STAT 32950: Homework 4

Robert Winter

Table of Contents

1 Exercise 2: MANOVA and Confidence Region **1**
1.1 Part (a) . . . 2
1.1.1 Part (i) . . . 2
1.1.2 Part (ii) . . . 3
1.1.3 Part (iii) . . . 3
1.1.4 Part (iv) . . . 5
1.2 Part (b) . . . 5
1.3 Part (c) . . . 7
1.3.1 Part (i) . . . 7
1.3.2 Part (ii) . . . 7
1.3.3 Part (iii) . . . 9

2 Exercise 3: Multidimensional Scaling **10**
2.1 Part (a) . . . 10
2.2 Part (b) . . . 11
2.3 Part (c) . . . 13

3 Exercise 4: Correspondence Analysis **14**
3.1 Part (a) . . . 14
3.2 Part (b) . . . 16
3.3 Part (c) . . . 16
3.4 Part (d) . . . 17

1 Exercise 2: MANOVA and Confidence Region

Researchers have suggested that a change in skull size over time is evidence of the interbreeding of a resident population with immigrant populations. Four measurements were made of male Egyptian skulls for three different time periods: Period 1 is 4000 B.C., Period 2 is 3300 B.C., and Period 3 is 1850 B.C. The measured variables are

$$X_1 = \text{maximum breadth of skull (mm)}$$
$$X_2 = \text{basibregmatic height of skull (mm)}$$
$$X_3 = \text{basialveolar length of skull (mm)}$$
$$X_4 = \text{nasal height of skull (mm)}$$

The data are in `T6-13.DAT`.

```
skull =
 ↪  read.table("C:/Users/rewin/OneDrive/Documents/STAT_32950/Homework/HW4/T6-13.DAT")
colnames(skull) = c("x1", "x2", "x3", "x4", "period")
skull = skull %>%
  mutate(period = as.factor(period))
```

1.1 Part (a)

Conduct a one-way MANOVA (periods as "treatments") of the Egyptian skull data.

1.1.1 Part (i)

State the numerical values of p (the number of component variables), g (the number of samples or treatments), and sample sizes n_i for $i = 1, \ldots, g$.

```
skull %>% group_by(period) %>% summarize(n = n())
```

```
# A tibble: 3 x 2
  period     n
  <fct>  <int>
1 1         30
2 2         30
3 3         30
```

In this case, we have:

- $p = 4$ (corresponding to the four different measurements for each skull),
- $g = 3$ (corresponding to the three different time periods), and
- $n_1 = n_2 = n_3 = 30$ (since we have data for 30 skulls from each of the three time periods, making this a balanced dataset).

1.1.2 Part (ii)

Write down the null hypothesis H_0 that the MANOVA table is used for (define your notations if you use any).

For each time period $t \in \{1, 2, 3\}$ and for each skull $j \in \{1, \dots, 30\}$ within each of those time periods, let

$$X_{tj} = \mu + \tau_t + \varepsilon_{tj},$$

where X_{tj} is a vector consisting of the four measurements for the j^{th} skull in time period t, μ is a vector consisting of the population mean skull measurements across all three time periods, τ_t is the average deviation from the total population mean skull measurements among the sub-population of skulls from time period t, and ε_{tj} is the j^{th} skull from time period t's personal deviation from the mean skull measurements associated with its time period (i.e., $\mu + \tau_t$).

The MANOVA table will test the null hypothesis

$$H_0 : \tau_1 = \tau_2 = \tau_3 = \mathbf{0},$$

where we have imposed the usual constraint that $\tau_1 + \tau_2 + \tau_3 = 0$ for identification purposes. Intuitively, the MANOVA table tests the null hypothesis that, on average, there are no differences between male Egyptians' skull measurements across the three time periods. Equivalently (since we have imposed the sum-zero constraint), the MANOVA table tests the null hypothesis that, on average, each time period has no effect on male Egyptians' skull measurements.

1.1.3 Part (iii)

Compute Wilks' Λ^* and the related F statistic under H_0 (ref. p. 303 Table 6.3 in Johnson & Wichern, 6th ed.). Use $\alpha = 0.05$ to conduct the hypothesis test and state your conclusion.

