## **Dimensionality Reduction and Visualization**

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**Exercise set 15 Solutions** 

## **Part I: Optional Problems**

### **Optional Problem I1: Exploration of Your Own Data**

The Principal Component Analysis (PCA) reduces the number of variables by finding a new, smaller set of variables.

The analysis made use of wine dataset obtained from UC Irvine Machine Learning Repository.

Source: http://ar chive.ics.uci.edu/ml/machine-learning-databases/wine/wine.data

```
str(wine)
```

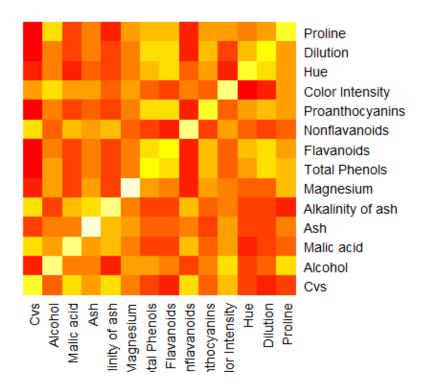
```
'data.frame': 178 obs. of 14 variables:
$ CVS : int 111111111...
$ Alcohol : num 14 2 12 2 12 2 14
                   : num 14.2 13.2 13.2 14.4 13.2 ...
$ Malic acid : num 1.71 1.78 2.36 1.95 2.59 1.76 1.87 2.15 1.64 1.35
$ Ash
                   : num 2.43 2.14 2.67 2.5 2.87 2.45 2.45 2.61 2.17 2.27 .
$ Alkalinity of ash: num 15.6 11.2 18.6 16.8 21 15.2 14.6 17.6 14 16 ...
$ Magnesium
                         127 100 101 113 118 112 96 121 97 98 ...
               : int
$ Total Phenols
                   : num 2.8 2.65 2.8 3.85 2.8 3.27 2.5 2.6 2.8 2.98 ...
$ Flavanoids
                   : num 3.06 2.76 3.24 3.49 2.69 3.39 2.52 2.51 2.98 3.15
$ Nonflavanoids : num 0.28 0.26 0.3 0.24 0.39 0.34 0.3 0.31 0.29 0.22 ...
$ Proanthocyanins : num 2.29 1.28 2.81 2.18 1.82 1.97 1.98 1.25 1.98 1.85
$ Color Intensity : num 5.64 4.38 5.68 7.8 4.32 6.75 5.25 5.05 5.2 7.22 ..
                   : num 1.04 1.05 1.03 0.86 1.04 1.05 1.02 1.06 1.08 1.01
$ Hue
```

```
$ Dilution : num 3.92 3.4 3.17 3.45 2.93 2.85 3.58 3.58 2.85 3.55 .
```

.. \$ Proline : int 1065 1050 1185 1480 735 1450 1290 1295 1045 1045 .

. .

The heatmap plot for correlation is as given below:



In the heatmap diagram above, dark heatmap signifies strong correlation among variables. Thus, it includes several s trong correlations.

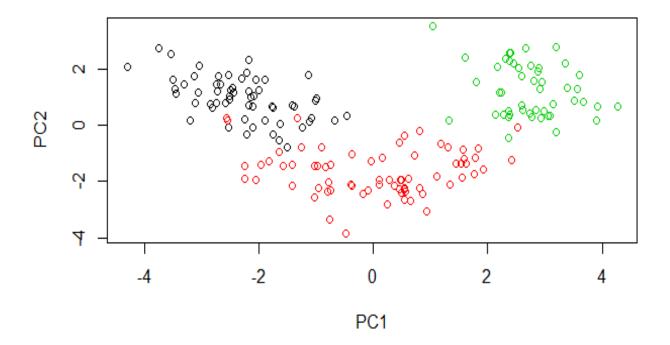
#### summary(winePCA)

Importance of components:

