \mathbf{r}\mathbf{c}'$

	none	light	medium	heavy
SM	0.003	-0.003	-0.003	0.003
JM	-0.009	-0.006	0.006	0.009
SE	0.046	-0.010	-0.023	-0.014
JE	-0.051	0.018	0.025	0.008
SC	0.011	0.001	-0.005	-0.006

- Residuals are naturally larger for the more abundant rows (employee ranks)

Standardised residuals

- To avoid the more abundant rows and columns from dominating downstream analyses, we normalise by row and column size.
- For each residual $P_{ij} - P_{\text{ind}_{ij}}$, we standardise by

$$\frac{P_{ij} - P_{\text{ind}_{ij}}}{\sqrt{r_i c_j}} = \frac{P_{ij} - r_i c_j}{\sqrt{r_i c_j}}$$

- Define the diagonal matrices $\mathbf{D}_r = \text{diag}(\mathbf{r})$ and $\mathbf{D}_c = \text{diag}(\mathbf{c})$.
- We then have that the matrix of standardised residuals is given by

$$\mathbf{S} = \mathbf{D}_r^{-1/2}(\mathbf{P} - \mathbf{P}_{\text{ind}})\mathbf{D}_c^{-1/2}.$$

Motivation for this form of residual I: Count distribution

- Consider the following residual:

$$\frac{\text{Observed} - \text{Expected}}{\sqrt{\text{Expected}}}$$

- This is equal to a residual with mean 0 and unit variance if the data are Poisson distributed, as for the Poisson distribution, the mean is equal to the variance.
  - Considering that we are dealing with abundance (e.g. count) data, the Poisson distribution seems appropriate.
  - We are accounting for the mean-variance relationship.

Motivation for this form of residual II: The χ^2 statistic

- Now if we square the residuals, we get a χ^2 statistic:

$$\frac{(\text{Observed} - \text{Expected})^2}{\text{Expected}}$$

- This tracks the deviation from the model with mean Expected and variance Expected.
- We can calculate this for all the elements in the matrix P under the assumption that P arose under independent rows and columns.
  - This yields the overall χ^2 statistic when we add them up:

$$\text{X}^2 = \sum_{i=1}^{I} \sum_{j=1}^{J} \frac{(\text{Observed}_{ij} - \text{Expected}_{ij})^2}{\text{Expected}_{ij}}$$

Role of independence assumption

- The assumption of independence is likely not true, but that is in fact the point:
  - We've created a way to highlight observation-variable (row-column) combinations that are more common than expected
    - In particular, the abundance of the row or column is now cancelled out
- We are *not* performing inference for a test of association between rows and columns
- Rather, this deviation-from-independence information (i.e. $\mathbf{S}$) will be used to represent rows in a lower-dimensional space that we can then interpret

Correspondence analysis as PCA on a transformed matrix

- What we've done up until this point is, essentially, transform the data appropriately
  - Calculated proportions ($\mathbf{X} \to \mathbf{P}$)
  - "Centred" it ($\mathbf{P} - \mathbf{r}\mathbf{c}'$)
  - "Standardised" it ($\mathbf{S} = \mathbf{D}_r^{-1/2}(\mathbf{P} - \mathbf{r}\mathbf{c}')\mathbf{D}_c^{-1/2}$)
- We then use the SVD to obtain a low-rank approximation to $\mathbf{S}$
  - Find the low-rank $s < \min(I-1, J-1)$ rank matrix $\tilde{S}$ such that the sum of squared differences is minimised
    - $\tilde{S} = \sum_{k=1}^{s} \lambda_i \mathbf{u}_k \mathbf{v}_k'$
  - PCA creates the same approximating matrix as the SVD, and so CA is essentially PCA on a transformed matrix
- Since this is an exploratory technique, we plot the points (transformed again) in a biplot
  - We have various options for how exactly to calculate the points, which we'll discuss

Views of correspondence analysis

- The previous description of CA is a bit handwavy, but serves to (help) give an intuition for what CA is doing
- There are two formal approaches to (or ways of developing) correspondence analysis:
  - Matrix approximation
  - Profile approximation

Matrix approximation view of correspondence analysis I

- The matrix approximation view to CA regards it as solving the following weighted least squares problem:

Matrix approximation angle on CA

- Find a reduced rank matrix $\hat{\mathbf{P}}$ such that

$$\sum_{i=1}^{I}\sum_{j=1}^{J}\frac{(p_{ij}-\hat{p}_{ij})^2}{r_i c_j}$$

is minimised.

- We upweight errors arising from more commonly observed rows and cells.
  - This makes sense from the mean-variance relationship we mentioned before.

