CSE574 Introduction to Machine Learning
Programming Assignment 3 (in R-Studio)
'Unsupervised Learning'
Project Report
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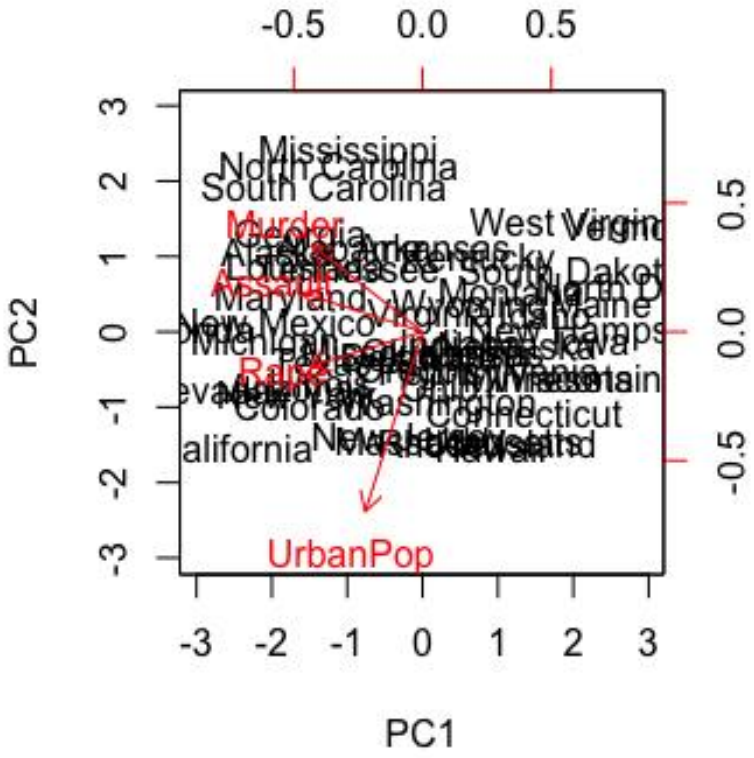
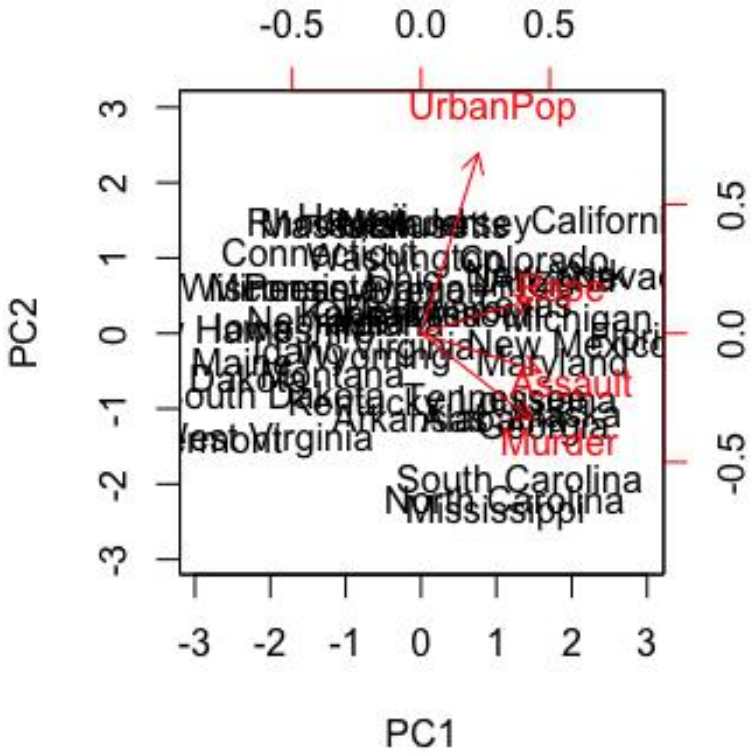
This is the project report for PA3 of CSE 574. Below is the output for Task1 lab1, Task2 lab2, Task3 Lab 3.