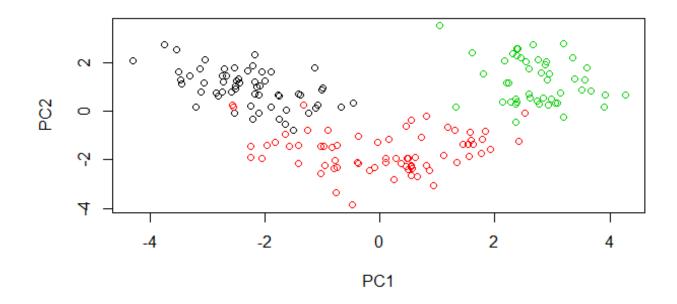
```
PC1
                                PC2
                                        PC3
                                                PC4
                                                        PC5
                                                                PC6
                                                                        PC7
Standard deviation
                       2.169 1.5802 1.2025 0.95863 0.92370 0.80103 0.74231
Proportion of Variance 0.362 0.1921 0.1112 0.07069 0.06563 0.04936 0.04239
                       0.362 0.5541 0.6653 0.73599 0.80162 0.85098 0.89337
Cumulative Proportion
                                   PC9
                                          PC10
                                                          PC12
                           PC8
                                                  PC11
Standard deviation
                       0.59034 0.53748 0.5009 0.47517 0.41082 0.32152
Proportion of Variance 0.02681 0.02222 0.0193 0.01737 0.01298 0.00795
Cumulative Proportion 0.92018 0.94240 0.9617 0.97907 0.99205 1.00000
```

It can be concluded that applying the PCA technique reduces the number of variables to 7, i.e. P C1 to PC7 as shown in summary table above.

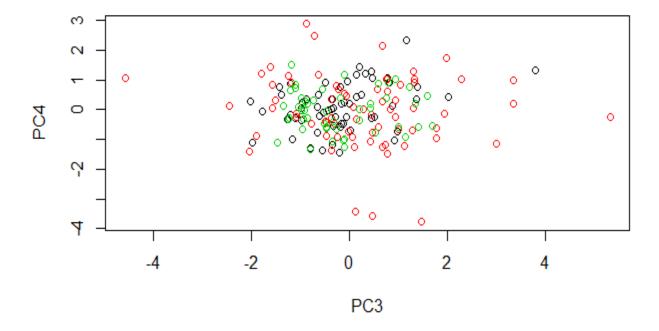
The PCA plot for 2 components, PC1 and PC2 are given below:



The PCA plot for all data is given below:



It can be seen that both plots above looks the same.



PC3 and PC4 look different from both PC1, PC2 and all PCA. In PC3 and PC4, most data points are stacked together especially at the middle of the plot, while for others they are spread with data points with white, black, and green not being overlapping.

## **Index**

# **Optional I1:**

### In [ ]:

```
library(doParallel)
registerDoParallel(cores = detectCores() - 1)
set.seed(10)
library(caret)
library(corrplot)
wine <- read.table("http://archive.ics.uci.edu/ml/machine-learning-databases/win</pre>
e/wine.data", sep=",", header=FALSE)
colnames(wine) <- c('Cvs', 'Alcohol', 'Malic acid', 'Ash',</pre>
                    'Alkalinity of ash', 'Magnesium', 'Total Phenols',
                    'Flavanoids', 'Nonflavanoids',
                    'Proanthocyanins', 'Color Intensity', 'Hue',
                    'Dilution', 'Proline')
str(wine)
heatmap(cor(wine),Rowv=NA, Colv=NA) #Plot heatmap to show correlation among vari
classes<- factor(wine$Cvs) # To declare classes as Cv1, Cv2, Cv3
winePCA <- prcomp(scale(wine[,-1])) # PCA; Normalize data and exclude the first
summary(winePCA) # To get the summary statistics on PCA
plot(winePCA$x[,1:2], col= classes) # Plotting PCA1 and PCA2 only; 3 colors
plot(winePCA$x, col= classes) # Plotting PCA of all data with 3 colors
plot(winePCA$x[,3:4], col= classes) # Plotting PCA3 and PCA4 only; 3 colors
```