Matrix approximation view of correspondence analysis II

Since

$$\sum_{i=1}^{I}\sum_{j=1}^{J}\frac{(p_{ij}-\hat{p}_{ij})^2}{r_i c_j} = \mathrm{tr}[(\mathbf{D}_r^{-1/2}(\mathbf{P}-\hat{\mathbf{P}})\mathbf{D}_c^{-1/2})(\mathbf{D}_r^{-1/2}(\mathbf{P}-\hat{\mathbf{P}})\mathbf{D}_c^{-1/2})'],$$

we have that

$$\begin{aligned}\sum_{i=1}^{I}\sum_{j=1}^{J}\frac{(p_{ij}-\hat{p}_{ij})^2}{r_i c_j} &= \mathrm{tr}[(\mathbf{D}_r^{-1/2}\mathbf{P}\mathbf{D}_c^{-1/2}-\mathbf{D}_r^{-1/2}\hat{\mathbf{P}}\mathbf{D}_c^{-1/2})(\mathbf{D}_r^{-1/2}\mathbf{P}\mathbf{D}_c^{-1/2}-\mathbf{D}_r^{-1/2}\hat{\mathbf{P}}\mathbf{D}_c^{-1/2})'],\\ &= \mathrm{tr}[(\mathbf{D}_r^{-1/2}\mathbf{P}\mathbf{D}_c^{-1/2}-\hat{\mathbf{P}}^*)(\mathbf{D}_r^{-1/2}\mathbf{P}\mathbf{D}_c^{-1/2}-\hat{\mathbf{P}}^*)'],\end{aligned}$$

,

where $\hat{\mathbf{P}}^* = \mathbf{D}_r^{-1/2}\hat{\mathbf{P}}\mathbf{D}_c^{-1/2}$.

- Thus the weighted least squares problem is essentially the same as an unweighted least squares problem, which we know how to solve - using the SVD on $\mathbf{D}_r^{-1/2}\mathbf{P}\mathbf{D}_c^{-1/2}$.

Results from matrix approximation view I

1. The reduced rank s approximation to $\mathbf{P}$ is given by

$$\sum_{k=1}^{s} \tilde{\lambda}_k (\mathbf{D}_r^{1/2} \tilde{\mathbf{u}}_k)(\mathbf{D}_c^{1/2} \tilde{\mathbf{v}}_k)',$$

where $\tilde{\lambda}_k$, $\tilde{\mathbf{u}}_k$ and $\tilde{\mathbf{v}}_k$ arise from the SVD of $\mathbf{D}_r^{-1/2}\mathbf{P}\mathbf{D}_c^{-1/2}$ and the approximation error is $\sum_{k=s+1}^{J} \tilde{\lambda}_k^2$.

2. We always have that

$$\tilde{\lambda}_k (\mathbf{D}_r^{1/2} \tilde{\mathbf{u}}_1)(\mathbf{D}_c^{1/2} \tilde{\mathbf{v}}_1) = \mathbf{r}\mathbf{c}'.$$

Results from matrix approximation view II

3. The reduced rank $K > 1$ approximation to $\mathbf{P} - \mathbf{r}\mathbf{c}'$ is given by

$$\sum_{k=1}^{K} \lambda_k (\mathbf{D}_r^{1/2}\mathbf{u}_k)(\mathbf{D}_c^{1/2}\mathbf{v}_k)',$$

where λ_k, $\mathbf{u}_k$ and $\mathbf{v}_k$ arise from the SVD of $\mathbf{D}_r^{-1/2}(\mathbf{P} - \mathbf{r}\mathbf{c}')\mathbf{D}_c^{-1/2}$.

4. $\mathbf{D}_r^{-1/2}\mathbf{P}\mathbf{D}_c^{-1/2}$ and $\mathbf{D}_r^{-1/2}(\mathbf{P} - \mathbf{r}\mathbf{c}')\mathbf{D}_c^{-1/2}$ share singular vectors and singular values, in that $\tilde{\lambda}_{k+1} = \lambda_k$, $\tilde{u}_{k+1} = u_k$ and $\tilde{v}_{k+1} = v_k$.

Comment on the previous results

- It's a lot - but I mention them because they shed light on a couple of things in CA, rather than that you memorise them all.
- The main point is that CA is an application of PCA on a transformed matrix, which is equivalent to a least-squares problem whose solution we find by the singular -vectors and -values of the matrix of standardised residuals, $\mathbf{S} = \mathbf{D}_r^{-1/2}(\mathbf{P} - \mathbf{r}\mathbf{c}')\mathbf{D}_c^{-1/2}$.

