MAST90138 Assignment 2

Haonan Zhong

Question 1a

```
wheat <- read.csv("Wheat data.txt", sep = "", header = F)
X <- scale(wheat[, -c(8)], scale = FALSE)
PCX <- prcomp(X, retx = TRUE)
(lambda <- PCX$sdev^2)
```

```
## [1] 1.079333e+01 2.129455e+00 7.363003e-02 1.288749e-02 2.748227e-03
## [6] 1.570450e-03 2.965544e-05
```

```
(gamma <- PCX$rotation)
```

```
##             PC1          PC2         PC3         PC4          PC5          PC6
## V1 -0.884228505  0.100805775  0.26453354  0.19944949 -0.137172970  0.280639558
## V2 -0.395405417  0.056489625 -0.28251995 -0.57881686  0.574756029 -0.301558638
## V3 -0.004311324 -0.002894744  0.05903584  0.05776023 -0.053104536 -0.045229054
## V4 -0.128544478  0.030621731 -0.40014946 -0.43610024 -0.786997760 -0.113437606
## V5 -0.111059139  0.002372293  0.31923869  0.23416358 -0.144802899 -0.896267845
## V6  0.127615624  0.989410476  0.06429754 -0.02514736 -0.001575639  0.003287998
## V7 -0.128966499  0.082233392 -0.76193973  0.61335659  0.087653609 -0.109923643
##             PC7
## V1 -0.025398239
## V2  0.065839904
## V3  0.994125646
## V4  0.001431435
## V5 -0.081549900
## V6  0.001142692
## V7  0.008971926
```

```
(fracvar <- lambda/sum(lambda))
```

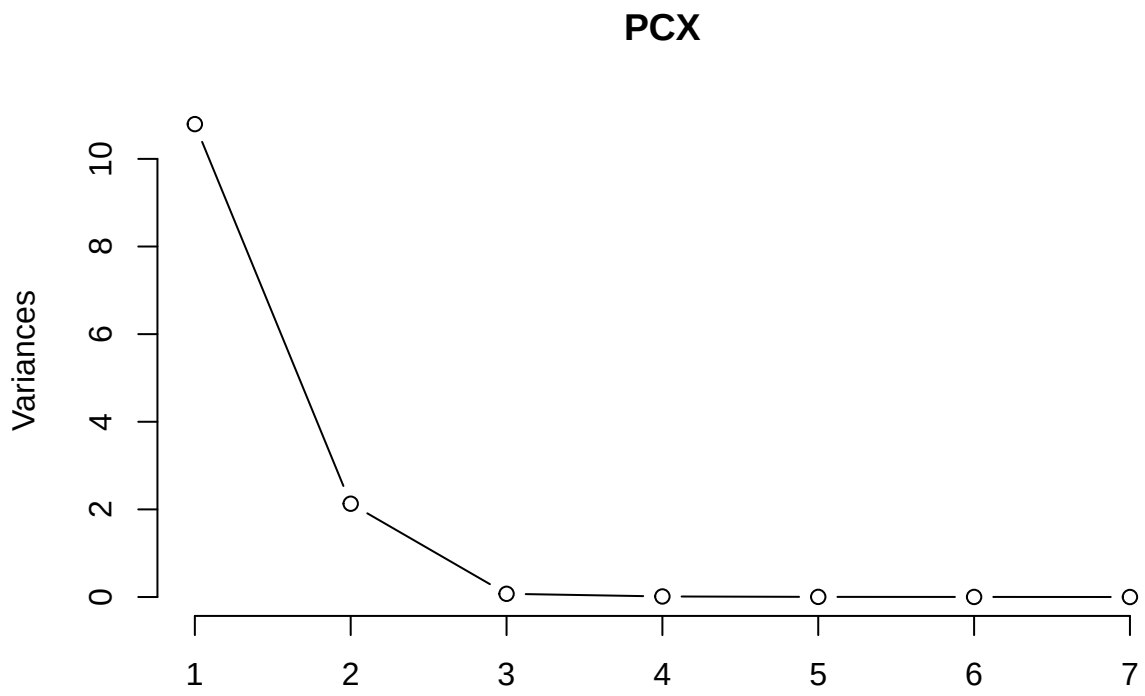
```
## [1] 8.293852e-01 1.636325e-01 5.657909e-03 9.903061e-04 2.111803e-04
## [6] 1.206771e-04 2.278796e-06
```

As we can see from the output, the first and the second principle components was able to explain about 82.9% and 16.4% of the variability of the data, respectively. And the third component explains around 0.57% of variances. Whilst, the rest of the PCs only explains a tiny portion of variances.

```
(cumuprop <- cumsum(lambda)/sum(lambda))
```

```
## [1] 0.8293852 0.9930176 0.9986756 0.9996659 0.9998770 0.9999977 1.0000000
```

```
screeplot(PCX, type = "line")
```



Visually, one can look for an elbow in the screeplot and stop there. In our case, we should keep the first three principle components, with the first three PCs we explain almost 100% of the variability of the data.