Using the `manova` function in R, we find that the between- and within-group matrices are (approximately) as follows:

```
q2manova = manova(cbind(skull$x1, skull$x2, skull$x3, skull$x4) ~ period,
                  data = skull)

B = summary(q2manova, test = "Wilks")$SS[1]$period %>% round(2)
W = summary(q2manova, test = "Wilks")$SS[2]$Residuals %>% round(2)

print("B = "); print(B)
```

```
[1] "B = "
```

```
        [,1]   [,2]    [,3]   [,4]
[1,]  150.20  20.30 -161.83   5.03
[2,]   20.30  20.60  -38.73   6.43
[3,] -161.83 -38.73  190.29 -10.86
[4,]    5.03   6.43  -10.86   2.02
```

```
print("W = "); print(W)
```

```
[1] "W = "
```

```
        [,1]   [,2]    [,3]   [,4]
[1,] 1785.40  172.5  128.97 289.63
[2,]  172.50 1924.3  178.80 171.90
[3,]  128.97  178.8 2153.00  -1.70
[4,]  289.63  171.9   -1.70 840.20
```

Thus, $|W| \approx 5.669 \times 10^{12}$, $|B+W| \approx 6.830 \times 10^{12}$, and so $\Lambda^* \approx \frac{5.879 \times 10^{12}}{6.830 \times 10^{12}} \approx 0.830$.

```
det(W); det(W+B); det(W)/det(W+B)
```

```
[1] 5.669254e+12
```

```
[1] 6.829577e+12
```

```
[1] 0.8301031
```

As shown in Table 6.3 of Johnson & Wichern, 6$^{\text{th}}$ ed., since $p = 4$ and $g = 3$, we have

$$\begin{aligned} \left(\frac{\sum_{t=1}^{3} n_t - p - 2}{p}\right)\left(\frac{1-\sqrt{\Lambda^*}}{\sqrt{\Lambda^*}}\right) &\sim F_{2p,2(\sum_{t=1}^{3} n_t - p - 2)} \\ \Rightarrow \left(\frac{(30+30+30)-4-2}{4}\right)\left(\frac{1-\sqrt{\Lambda^*}}{\sqrt{\Lambda^*}}\right) &\sim F_{2(4),2(30+30+30-4-2)} \\ \Rightarrow \frac{21(1-\sqrt{\Lambda^*})}{\sqrt{\Lambda^*}} &\sim F_{8,168} \end{aligned}$$

Our F statistic is therefore $\frac{21(1-\sqrt{\Lambda^*})}{\sqrt{\Lambda^*}} \approx \frac{21(1-\sqrt{0.830})}{\sqrt{0.830}} \approx 2.049$, and the associated p-value is $\mathbb{P}(F_{8,168} > 2.049) \approx 0.044 < 0.05$. Thus, at the $\alpha = 0.05$ level, we reject the null hypothesis

that, on average, there were no differences between male Egyptians' skull measurements across the three time periods in favor of the alternative hypothesis that male Egyptians' skull measurements were significantly different during at least one of the three time periods as compared to the remaining periods.

```
L = det(W)/det(W+B) # Wilks' Lambda
21*(1-sqrt(L))/sqrt(L) # F statistic
```

```
[1] 2.049063
```

```
1-pf(21*(1-sqrt(L))/sqrt(L), 8, 168) # p-value
```

```
[1] 0.04358321
```

1.1.4 Part (iv)

What are the assumptions on the data to make the hypothesis test valid?

For the hypothesis test to be valid, we must assume that $\varepsilon_{tj} \sim \text{iid } N_4(\mathbf{0}, \Sigma)\ \forall t \in \{1, 2, 3\}, j \in \{1, \dots, 30\}$, where ε_{tj} is defined as in Part (ii) above. That is, within each time period, we assume that each skull's 4-vector of residuals are independently and identically multivariate normally distributed. Moreover, we must also assume that each time periods' skulls have equal population covariance matrices.

1.2 Part (b)

Apply Hotelling's T^2 to determine which pair of time periods differ, treating each pair of time periods as two independent samples of equal covariance structure.

We perform three Hotelling's T^2 tests to evaluate differences in skull measurements between pairs of time periods.

- In our pairwise comparison of Periods 1 and 2, we recover a T^2 statistic of approximately 0.028 and a corresponding p-value of 0.814; there is *not* statistical evidence that the four skull measurements were significantly different among Egyptian males in Period 1 and those in Period 2.
- In our pairwise comparison of Periods 1 and 3, we recover a T^2 statistic of approximately 0.231 and a corresponding p-value of $0.020 < 0.05$. As such, there *is* statistical evidence of significant differences in the four skull measurements between Egyptian males in Period 1 and those in Period 3.

- In our pairwise comparison of Periods 2 and 3, we recover a T^2 statistic of approximately 0.234 and a corresponding p-value of $0.019 < 0.05$. As such, there *is* statistical evidence of significant differences in the four skull measurements between Egyptian males in Period 2 and those in Period 3.

