# STAT 441: Lecture 26 Multivariate analysis with qualitative variables Correspondence analysis

Venables and Ripley, 11.4

# $\chi^2$ -statistic

Let us, say, test independence in a  $r \times c$  contingency table. The probabilities of observations in cells are  $p_{ij}$ ; under the hypothesis of independence,  $p_{ij} = p_{i\cdot}p_{\cdot j}$ , where  $p_{i\cdot}$  and  $p_{\cdot j}$  are column and row sums - marginal probabilities.

We observe cells frequencies  $n_{ij}$ ; the estimates for  $p_{i\cdot}$ , and  $p_{\cdot j}$  are  $\widehat{p}_{i\cdot} = n_{i\cdot}/n$  and  $\widehat{p}_{\cdot j} = n_{\cdot j}/n$ , respectively; n is the total number of observations. Under the hypothesis of independence, the estimate for the cell probability is  $\widehat{p}_{ij} = \widehat{p}_{i\cdot}\widehat{p}_{\cdot j} = (n_{i\cdot}/n)(n_{\cdot j}/n)$  and therefore the predicted number of observations is  $P = n \cdot \frac{n_i \cdot n_{\cdot j}}{n^2} = \frac{n_i \cdot n_{\cdot j}}{n}$  and the observed number is  $O = n_{ij}$ 

The test statistic can be written as  $\sum_{\text{all cells}} \frac{(O_k - P_k)^2}{P_k}$ 

We use  $\chi^2$  distribution with (r-1)(c-1) degrees of freedom to assess how large is this statistic is large enough, via its right tail value, which gives the p-value for the hypothesis of independence. If this p-value is low, we may reject the hypothesis - but what then?

Note: the statistic sums squares of "Pearson residuals"  $\frac{O_k - P_k}{\sqrt{P_k}}$ 

### Correspondence analysis

Suppose that E is the matrix formed from  $n_{ij}/n$  (the estimates of cell probabilities not assuming the independence hypothesis) and R, C are diagonal matrices formed from vectors r and c, with elements  $r_i = n_{i\cdot}/n$  and  $c_j = n_{\cdot j}/n$ , respectively.

Consider the matrix  $R^{-1/2}EC^{-1/2}$  (it is easy to form the square roots of diagonal matrices with positive elements). This matrix has elements

 $\frac{e_{ij}}{\sqrt{r_i c_j}}$ 

SVD of this matrix can be viewed as returning "scores giving maximal correlations for rows and columns". The largest singular value is always one, corresponding to constant scores; hence we dismiss it, and look only for nontrivial solutions corresponding to singular values beginning with the second largest. That is, we form the SVD of

$$R^{-1/2}(E - rc^{T})C^{-1/2}$$

instead, and then we may take first one or two singular values.

# Aggregated hair/eye color data: r = c = 4

```
> haireye=apply(HairEyeColor,1:2,sum)
> haireye
      Eye
Hair
       Brown Blue Hazel Green
          68
               20
 Black
                     15
                            5
         119 84
                     54
                           29
 Brown
 Red
          26 17
                           14
                     14
           7
             94
                           16
  Blond
                     10
> r = apply(haireye,1,sum)/sum(haireye)
> c = apply(haireye,2,sum)/sum(haireye)
> E = haireye/sum(haireye)
```

```
> svd(diag(1/sqrt(r)) %*% E %*% diag(1/sqrt(c)))
$d
[1] 1.00000000 0.45691646 0.14908593 0.05097489
$u
           [,1]
                       [,2]
                                  [,3]
                                             [,4]
[1,] -0.4271211  0.47166009  0.6154461  0.4651134
[2,] -0.6950598  0.22552151 -0.1522951 -0.6654608
[3,] -0.3463126  0.09817011 -0.7424993  0.5649115
[4,] -0.4631706 -0.84678181 0.2161646 0.1473309
$v
           [,1]
                      [,2]
                                 [,3]
                                             [,4]
[1,] -0.6096078  0.6566258  0.3611439  0.25844921
[2,] -0.6026406 -0.7220003 0.3353208 -0.05567605
[3,] -0.3963516  0.1844169 -0.4450167 -0.78157274
[4,] -0.3287980 -0.1163980 -0.7477267 0.56502056
> svd(diag(1/sqrt(r)) %*% (E - r %*% t(c)) %*% diag(1/sqrt(c)))
$d
[1] 4.569165e-01 1.490859e-01 5.097489e-02 2.929785e-19
$u
                       [,2]
                                  [,3]
            [,1]
                                            [,4]
[1,] -0.47166009   0.6154461 -0.4651134   0.4271211
[2,] -0.22552151 -0.1522951 0.6654608 0.6950598
[3,] -0.09817011 -0.7424993 -0.5649115 0.3463126
[4,] 0.84678181 0.2161646 -0.1473309 0.4631706
$v
           [,1]
                      [,2]
                                  [,3]
                                             [,4]
[1,] -0.6566258  0.3611439 -0.25844921 -0.6096078
[2,] 0.7220003 0.3353208 0.05567605 -0.6026406
[3,] -0.1844169 -0.4450167 0.78157274 -0.3963516
[4,] 0.1163980 -0.7477267 -0.56502056 -0.3287980
```