Question 1b

According to the eigenvectors given in the question 1a, we have

$$Y_1 = -0.884X_1 - 0.395X_2 - 0.004X_3 - 0.129X_4 - 0.111X_5 + 0.127X_6 - 0.129X_7$$

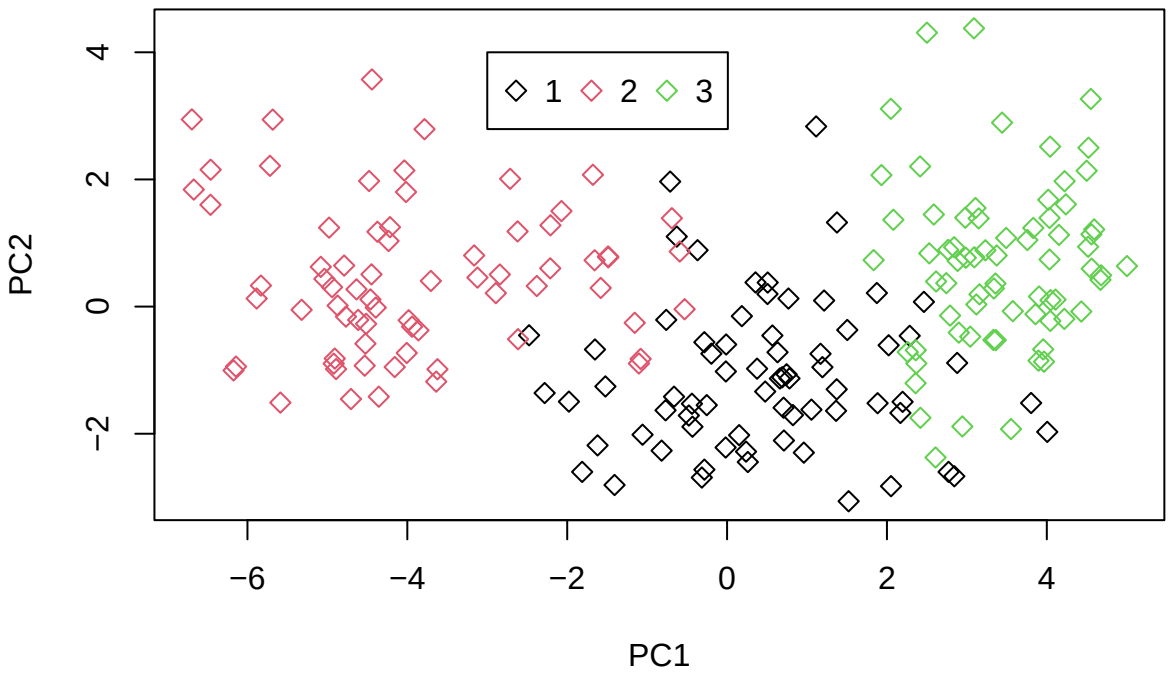
Thus, the first PC puts the most weight on the first variable X_1, which has an negative effect on PC1, followed by X_2 with a positive effect. On the other hand, X_4, X_5, X_6, and X_7 are quite similar in terms of contribution, whilst X_3 plays the smallest role in the construction of the first PC.

$$Y_2 = 0.101X_1 + 0.056X_2 - 0.003X_3 + 0.031X_4 + 0.002X_5 + 0.989X_6 + 0.082X_7$$

Thus, X_6 plays the major role in the construction of the second PC with a positive effect, followed by X_1.

Question 1c

```
plot(x = PCX$x[,1], y = PCX$x[,2], col = wheat$V8, pch=5, xlab = 'PC1', ylab = 'PC2')
legend(-3, 4, horiz = TRUE, unique(wheat$V8), col=1:length(wheat$V8), pch=5)
```



Based on the scatter plot between the first two principle components, we can see that PC1 captured most of the variation driven by the different varieties of wheat, as it divides the data points into three distinct clusters, where black points indicates data point from group 1, red points indicates data point from group 2, and green points represents data point from group 3. On the other hand, no clear group separation can be seen from PC2, other than group 1 seems to have a low value of PC2 compare to the other two groups.