Inertia

- For $\mathbf{S} = \mathbf{D}_r^{-1/2}(\mathbf{P} - \mathbf{r}\mathbf{c}')\mathbf{D}_c^{-1/2}$, total inertia is the weighted sum of squares of residuals:

$$\mathrm{tr}[\mathbf{S}\mathbf{S}'] = \sum_i \sum_j \frac{(p_{ij} - r_i c_j)^2}{r_i c_j} = \sum_{k=1}^{J-1} \lambda_k^2$$

- λ_k is the k-th singular value of $\mathbf{S}$
  - This follows from the fact that $\mathbf{r}\mathbf{c}'$ is in fact the best rank-one approximation to $\mathbf{P}$
    - It is therefore the first term in the SVD approximation, and the rank one SVD matrice's approximation error is equal to $\sum_{k=2}^{J} \tilde{\lambda}_k^2 = \sum_{k=1}^{J-1} \lambda_k^2$.
- The inertia captured by the first s components represents the variation captured in $\mathbf{S}$, and the proportion of variation captured is given by $(\sum_{k=1}^{s} \lambda_k^2)/(\sum_{k=1}^{J-1} \lambda_k^2)$.

Examinig the raw data using CA concepts

```
> CrossTable(smokelong$Rank, smokelong$smoke)

   Cell Contents
|-------------------------|
|                       N |
| Chi-square contribution |
|           N / Row Total |
|           N / Col Total |
|         N / Table Total |
|-------------------------|

Total Observations in Table:  193

                | smokelong$smoke
smokelong$Rank  |         1 |         2 |         3 |         4 | Total
----------------|-----------|-----------|-----------|-----------|------
              1 |         4 |         2 |         3 |         2 |    11
                |     0.079 |     0.124 |     0.081 |     0.232 |
                |     0.364 |     0.182 |     0.273 |     0.182 |     0.057
             SM |     0.066 |     0.044 |     0.048 |     0.080 |
                |     0.021 |     0.010 |     0.016 |     0.010 |
----------------|-----------|-----------|-----------|-----------|------
                |         4 |         3 |         7 |         4 |    18
             JM |     0.502 |     0.341 |     0.256 |     1.194 |
                |     0.222 |     0.167 |     0.389 |     0.222 |     0.093
                |     0.066 |     0.067 |     0.113 |     0.160 |
                |     0.021 |     0.016 |     0.036 |     0.021 |
----------------|-----------|-----------|-----------|-----------|------
              3 |        25 |        10 |        12 |         4 |    51
                |     4.893 |     0.301 |     1.173 |     1.028 |
                |     0.490 |     0.196 |     0.235 |     0.078 |     0.264
             SE |     0.410 |     0.222 |     0.194 |     0.160 |
                |     0.130 |     0.052 |     0.062 |     0.021 |
----------------|-----------|-----------|-----------|-----------|------
              4 |        18 |        24 |        33 |        13 |    88
                |     3.463 |     0.591 |     0.792 |     0.225 |
             JE |     0.205 |     0.273 |     0.375 |     0.148 |     0.456
                |     0.295 |     0.533 |     0.532 |     0.520 |
                |     0.093 |     0.124 |     0.171 |     0.067 |
----------------|-----------|-----------|-----------|-----------|------
              5 |        10 |         6 |         7 |         2 |    25
                |     0.557 |     0.005 |     0.132 |     0.474 |
            SEC |     0.400 |     0.240 |     0.280 |     0.080 |     0.130
                |     0.164 |     0.133 |     0.113 |     0.080 |
                |     0.052 |     0.031 |     0.036 |     0.010 |
----------------|-----------|-----------|-----------|-----------|------
   Column Total |        61 |        45 |        62 |        25 |   193
                |     0.316 |     0.233 |     0.321 |     0.130 |
----------------|-----------|-----------|-----------|-----------|------
```

$$\left(\frac{(o_{ij} - e_{ij})}{\sqrt{e_{ij}}}\right)^2$$

Third row = row profile=row percentages =distribution of row frequencies across columns

Fourth entry in every column cell = column profiles = column percentages=distribution of column frequencies across rows

Row margins = percentage of overall mass/total accounted for by each row. So JE and SE contribute more than other rows.

Column margins = percentage of overall mass/total accounted for by each column. Even distribution across columns, except for column 4.