### Mechanized way

```
> library(MASS)
> hc1 = corresp(haireye)
First canonical correlation(s): 0.4569165
Hair scores:
    Black Brown
                      R.e.d
                                    Blond
-1.1042772 -0.3244635 -0.2834725 1.8282287
Eye scores:
    Brown
                Blue
                          Hazel
                                    Green
-1.0771283 1.1980612 -0.4652862 0.3540108
> hc2 = corresp(haireye,nf=2)
First canonical correlation(s): 0.4569165 0.1490859
Hair scores:
           [,1] \qquad [,2]
Black -1.1042772 1.4409170
Brown -0.3244635 -0.2191109
Red -0.2834725 -2.1440145
Blond 1.8282287 0.4667063
Eye scores:
           [,1]
                      [,2]
Brown -1.0771283 0.5924202
Blue 1.1980612 0.5564193
Hazel -0.4652862 -1.1227826
Green 0.3540108 -2.2741218
```

### Interpretation I

```
Can be thought of as analysis of the \chi^2 statistic for
independence, because the elements of the matrix
R^{-1/2}(E-rc^{T})C^{-1/2} are Pearson residuals, up to a factor \sqrt{n}.
> class(haireye)='table'
> matrix(residuals(glm(Freq~Hair+Eye,family=poisson,
data=as.data.frame(haireye)),type='pearson'),4,4)/sqrt(sum(haireye))
             \lceil .1 \rceil \qquad \lceil .2 \rceil
                                     [.3]
[1.] 0.180773066 -0.12615064 -0.01961905 -0.08029590
[2,] 0.050694815 -0.08012300 0.05561963 -0.01418351
[3,] -0.003081574 -0.07110772 0.03502737 0.09381990
[4,] -0.240474512  0.28973637 -0.09156384  0.02518174
> diag(1/sqrt(r)) %*% (E - r %*% t(c)) %*% diag(1/sqrt(c))
             [.1]
                        [.2]
                                     [,3]
[1,] 0.180773066 -0.12615064 -0.01961905 -0.08029590
[2,] 0.050694815 -0.08012300 0.05561963 -0.01418351
[3,] -0.003081574 -0.07110772 0.03502737 0.09381990
[4,] -0.240474512  0.28973637 -0.09156384  0.02518174
```

### Another interpretation - and plotting

Can be viewed also as a search for the linear combination giving maximal contingency ("correlation") - not accounting for the trivial constant solution

can be a comparison of distances between "profiles", rowwise or columnwise conditional distributions.