Thus, Egyptian males who lived during Period 3 appear to be the "odd ones out," having significantly different skull measurements than their ancestors during Periods 1 and 2 (whose measurements were not significantly different from one another).

```
# Pairwise Comparison: Periods 1 and 2
periods12 = filter(skull, period != 3)
manova(cbind(periods12$x1, periods12$x2, periods12$x3, periods12$x4) ~
 ↪  period,
       data = periods12) %>%
  summary(test = "Hotelling")
```

```
          Df Hotelling-Lawley approx F num Df den Df Pr(>F)
period     1         0.028462  0.39135      4     55 0.8139
Residuals 58
```

```
# Pairwise Comparison: Periods 1 and 3
periods13 = filter(skull, period != 2)
manova(cbind(periods13$x1, periods13$x2, periods13$x3, periods13$x4) ~
 ↪  period,
       data = periods13) %>%
  summary(test = "Hotelling")
```

```
          Df Hotelling-Lawley approx F num Df den Df  Pr(>F)
period     1          0.23087   3.1744      4     55 0.02035 *
Residuals 58
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Pairwise Comparison: Periods 2 and 3
periods23 = filter(skull, period != 1)
manova(cbind(periods23$x1, periods23$x2, periods23$x3, periods23$x4) ~
 ↪  period,
       data = periods23) %>%
  summary(test = "Hotelling")
```

```
          Df Hotelling-Lawley approx F num Df den Df  Pr(>F)
period     1           0.2342   3.2203      4     55 0.01908 *
```

```
Residuals 58
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

1.3 Part (c)

Assume that you would like to construct confidence intervals for pairwise differences of component means simultaneously for all component pairs and all time periods.

1.3.1 Part (i)

How many simultaneous confidence intervals do you need to construct? (Show how you get the number.)

Since there are three time periods, there are $\binom{3}{2} = \frac{3!}{2!(3-2)!} = 3$ possible pairwise comparisons of time periods. Therefore, since there are four variables in total, we must construct $3 \times 4 = 12$ simultaneous confidence intervals.

1.3.2 Part (ii)

Based on Part (i), there are quite a few (simultaneous) confidence intervals. To save time, in this part you are asked to write out a subset of the simultaneous confidence intervals.

Assume that you construct 85% Bonferroni confidence intervals for pairwise differences of component means simultaneously for all component pairs and all time periods.

Write out the Bonferroni simultaneous confidence intervals for the difference of the component means between samples of Periods 1 and 2, only. Provide the details (including formula for the estimated variance, formula and numerical value of the multiplier).

Since we are interested in constructing 85% Bonferroni confidence intervals, we have $\alpha = 1 - 0.85 = 0.15$. Since we have to construct 12 confidence intervals in all, we have $p = 12$. And since each confidence interval is comparing measurements between two time periods, each of which has 30 skulls, we have $n_1 = n_2 = 30$.

Thus, for variable $X_i,\ i \in \{1, 2, 3, 4\}$, the confidence interval for the difference in means between Period 1 skulls and Period 2 skulls has the form

$$\left(\bar{x}_{i1} - \bar{x}_{i2} - t_{n_1+n_2-2,1-\alpha/2p}\sqrt{s_i^2\left(\frac{1}{n_1}+\frac{1}{n_2}\right)},\ \bar{x}_{i1} - \bar{x}_{i2} + t_{n_1+n_2-2,1-\alpha/2p}\sqrt{s_i^2\left(\frac{1}{n_1}+\frac{1}{n_2}\right)}\right)$$

$$= \left(\bar{x}_{i1} - \bar{x}_{i2} - t_{30+30-2,1-0.15/2(12)}\sqrt{s_i^2\left(\frac{1}{30}+\frac{1}{30}\right)},\ \bar{x}_{i1} - \bar{x}_{i2} + t_{30+30-2,1-0.15/2(12)}\sqrt{s_i^2\left(\frac{1}{30}+\frac{1}{30}\right)}\right)$$

$$= \left(\bar{x}_{i1} - \bar{x}_{i2} - t_{58,0.99375}\sqrt{\frac{s_i^2}{15}},\ \bar{x}_{i1} - \bar{x}_{i2} + t_{58,0.99375}\sqrt{\frac{s_i^2}{15}}\right)$$

$$\approx \left(\bar{x}_{i1} - \bar{x}_{i2} - 2.578\sqrt{\frac{s_i^2}{15}},\ \bar{x}_{i1} - \bar{x}_{i2} + 2.578\sqrt{\frac{s_i^2}{15}}\right)$$

where $\bar{x}_{it}$ denotes the mean of measurement i among skulls from Period t, and s_i^2 is the i^{th} diagonal element of the pooled sample covariance matrix $S_{pool} = \frac{(30-1)S_1+(30-1)S_2}{30+30-2} = \frac{29(S_1+S_2)}{58} = \frac{S_1+S_2}{2}$. Here, S_t is the sample covariance matrix for skulls from Period t, $S_t = \frac{1}{30-1}\sum_{j=1}^{30}(\mathbf{x}_{tj} - \bar{\mathbf{x}}_t)(\mathbf{x}_{tj} - \bar{\mathbf{x}}_t)^T$, where $\mathbf{x}_{tj}$ is the 4-vector of skull measurements for skull j from Period t, and $\bar{\mathbf{x}}_t$ is the 4-vector of mean skull measurements for the skulls from Period t.