Calculating the solution to the least-squares problem

```
> #CA from first principles
> N<-smoke> N
   none light medium heavy
SM    4     2      3     2
JM    4     3      7     4
SE   25    10     12     4
JE   18    24     33    13
SC   10     6      7     2
> P<-N/sum(N)
> P
         none      light     medium      heavy
SM 0.02072539 0.01036269 0.01554404 0.01036269
JM 0.02072539 0.01554404 0.03626943 0.02072539
SE 0.12953368 0.05181347 0.06217617 0.02072539
JE 0.09326425 0.12435233 0.17098446 0.06735751
SC 0.05181347 0.03108808 0.03626943 0.01036269
> rm<-apply(P,1,sum)
> rm
       SM        JM        SE        JE        SC
0.05699482 0.09326425 0.26424870 0.45595855 0.12953368
> cm<-apply(P,2,sum)
> cm
     none     light    medium     heavy
0.3160622 0.2331606 0.3212435 0.1295337
> Dr<-diag(rm)
> Dr
           [,1]       [,2]      [,3]      [,4]      [,5]
[1,] 0.05699482 0.00000000 0.0000000 0.0000000 0.0000000
[2,] 0.00000000 0.09326425 0.0000000 0.0000000 0.0000000
[3,] 0.00000000 0.00000000 0.2642487 0.0000000 0.0000000
[4,] 0.00000000 0.00000000 0.0000000 0.4559585 0.0000000
[5,] 0.00000000 0.00000000 0.0000000 0.0000000 0.1295337
> Dc<-diag(cm)
> Dc
          [,1]      [,2]      [,3]      [,4]
[1,] 0.3160622 0.0000000 0.0000000 0.0000000
[2,] 0.0000000 0.2331606 0.0000000 0.0000000
[3,] 0.0000000 0.0000000 0.3212435 0.0000000
[4,] 0.0000000 0.0000000 0.0000000 0.1295337
```

Show how 1 unit of mass is distributed across cells

Or across rows, = row margins or "masses"

Or across columns, = column margins or "masses"

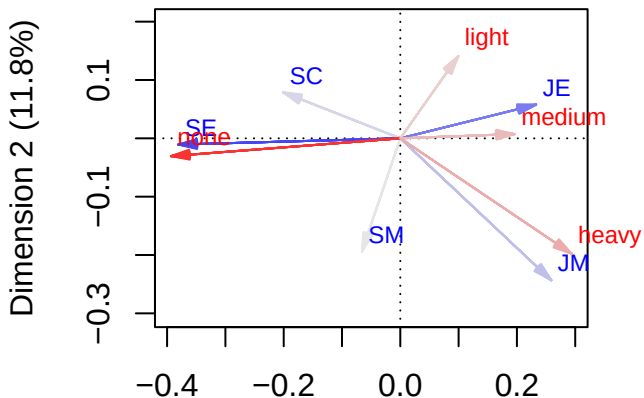
```
> S<-diag(sqrt(1/rm))%*%(as.matrix(P)-rm%*%t(cm))%*%diag(sqrt(1/cm))

> svdS<-svd(S)
> svdS
$d
[1] 2.734211e-01 1.000859e-01 2.033652e-02 5.571478e

$u
           [,1]        [,2]       [,3]        [,4]
[1,] -0.05742524 -0.46212293  0.8332653 -0.09239316
[2,]  0.28923816 -0.74239515 -0.5061482 -0.17736175
[3,] -0.71554563 -0.05475038 -0.1303234 -0.68022273
[4,]  0.57530335  0.38957951  0.1097504 -0.67979717
[5,] -0.26469630  0.28376408 -0.1430158  0.18756108

$v
           [,1]        [,2]       [,3]      [,4]
[1,] -0.8087001 -0.17127755 -0.0246170 0.5621941
[2,]  0.1756411  0.68056865  0.5223178 0.4828671
[3,]  0.4069601  0.04167443 -0.7151246 0.5667835
[4,]  0.3867013 -0.71116353  0.4638695 0.3599079

> smoke_F<-diag(1/sqrt(rm))%*%svdS$u%*%diag(svdS$d)
> smoke_F
           [,1]        [,2]        [,3]          [,4]
[1,] -0.06576838 -0.19373700  0.07098102 -2.156217e-17
[2,]  0.25895842 -0.24330457 -0.03370519 -3.235734e-17
[3,] -0.38059489 -0.01065991 -0.00515575 -7.372506e-17
[4,]  0.23295191  0.05774391  0.00330537 -5.609021e-17
[5,] -0.20108912  0.07891123 -0.00808107  2.903500e-17

> smoke_G<-diag(1/sqrt(cm))%*%svdS$v
> smoke_G
           [,1]        [,2]       [,3] [,4]
[1,] -1.4384714 -0.30465911 -0.04378737    1
[2,]  0.3637463  1.40943267  1.08170100    1
[3,]  0.7180168  0.07352795 -1.26172451    1
[4,]  1.0744451 -1.97595989  1.28885615    1
```

Taking SVD of weighted difference between observed and expected relative frequencies.

Principal coordinates for plotting, though they usually are scaled.