Question 1d

```
corr_matrix <- matrix(0, 7, 7)

for (j in 1:7) {
  for (k in 1:7) {
    corr_matrix[j, k] <- (gamma[j, k] * lambda[k]) / sqrt(cov(X)[j, j] * lambda[k])
  }
}
corr_matrix[, c(1, 2)]
```

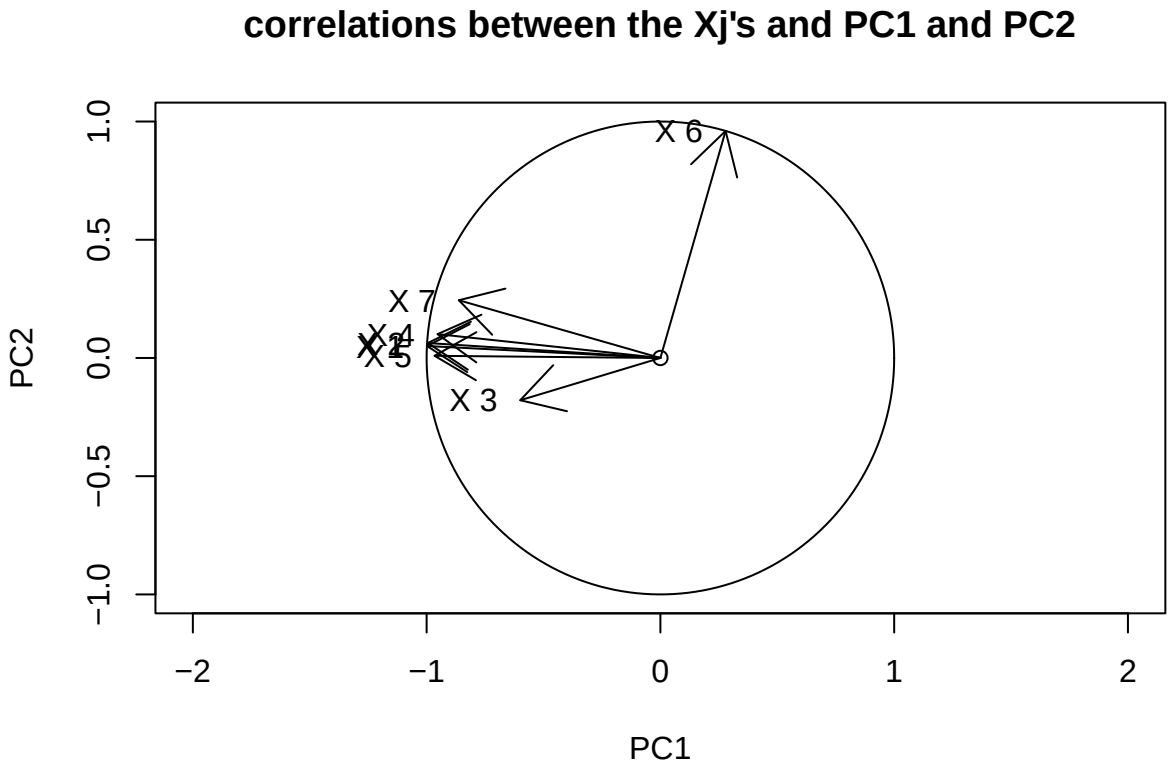
```
##            [,1]         [,2]
## [1,] -0.9983758  0.050555863
## [2,] -0.9946970  0.063120944
## [3,] -0.5994257 -0.178768653
## [4,] -0.9531585  0.100855139
## [5,] -0.9659805  0.009165136
## [6,]  0.2788442  0.960264370
## [7,] -0.8620814  0.244160925
```

```
corr_matrix[,1]^2 + corr_matrix[,2]^2
```

```
## [1] 0.9993101 0.9934065 0.3912694 0.9186829 0.9332024 0.9998617 0.8027989
```

```
plot(x = 0, y = 0, xlim = c(-2, 2), ylim = c(-1, 1), xlab = 'PC1', ylab = 'PC2',
     main = "correlations between the Xj's and PC1 and PC2")
for (i in 1:7) {
  arrows(0, 0, corr_matrix[i, 1], corr_matrix[i, 2])
  text(corr_matrix[i, 1] - 0.2,
       corr_matrix[i, 2],
       paste("X", as.character(i)))
}

radius <- 1
theta <- seq(0, 2 * pi, length = 200)
lines(x = radius * cos(theta), y = radius * sin(theta))
```



As the plot above depicted, most of the variables, except for $X3$, are relatively close to the periphery of the circle, which indicates that they are strongly correlated with the first two PCs. Furthermore, PC1 is strongly negatively correlated with $X1$, $X2$, $X4$, $X5$ and $X7$. Whilst PC2 is highly positively correlated with $X6$.

We also know that together the first two PCs explains a large portion of the variability of the data, therefore we could also use the direction of the arrow in conjunction with the scatter plot of the first two PCs to learn the effect of these variables on individuals.