```
# Period 1 and 2 means for each variable
periods12means = periods12 %>%
  group_by(period) %>%
  summarize(m1 = mean(x1),
            m2 = mean(x2),
            m3 = mean(x3),
            m4 = mean(x4))

# Period 1, Period 2, and Pooled sample covariance matrices
S1 = cov(select(filter(periods12, period == 1), select = -period))
S2 = cov(select(filter(periods12, period == 2), select = -period))
Sp = 0.5*S1 + 0.5*S2
```

In particular, for X_1 = maximum breadth of skull, we have $\bar{x}_{11} \approx 131.367$, $\bar{x}_{12} \approx 132.367$, and $s_1^2 \approx 24.723$, so our confidence interval is approximately $(-4.310, 2.310) \ni 0$.

```
c(periods12means$m1[1] - periods12means$m1[2] - qt(1-0.00625,
↪  58)*sqrt(Sp[1,1]/15),
  periods12means$m1[1] - periods12means$m1[2] + qt(1-0.00625,
↪  58)*sqrt(Sp[1,1]/15))
```

```
[1] -4.309679  2.309679
```

For X_2 = basibregmatic height of skull, we have $\bar{x}_{21} = 133.6$, $\bar{x}_{22} = 132.7$, and $s_2^2 \approx 20.784$, so our confidence interval is approximately $(-2.135, 3.935) \ni 0$.

```
c(periods12means$m2[1] - periods12means$m2[2] - qt(1-0.00625,
↪  58)*sqrt(Sp[2,2]/15),
 periods12means$m2[1] - periods12means$m2[2] + qt(1-0.00625,
↪  58)*sqrt(Sp[2,2]/15))
```

```
[1] -2.134624  3.934624
```

For X_3 = basialveolar length of skull, we have $\bar{x}_{31} \approx 99.167$, $\bar{x}_{32} \approx 99.067$, and $s_3^2 \approx 26.759$, so our confidence interval is approximately $(-3.343, 3.543) \ni 0$.

```
c(periods12means$m3[1] - periods12means$m3[2] - qt(1-0.00625,
↪  58)*sqrt(Sp[3,3]/15),
 periods12means$m3[1] - periods12means$m3[2] + qt(1-0.00625,
↪  58)*sqrt(Sp[3,3]/15))
```

```
[1] -3.343276  3.543276
```

For X_4 = nasal height of skull, we have $\bar{x}_{41} \approx 50.533$, $\bar{x}_{42} \approx 50.233$, and $s_4^2 \approx 8.187$, so our confidence interval is approximately $(-1.605, 2.205) \ni 0$.

```
c(periods12means$m4[1] - periods12means$m4[2] - qt(1-0.00625,
↪  58)*sqrt(Sp[4,4]/15),
 periods12means$m4[1] - periods12means$m4[2] + qt(1-0.00625,
↪  58)*sqrt(Sp[4,4]/15))
```

```
[1] -1.604548  2.204548
```

1.3.3 Part (iii)

Determine which mean components differ statistically significantly at 85% confidence level between Periods 1 and 2.

Since all four confidence intervals in Part (ii) contained 0, we conclude that none of the four mean skull components differ statistically significantly at the 85% confidence level between Periods 1 and 2. This result coheres with our finding in Part (b) that the mean vectors of Periods 1 and 2 were not statistically significantly different from one another at the $\alpha = 0.05$ level.

2 Exercise 3: Multidimensional Scaling

The table in `T12-13.DAT` gives the "distances" between certain archaeological sites from different periods, based upon the frequencies of different types of potsherds found at the sites. The dates of the periods $1, 2, \ldots, 9$ correspond to A.D. years 918, 1131, 960, 987, 1024, 1005, 945, 1137, and 1062, respectively.