Displaying the results of a correspondence analysis

- We've discussed the first three steps in performing CA:
  1. Calculating the matrix of standardised residuals, $\mathbf{S} = \mathbf{D}_r^{-1/2}(\mathbf{P} - \mathbf{r}\mathbf{c}')\mathbf{D}_c^{-1/2}$.
  2. Calculating SVD of this (to obtain its least-squares approximation).
  3. Assessing the quality of the dimensionality reduction (via inertia).
- We now turn our attention to to displaying the rows and columns:



Choosing coordinate scales

- A biplot is a graphical display of a matrix $\mathbf{X}_{m\times n}$ such that

$$\mathbf{X}_{m\times n} = \mathbf{F}_{m\times k}(\mathbf{G}_{n\times k})' \text{ for } k \leq \min(m, n),$$

where each row of $\mathbf{F}$ is a lower-dimensional representation of a row in $\mathbf{X}$ and each column of $\mathbf{G}$ is a lower-dimensional representation of a column in $\mathbf{X}$.

- Here we term $\mathbf{F}$ and $\mathbf{G}$ the *row* and *column* coordinates, respectively.
- Clearly, in our case $\mathbf{X} = \mathbf{S} = \mathbf{D}_r^{-1/2}(\mathbf{P} - \mathbf{rc}')\mathbf{D}_c^{-1/2}$.

Principal vs standard coordinates

- We need to choose the scaling for our row coordinates. Typical choices:
  - *Principal* coordinates:
    - Rows: $\mathbf{F} = \mathbf{D}_r^{-1/2}\mathbf{U}\mathbf{\Lambda}$
    - Columns: $\mathbf{G} = \mathbf{D}_c^{-1/2}\mathbf{V}\mathbf{\Lambda}$
  - *Standard* coordinates:
    - Rows: $\mathbf{F} = \mathbf{D}_r^{-1/2}\mathbf{U}$
    - Columns: $\mathbf{G} = \mathbf{D}_c^{-1/2}\mathbf{V}$
- When rows are plotted using principal coordinates, the χ^2 distance between the rows is optimally displayed. Similarly for columns.

Symmetric vs asymmetric biplots

- In symmetric biplots, the both rows and columns are plotted using principal coordinates, or both rows and columns are plotted using standard coordinates.
  - This is great for displaying relationships between rows, or between columns. But:
    - Relationships between rows and columns are not necessarily displayed correctly.
    - It's not a true biplot, as $\mathbf{X}$ is not even approximately equal to $\mathbf{FG}'$.
- In asymmetric biplots, one uses principal coordinates and the other uses standard coordinates.
  - The motivation is that the relationships between rows and columns are more accurately displayed.
  - However:
    - The standard and principal coordinates may be on fairly different scales, depending on the size of the singular values.
    - Neither distances between rows nor distances between columns are optimally displayed.
- However, at the end of the day it's all quite fuzzy as even principal coordinates are approximations.
  - It seems to me like dividing Λ up between the row and column coordinates (e.g. $\Lambda^{0.5}$ for both) is the best option unless you have a particular interest in either the rows or columns.

Terminology for scaling choices:

- Both principal: symmetric
- Row principal and column standard: row-principal
- Column principal and row standard: column-principal

`ca.plot` function

Example: symmetric plot

Symmetric Plots:

NORMALIZATION of coordinates determines whether and how the similarity of the row categories, the similarity of the column categories and the relationship between the row and column variables can be interpreted in terms of the row and column coordinates and the origin of the plot.

The Euclidean distance between the row points approximates the chi-squared distances between the corresponding row profiles (i.e., the distributions on the column variables are similar). . So categories mapped close together have similar row profiles

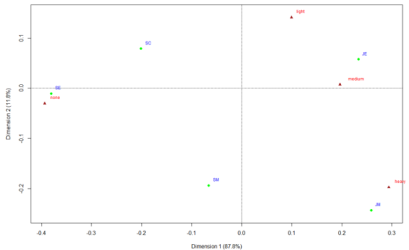
The Euclidean distance between a row point and the origin approximates the chi-square distance from the row profile to the row centroid, indicating how different a category is from the population.

Similarly for column points.

Cannot interpret distances between rows and columns except in a very general sense.

> plot(ca(smoke),map="symmetric",col=c("green","brown"))

- Rows and columns plotted using principal coordinates but scaled so that each have variance equal to singular values.
- Can interpret distances between rows and distances between columns but not distances between rows and columns.



→ First axis contrasts “none” to other smoking categories
→ First axis contrasts SE to JE&JM
→ SE lies in proximate area to “none”
→ JE lies in proximate area to “medium”
→ JM lies in proximate area to “heavy”

But cannot interpret actual distances between rows and cols

Example: asymmetric plot I

Asymmetric biplots

ROWPRINCIPAL
You can choose to plot the rows using principal coordinates and the columns as scaled standard coordinates. This is referred to as a row-preserving metric and represent the columns in row space. Distances between columns will not be correct.

