## Psych 6136: Correspondence analysis tutorial

This exercise invites you to carry out a correspondence analysis to examine the data on hair color and eye color from the lecture and the text (see: Example 6.1). The dataset is HairEyeColor in the datasets package. As you can see, it is a 4 x 4 x 2 table.

```
> data("HairEyeColor")
> str(HairEyeColor)
'table' num [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"
```

- We will just consider the relation between hair and eye color here. So as a first step, collapse this to a twoway table, haireye, by summing over Sex. [Hint: margin.table()]
- 2. Load the capackage, and perform a correspondence analysis on the haireye table, assigning the result to haireye.ca

```
library(ca)
haireye.ca <- ???
...</pre>
```

3. Examine the result you get by printing the haireye.ca object. What do the Principal inertias tell you? Interpret what you get from summary(), in particular the columns labeled mass and qlt. [Hint: read help(summary.ca)]

```
print(haireye.ca)
summary(haireye.ca)
```

4. Examine the components of the haireye.ca object. Which components give the CA scores on the dimensions for rows and columns?

names(haireye.ca)

5. Plot the haireye.ca object. Examine help (plot.ca) and find an argument to draw lines connecting the category points for hair and eye colors. What argument would you use to change the color of points to green and purple?

```
plot(haireye.ca, ???)
```

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6. Supplementary rows: In correspondence analysis you can include additional rows (or columns) which are treated as "supplementary", meaning that they are not used in the analysis, but can be projected into the correspondence analysis solution. Re-analyse the hair- eye-color table treating Sex as supplementary. The code below constructs the new table, adding the table of Sex x Hair to that of Eye x Hair.

```
eh <- margin.table(HairEyeColor, 2:1)  # Eye x Hair
sh <- margin.table(HairEyeColor, c(3,1))  # Sex x Hair
ehs <- rbind(eh, sh)</pre>
```

Figure out how to do a CA of the new ehs table, treating the last two rows as supplementary. Plot the result, and interpret the location of the points for Male and Female.