```
potsherds = matrix(0, 9, 9)
potsherds[row(potsherds) <= col(potsherds)] =
 ↪  scan("C:/Users/rewin/OneDrive/Documents/STAT_32950/Homework/HW4/T12-13.DAT")
potsherds = t(potsherds)
```

2.1 Part (a)

Given these distances, determine the coordinates of the sites in $q = 3, 4, 5$ dimensions using (classical metric) multidimensional scaling.

The coordinates of the nine sites in $q = 3$ dimensions are as follows:

```
# q = 3
cmdscale(as.dist(potsherds), k = 3) %>% round(3)
```

```
       [,1]   [,2]   [,3]
 [1,]  0.512 -0.278  0.242
 [2,] -1.318  0.692  0.623
 [3,]  0.470 -0.071  0.186
 [4,]  0.387  0.088  0.049
 [5,]  0.234  0.296 -0.325
 [6,]  0.469  0.137 -0.219
 [7,]  0.581 -0.349  0.457
 [8,] -1.118 -1.122 -0.316
 [9,] -0.216  0.608 -0.697
```

The coordinates of the nine sites in $q = 4$ dimensions are as follows:

```
# q = 4
cmdscale(as.dist(potsherds), k = 4) %>% round(3)
```

```
       [,1]   [,2]   [,3]   [,4]
 [1,]  0.512 -0.278  0.242  0.676
 [2,] -1.318  0.692  0.623  0.050
 [3,]  0.470 -0.071  0.186 -0.302
```

```
 [4,]  0.387  0.088  0.049 -0.344
 [5,]  0.234  0.296 -0.325 -0.052
 [6,]  0.469  0.137 -0.219  0.139
 [7,]  0.581 -0.349  0.457 -0.178
 [8,] -1.118 -1.122 -0.316 -0.052
 [9,] -0.216  0.608 -0.697  0.062
```

The coordinates of the nine sites in $q = 5$ dimensions are as follows:

```
# q = 5
cmdscale(as.dist(potsherds), k = 5) %>% round(3)
```

```
       [,1]   [,2]   [,3]   [,4]   [,5]
 [1,]  0.512 -0.278  0.242  0.676  0.119
 [2,] -1.318  0.692  0.623  0.050 -0.024
 [3,]  0.470 -0.071  0.186 -0.302  0.059
 [4,]  0.387  0.088  0.049 -0.344  0.102
 [5,]  0.234  0.296 -0.325 -0.052  0.121
 [6,]  0.469  0.137 -0.219  0.139 -0.281
 [7,]  0.581 -0.349  0.457 -0.178 -0.102
 [8,] -1.118 -1.122 -0.316 -0.052 -0.005
 [9,] -0.216  0.608 -0.697  0.062  0.010
```

2.2 Part (b)

The $Stress(q)$ can be calculated as

$$Stress(q) = \left[\frac{\sum_{j<i} \left(x_{ij} - d_{ij}^{(q)} \right)^2}{\sum_{j<i} x_{ij}^2} \right]^{1/2}$$

where $d_{ij}^{(q)}$ is the distance between sites i and j in q-dimensional representation by using (classical metric) multidimensional scaling method, and x_{ij} is the corresponding distance matrix X given by the data. Plot (the minimum) $Stress(q)$ versus q and interpret the graph.

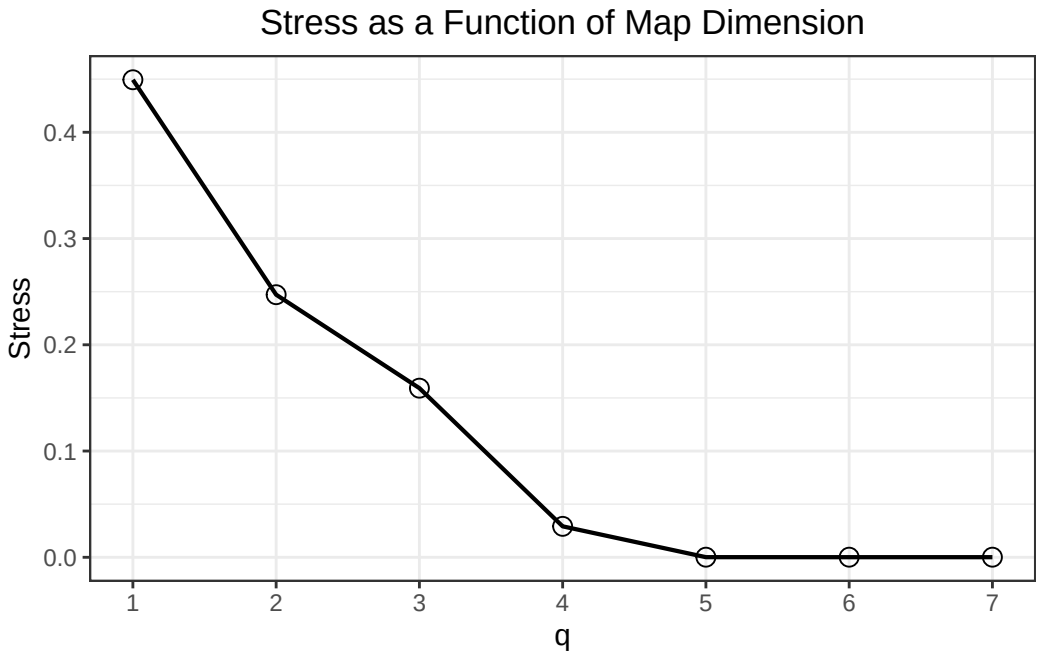
Below, we plot $Stress(q)$ against q for $q \in \{1, \ldots, 7\}$ (the $q = N - 1 = 8$ configuration is identical to the $q = 7$ configuration, so is not included in the plot). For these data, we see that as the dimension of our map increases, the stress associated with the map generally decreases. (It is difficult to see in the plot, but the stress actually increases by a very small amount from $q = 6$ to $q = 7$.) We also see that once $q = 5$ dimensions are used, the q-dimensional map almost perfectly captures the true distances between the sites, such that moving into 6- or 7-dimensional representations of the sites barely improves the fit. Using the rule of

thumb that a value of *Stress* less than 0.05 is "good", even a 4-dimensional representation of the data is good enough, as the associated *Stress* is approximately 0.029.