COLUMN PRINCIPAL
You can choose to plot the columns using principal coordinates and the rows as scaled standard coordinates. This is referred to as a column-preserving metric and represent the rows in column space. Distances between rows will not be correct.

The angles between arrows representing rows and columns give an indication of associations. The more acute, the more strongly associated.

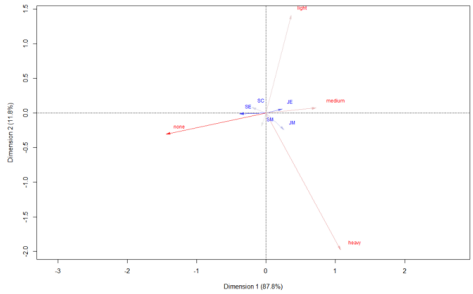
A further scaling according to Greenacre allows for interpretation of contribution of columns or rows to dimensions.

Example: asymmetric plot II

Row principal plots:

```
> plot(ca(smoke), mass = TRUE, contrib = "absolute",map = "rowprincipal", arrows = c(TRUE, TRUE))
```

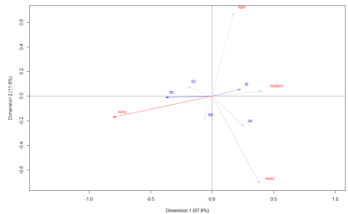
```
Rows in principal coordinates, column in standard coordinates
```



Based on angles.
So SE close to “none”.
And JE close to “medium”.
Whereas SM and JM closer to “heavy”.

```
> plot(ca(smoke), mass = TRUE, contrib = "absolute",
map = "rowgreen", arrows = c(TRUE, TRUE))
```

```
Rows in principal and columns in standard coordinates,
columns scaled to reflect contribution to inertia through
distance from origin. Allows interpretation of
contribution of columns to axes.
```



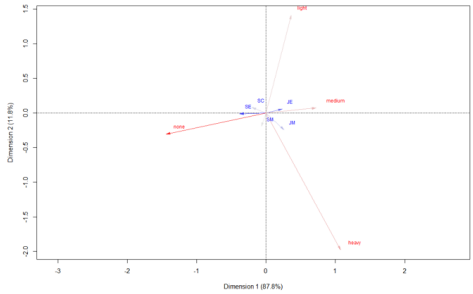

```
“none and “medium” close to dimension 1
“light” close to dimension 2
Column points closer to origin contributed less than
column point further away.
```

Example: asymmetric plot III

Row principal plots:

```
> plot(ca(smoke), mass = TRUE, contrib = "absolute",map = "rowprincipal", arrows = c(TRUE, TRUE))
```

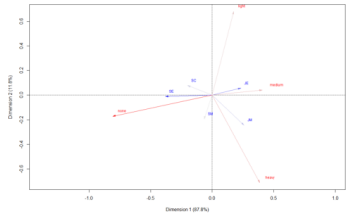
```
Rows in principal coordinates, column in standard coordinates
```



Based on angles.
So SE close to “none”.
And JE close to “medium”.
Whereas SM and JM closer to “heavy”.

```
> plot(ca(smoke), mass = TRUE, contrib = "absolute",
map = "rowgreen", arrows = c(TRUE, TRUE))
```

```
Rows in principal and columns in standard coordinates,
columns scaled to reflect contribution to inertia through
distance from origin. Allows interpretation of
contribution of columns to axes.
```




```
“none and “medium” close to dimension 1
“light” close to dimension 2
Column points closer to origin contributed less than
column point further away.
```

Example: quality of approximation

```
> summary(ca(smoke))

Principal inertias (eigenvalues):

 dim    value      %    cum%   scree plot
 1      0.074759  87.8  87.8   ***********************
 2      0.010017  11.8  99.5   ***
 3      0.000414   0.5 100.0
        -------- -----
 Total: 0.085190 100.0


Rows:
     name   mass  qlt  inr    k=1 cor  ctr    k=2 cor  ctr
1 |   SM |   57  893   31 |  -66  92    3 | -194 800  214 |
2 |   JM |   93  991  139 |  259 526   84 | -243 465  551 |
3 |   SE |  264 1000  450 | -381 999  512 |  -11   1    3 |
4 |   JE |  456 1000  308 |  233 942  331 |   58  58  152 |
5 |   SC |  130  999   71 | -201 865   70 |   79 133   81 |

Columns:
     name   mass  qlt  inr    k=1 cor  ctr    k=2 cor  ctr
1 | none |  316 1000  577 | -393 994  654 |  -30   6   29 |
2 | lght |  233  984   83 |   99 327   31 |  141 657  463 |
3 | medm |  321  983  148 |  196 982  166 |    7   1    2 |
4 | hevy |  130  995  192 |  294 684  150 | -198 310  506 |
>
```