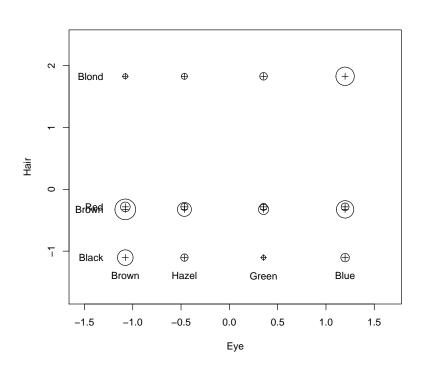
If the resulting SVD is  $U\Lambda V^T$ , then of interest are first columns of  $A=R^{-1/2}U\Lambda$  and  $B=C^{-1/2}V\Lambda$ 

"Classical correspondence analysis": first two columns of A and B are plotted on the same figure. "Asymmetric approach" plots either first two columns of A with first two columns of  $C^{-1/2}V$  (rows) or B with first two columns of  $R^{-1/2}U$  (columns). Row plot can be viewed as that A is a convex combination of row profiles, given by  $C^{-1/2}V$ 

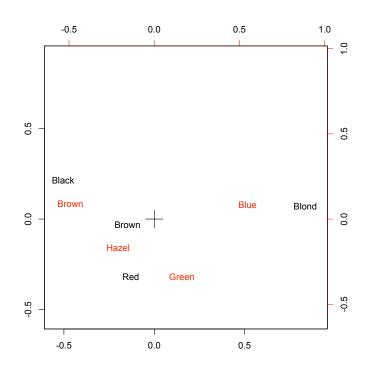
Inertia: the sum of squares of omitted singular values.

## Symmetric view

### First column

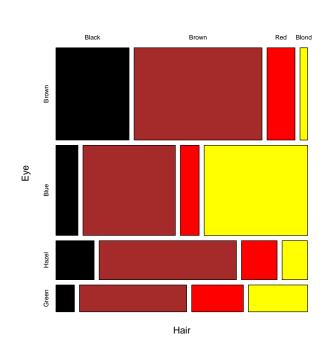


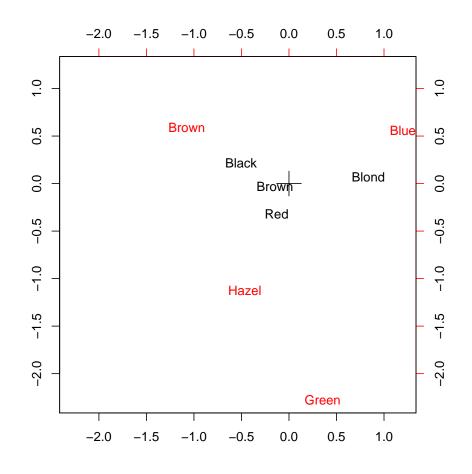
### First two columns



- > plot(hc2)
- > biplot(hc2)
- > biplot(hc2,xlim=c(-0.55,0.9),ylim=c(-0.55,0.9))

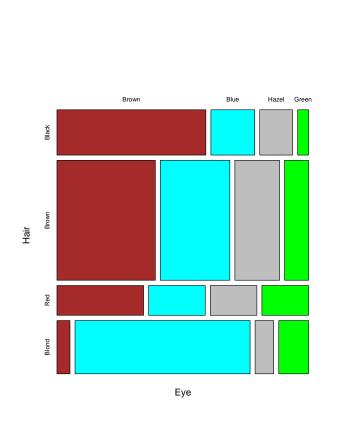
### Asymmetric view: rows

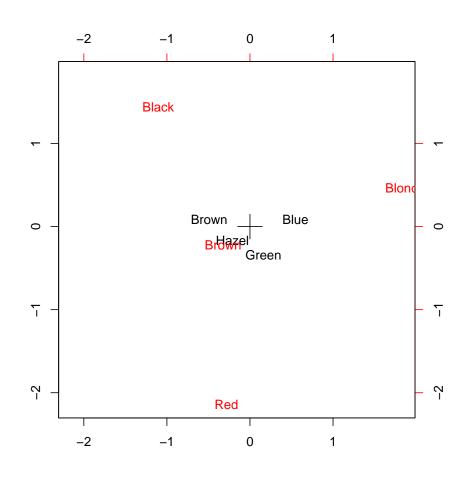




- > plot(hc2,type="rows")
- > biplot(hc2,type="rows")
- > mosaicplot(haireye,sort=c(2,1),dir=c('v','h'))

### Asymmetric view: columns





- > plot(hc2,type="columns")
- > biplot(hc2,type="columns")
- > mosaicplot(haireye,sort=c(1,2),dir=c('h','v'))