```
stress = rep(0, 7)
for(i in 1:7){
  fit = cmdscale(as.dist(potsherds), k = i)
  diffS2 = sum((as.dist(potsherds) - dist(fit))^2)
  dist2 = sum((as.dist(potsherds))^2)
  stress[i] = sqrt(diffS2/dist2)
}

stress = stress %>% as.data.frame()
stress = rename(stress, Stress = .) %>%
  mutate(q = row_number())
```

```
ggplot(data = stress, aes(x=q, y=Stress)) +
  theme_bw() +
  geom_line(linewidth = 0.75) +
  geom_point(shape = 1, size = 3) +
  scale_x_continuous(breaks = scales::pretty_breaks(n=7),
                     minor_breaks = NULL) +
  ggtitle("Stress as a Function of Map Dimension") +
  theme(plot.title = element_text(hjust = 0.5))
```



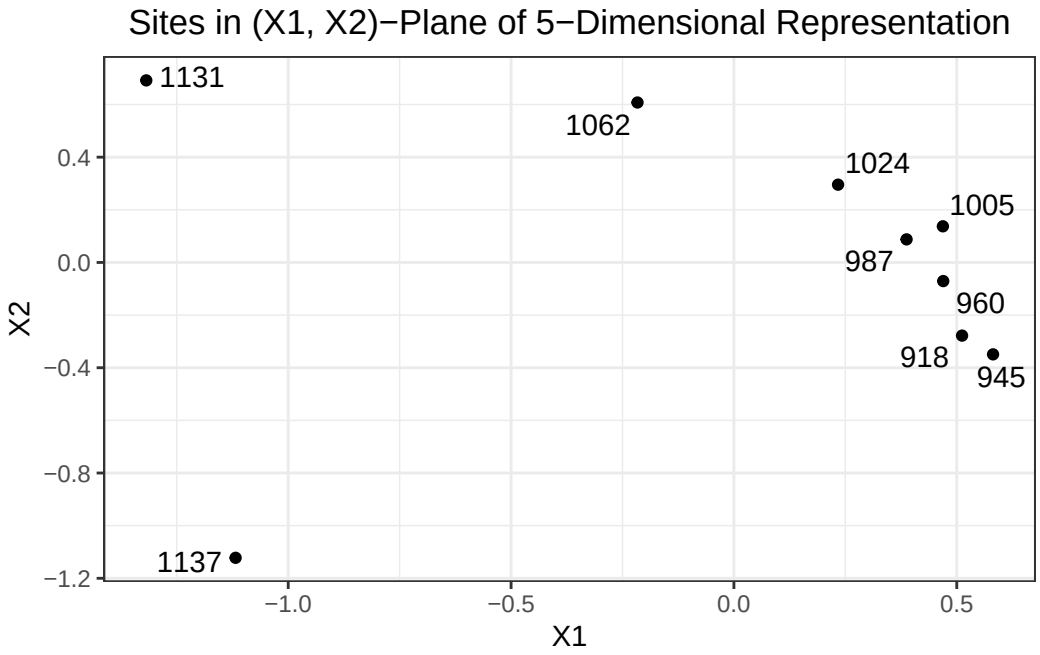
2.3 Part (c)

Plot the nine sites (treated as variables) in two dimensions using the first two coordinates for $q = 5$ dimensional solutions. Note the periods associated with the sites. Archaeologists would say that the two dimensional configuration contains a time trend or movement pattern. Do you see it (admittedly the pattern is very vague)?

Below, we plot the nine sites using the first two coordinates of their 5-dimensional representations. In general, it appears that more recent sites have progressively smaller X_1 coordinates and progressively larger X_2 coordinates, though this is not a perfect rule (for example, the most recent site, dated 1137 A.D., actually has the smallest X_2 coordinate). The imperfect quality of this pattern may be because there is additional information captured in the third through fifth coordinates of each site that are not visualized.