λ^2 *analysis*

Row totals*1000

Quality in each dimension = the correlation of point with dimension

Ctr refers to contribution of each row/ column to specific dimension

Qlt = Quality = $\frac{\textit{squared distance of point from origin in 2 dimensions}}{\textit{squared distance of point from origin in maximum \# dimensions}}$

inr=Relative Inertia
=proportion of inertia accounted for by respective point

$k = 1$ & $k = 2$ are the plotting coordinates

SM not well presented by dimension 1 because cor very low
SE not well presented by dimension 2 because cor very low

Multiple correspondence analysis (MCA)

For multilevel contingency tables when you are cross-tabulating more than two variables.
There are different approaches for adjusting Correspondence Analysis to cope with this, including

1. CA on an indicator matrix
2. CA on a Burt matrix
3. Adjusted MCA through rescaling
4. Joint Correspondence Analysis

For example, consider 10 observations on 3 categorical variables, w , x and y, each with 2 categories:
Then you can form the indicator matrix as follows:

$$Z = \begin{array}{c} \\ 1 \\ 2 \\ 3 \\ 4 \\ 5 \\ 6 \\ 7 \\ 8 \\ 9 \\ 10 \end{array} \begin{array}{c} \begin{array}{cccccc} w_1 & w_2 & x_1 & x_2 & y_1 & y_2 \end{array} \\ \begin{pmatrix} 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 1 & 0 \\ 1 & 0 & 0 & 1 & 0 & 1 \\ 1 & 0 & 0 & 1 & 0 & 1 \\ 1 & 0 & 1 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 & 0 \\ 1 & 0 & 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 1 & 0 \end{pmatrix} \end{array}$$

And the Burt matrix corresponding to Z is:

There were 7 observations with w_1=1, 4 observations with w_1=1 and x_1=1, etc.

$$B = Z^T Z = \begin{array}{c} \\ w_1 \\ w_2 \\ x_1 \\ x_2 \\ y_1 \\ y_2 \end{array} \begin{array}{c} \begin{array}{cccccc} w_1 & w_2 & x_1 & x_2 & y_1 & y_2 \end{array} \\ \begin{pmatrix} 7 & 0 & 4 & 3 & 3 & 4 \\ 0 & 3 & 1 & 2 & 3 & 0 \\ 4 & 1 & 5 & 0 & 3 & 2 \\ 3 & 2 & 0 & 5 & 3 & 2 \\ 3 & 3 & 3 & 3 & 6 & 0 \\ 4 & 0 & 2 & 2 & 0 & 4 \end{pmatrix} \end{array}$$

That summarises the number of observations with the pairwise frequencies.

MCA: example introduction

wg93 {ca}R Documentation
International Social Survey Program on Environment 1993

This data frame contains 871 records of four questions on attitude towards science with responses on a five-point scale (1=agree strongly to 5=disagree strongly) and three demographic variables (sex, age and education).

The questions were:
A: We believe too often in science, and not enough in feelings and faith.
B: Overall, modern science does more harm than good.
C: Any change humans cause in nature, no matter how scientific, is likely to make things worse.
D: Modern science will solve our environmental problem with little change to our way of life.

Source: ISSP (1993). International Social Survey Program: Environment. http://www.issp.org

```
> data("wg93")
> head(wg93)
  A B C D sex age edu
1 2 3 4 3   2   2   3
2 3 4 2 3   1   3   4
3 2 3 2 4   2   3   2
4 2 2 2 2   1   2   3
5 3 3 3 3   1   5   2
6 3 4 4 5   1   3   2
```

So we have 4 categorical variables each with 5 levels,
Plus some additional demographic characteristics.
The 4 categorical variables can each turn into 5 binary indicator variables, for example A1(0/1), A2(0/1),A3(0/1),A4(0/1),A5(0/1), etc.
The first observation will have A2=1 and all the other A-variables =0, etc.

MCA: example application

```
> summary(mica(wg93[,1:4],lambda="adjusted"))

Principal inertias (eigenvalues):

 dim    value      %    cum%   scree plot
 1      0.076455  44.9  44.9   ************
 2      0.058220  34.2  79.1   **********
 3      0.009197   5.4  84.5   **
 4      0.005670   3.3  87.8   *
 5      0.001172   0.7  88.5
 6      7e-06000   0.0  88.5
        -------- -----
 Total: 0.170246
```

Use mica function with "adjusted" option

First 2 dimensions account for 79% of associations among responses to 4 questions.

Now only have column variables since all variables have been turned into column variables.