```
q3dim5 = cmdscale(as.dist(potsherds), k = 5) %>%
  as.data.frame() %>%
  mutate(year = c(918, 1131, 960, 987, 1024, 1005, 945, 1137, 1062))

ggplot(q3dim5, aes(x=V1, y=V2, label = year)) +
  theme_bw() +
  geom_point() +
  geom_text_repel() +
  xlab("X1") +
  ylab("X2") +
  ggtitle("Sites in (X1, X2)-Plane of 5-Dimensional Representation") +
  theme(plot.title = element_text(hjust = 0.5))
```



3 Exercise 4: Correspondence Analysis

A sample of 592 students is cross-classified according to hair colors and eye colors in the table in `HairEyeAll.txt`.

```
haireyeall =
 ↪  read.table("C:/Users/rewin/OneDrive/Documents/STAT_32950/Homework/HW4/HairEyeAll.txt")
rownames(haireyeall) = c("Black", "Brown", "Red", "Blond") # for variable
 ↪  Hair
colnames(haireyeall) = c("Brown", "Blue", "Hazel", "Green") # for variable
 ↪  Eye
```

3.1 Part (a)

Obtain the tables of cell percentages ($p_{ij} = x_{ij}/n$), row percentages, and column percentages.

First, we display a table of cell percentages:

```
round(as.matrix(haireyeall)/sum(as.matrix(haireyeall)), 3)
```

```
      Brown  Blue Hazel Green
Black 0.115 0.034 0.025 0.008
Brown 0.201 0.142 0.091 0.049
Red   0.044 0.029 0.024 0.024
Blond 0.012 0.159 0.017 0.027
```

Next, we display a table of within-row percentages (i.e., a row profile matrix):

```
rowtotals = as.matrix(haireyeall) %*% c(1,1,1,1)
rowprofile = round(diag(c(1/rowtotals)) %*% as.matrix(haireyeall), 3)
rownames(rowprofile) = c("Black", "Brown", "Red", "Blond")
rowprofile %>%
  as.data.frame() %>%
  mutate(Total = Brown + Blue + Hazel + Green) %>%
  as.matrix()
```

```
      Brown  Blue Hazel Green Total
Black 0.630 0.185 0.139 0.046 1.000
Brown 0.416 0.294 0.189 0.101 1.000
Red   0.366 0.239 0.197 0.197 0.999
Blond 0.055 0.740 0.079 0.126 1.000
```

Finally, we display a table of within-column percentages (i.e., a column profile matrix):

```
coltotals = c(1,1,1,1) %*% as.matrix(haireyeall)
colprofile = round(as.matrix(haireyeall) %*% diag(c(1/coltotals)), 3)
colnames(colprofile) = c("Brown", "Blue", "Hazel", "Green")
colprofile %>% t() %>%
  as.data.frame() %>%
  mutate(Total = Black + Brown + Red + Blond) %>%
  as.matrix() %>% t()
```

```
      Brown  Blue Hazel Green
Black 0.309 0.093 0.161 0.078
Brown 0.541 0.391 0.581 0.453
Red   0.118 0.079 0.151 0.219
Blond 0.032 0.437 0.108 0.250
Total 1.000 1.000 1.001 1.000
```

3.2 Part (b)

Obtain the table of expected cell counts (i.e., expected cell frequencies) E_{ij} if the variables $Hair$ and Eye were independent (for the given data).

If $Hair$ color and Eye color were independent, we would expect to observe the following counts:

```
E = (as.matrix(haireyeall)%*%c(1,1,1,1)) %*%
 ↪  (c(1,1,1,1)%*%as.matrix(haireyeall)) /
  sum(haireyeall)
round(E, 1)
```

```
      Brown  Blue Hazel Green
Black  40.1  39.2  17.0  11.7
Brown 106.3 103.9  44.9  30.9
Red    26.4  25.8  11.2   7.7
Blond  47.2  46.1  20.0  13.7
```

3.3 Part (c)

Obtain the table of cell $mass = \frac{(x_{ij}-E_{ij})^2}{E_{ij}}$. Conduct a Pearson's chi-square test (What is the hypothesis? What is the degrees of freedom of the χ^2?) and check that the χ^2-statistic$/n$ = total inertia.

First, we present the table of cell masses:

```
(((as.matrix(haireyeall) - E)^2)/E) %>% round(3)
```

```
       Brown   Blue Hazel Green
Black 19.346  9.421 0.228 3.817
Brown  1.521  3.800 1.831 0.119
Red    0.006  2.993 0.726 5.211
Blond 34.234 49.697 4.963 0.375
```

We now test the null hypothesis H_0 : hair color is independent of eye color using a Pearson's chi-square test. The χ^2 statistic is the sum of the entries in the mass table above: $X^2 \approx 138.29$. Moreover, under H_0, the chi-square statistic $X^2 \sim_{H_0} \chi^2_{(4-1)(4-1)} = \chi^2_9$. As such, we recover a p-value of $p = \mathbb{P}(X^2 > 138.29) < 2.2 \times 10^{-16}$, and we reject the null hypothesis that hair color and eye color are independent in favor of the alternative hypothesis that there is a relationship between an individual's hair color and their eye color.

```r
chisq.test(haireyeall)
```

```
    Pearson's Chi-squared test

data:  haireyeall
X-squared = 138.29, df = 9, p-value < 2.2e-16
```

The total inertia is $\frac{X^2}{n} \approx \frac{138.29}{592} \approx 0.234$. To confirm our calculation, we can use the `ca` function in R, which returns "principal inertias" that total approximately $0.209 + 0.022 + 0.003 \approx 0.234$ (as shown in Part (d) below).

3.4 Part (d)

Perform a correspondence analysis of the data. What percentage of variation in the data is captured in the 2-dimensional CA plot? Are there any associations of *Eye* category and *Hair* category reflected in the plot?

We first summarize the results of a correspondence analysis below. Notice that the first two dimensions of the output cumulatively capture 98.9% of the variation in the data.

```r
ca(haireyeall) %>% summary()
```

```
Principal inertias (eigenvalues):

 dim    value      %    cum%   scree plot
 1      0.208773  89.4  89.4  **********************
 2      0.022227   9.5  98.9  **
 3      0.002598   1.1 100.0
        -------- -----
 Total: 0.233598 100.0


Rows:
    name   mass  qlt  inr    k=1 cor ctr    k=2 cor ctr
1 | Blck |  182  990  237 | -505 838 222 |  215 152 379 |
2 | Brwn |  483  906   53 | -148 864  51 |  -33  42  23 |
3 |  Red |  120  945   65 | -130 133  10 | -320 812 551 |
4 | Blnd |  215 1000  646 |  835 993 717 |   70   7  47 |

Columns:
```

```
    name   mass  qlt  inr    k=1 cor ctr    k=2 cor ctr
1 | Brwn |  372  998  398 | -492 967 431 |   88  31 130 |
2 | Blue |  363 1000  477 |  547 977 521 |   83  22 112 |
3 | Hazl |  157  879   56 | -213 542  34 | -167 336 198 |
4 | Gren |  108  948   69 |  162 176  14 | -339 773 559 |
```

Now, we plot the coordinates of each hair and eye color using the standard symmetric scaling of the corresponding coordinate systems. As implied by the table above, this plot captures 98.9% of the variation in the data. In the upper-right corner of the plot, we see that blond hair and blue eyes are both fairly far from the origin and have a small angle between them; this suggests a strong association between having blond hair and having blue eyes. Similarly, in the upper-left corner of the plot, we see that black hair and brown eyes are both fairly far from the origin and have a fairly small angle between them; this suggests a strong association between having black hair and having brown eyes.

```
plot(ca(haireyeall), arrows = c(T,T))
```