Some relatively low correlations of columns with dimensions 1 and 2

Columns:

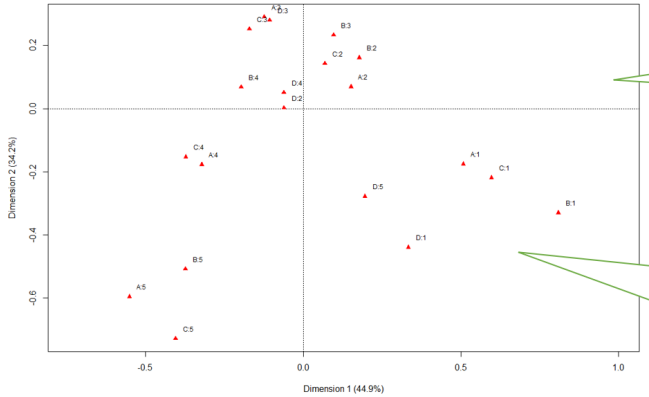
	name	mass	qlt	inr	k=1 cor	ctr	k=2 cor	ctr
1	A:1	34	963	55	508 860	115	-176 103	18
2	A:2	92	659	38	151 546	28	69 113	7
3	A:3	59	929	47	-124 143	12	289 786	84
4	A:4	51	798	50	-322 612	69	-178 186	28
5	A:5	14	799	60	-552 369	55	-596 430	84
6	B:1	20	911	62	809 781	174	-331 131	38
7	B:2	50	631	47	177 346	21	161 285	22
8	B:3	59	806	45	96 117	7	233 690	55
9	B:4	81	620	41	-197 555	41	68 65	6
10	B:5	40	810	60	-374 285	74	-509 526	179
11	C:1	44	847	60	597 746	203	-219 101	36
12	C:2	91	545	38	68 101	6	143 444	32
13	C:3	57	691	48	-171 218	22	252 473	62
14	C:4	44	788	52	-373 674	80	-153 114	18
15	C:5	15	852	60	-406 202	32	-728 650	136
[illegible]	D:1	17	782	56	333 285	25	-440 497	57
17	D:2	67	126	42	-61 126	3	2 0	0
18	D:3	58	688	48	-106 87	9	280 601	78
19	D:4	65	174	43	-61 103	3	51 71	3
20	D:5	43	869	50	196 288	22	-278 581	57

For the BURT matrix, the main diagonal is a cross-tabulation of each variable with itself, thus the solution will overestimate the total inertia.
To correct for this, MCA rescales the coordinates to best fit the pairwise cross-tabulations on the off-diagonals of the Burt matrix. Use the lambda-"adjusted" option which is also the default option.
Another option is to use Joint Correspondence Analysis that uses a different algorithm to find an optimal least squares fit to the off-diagonal elements.

D3 and D4 not well represented in first 2 dimensions

MCA: example plot

```
plot(mjca(wg93[,1:4]), mass = TRUE, contrib = "absolute",map = "colprincipal", arrows = c(TRUE, TRUE))
```



All column variables so can interpret proximity to each other. Horse shoe effect often seen

Looks as if first dimension orders level of response to all questions, grouping 5's together, etc to 1's on right hand side. And second dimension contrasts extreme responses (1 and 5) to more moderate responses.

Summary

To Summarize:
CA is a method for displaying the associations between levels of categorical variables in low dimensions.

It does so by decomposing the inertia, a transformation of the Chi-Square statistic, which is a measure of the amount of information contained in the cross tabulation of the categorical variables.

Starting with a weighted least squares problem, you end up having to take the SVD of $D_r^{-\frac{1}{2}}(P - rc')D_c^{-1/2}$.

From there you can calculate row coordinates and column coordinates in lower dimensions, either Principal coordinates of rows and columns $F = D_r^{-1/2}U\Lambda, G = D_c^{-1/2}V\Lambda$ or Standardized coordinates of rows: $X = D_r^{-1/2}U$ and columns $Y = D_c^{-1/2}V$.

Different combinations of these lead to different biplots:
Symmetric biplot plots rows and columns using principal coordinates. You can interpret distance between rows or between columns but can only make general statements about association between rows and columns.
For Asymetric biplots, you have to choose whether you plot rows using principal coordinates and columns using scaled standard coordinates or vice versa. For either, the best is to interpret angles between arrows to row and column points.

DO need to take into account quality of row or column profiles in low dimensions:
Qlt = Quality = $\frac{squared\ distance\ of\ point\ from\ origin\ in\ 2\ dimensions}{squared\ distance\ of\ point\ from\ origin\ in\ maximum\ \#\ dimensions}$
inr=Relative Inertia=proportion of inertia accounted for by respective point
Cor=Quality in each dimension = the correlation of point with dimension

MCA for more than 2 categorical variables best done by analysing “Burt” matrix.