TASK Lab 1 : Chapter 10 Lab 1: Principal Components Analysis

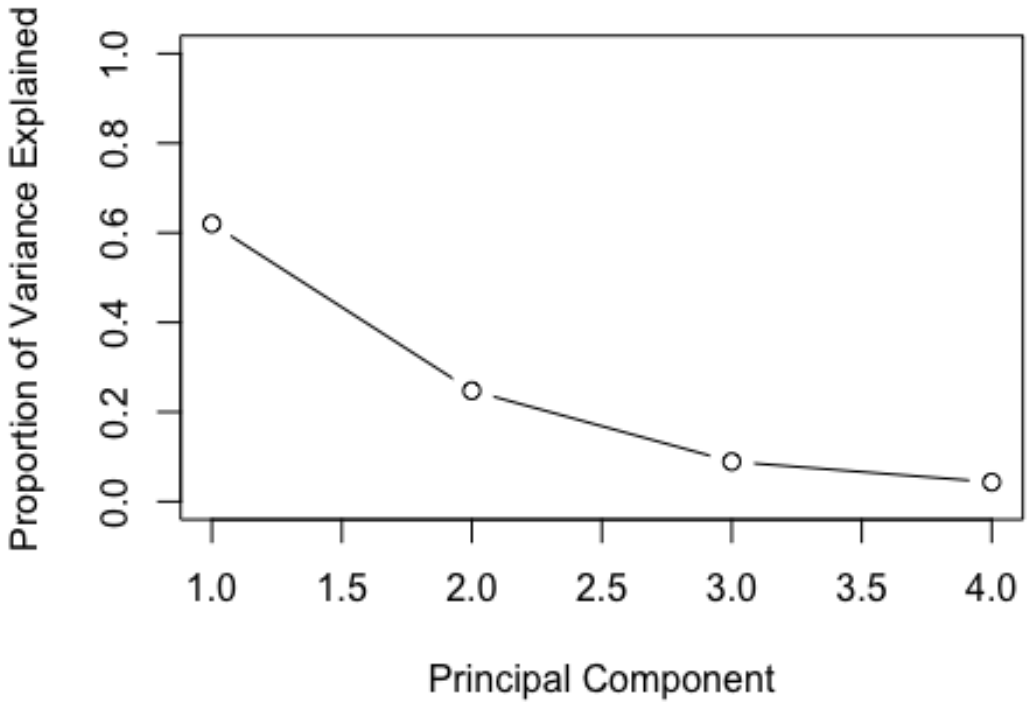
```
names(USArrests)
## [1] "Murder"   "Assault"  "UrbanPop" "Rape"
apply(USArrests, 2, mean)
##   Murder  Assault UrbanPop     Rape
##    7.788  170.760   65.540   21.232
apply(USArrests, 2, var)
##     Murder    Assault   UrbanPop       Rape
##   18.97047 6945.16571  209.51878   87.72916
pr.out=prcomp(USArrests, scale=TRUE)
names(pr.out)
## [1] "sdev"     "rotation" "center"   "scale"    "x"
pr.out$center
##   Murder  Assault UrbanPop     Rape
##    7.788  170.760   65.540   21.232
pr.out$scale
##    Murder   Assault  UrbanPop      Rape
##  4.355510 83.337661 14.474763  9.366385
pr.out$rotation
##                 PC1        PC2        PC3         PC4
## Murder   -0.5358995  0.4181809 -0.3412327  0.64922780
## Assault  -0.5831836  0.1879856 -0.2681484 -0.74340748
## UrbanPop -0.2781909 -0.8728062 -0.3780158  0.13387773
## Rape     -0.5434321 -0.1673186  0.8177779  0.08902432
dim(pr.out$x)
## [1] 50  4
biplot (pr.out , scale =0)
```



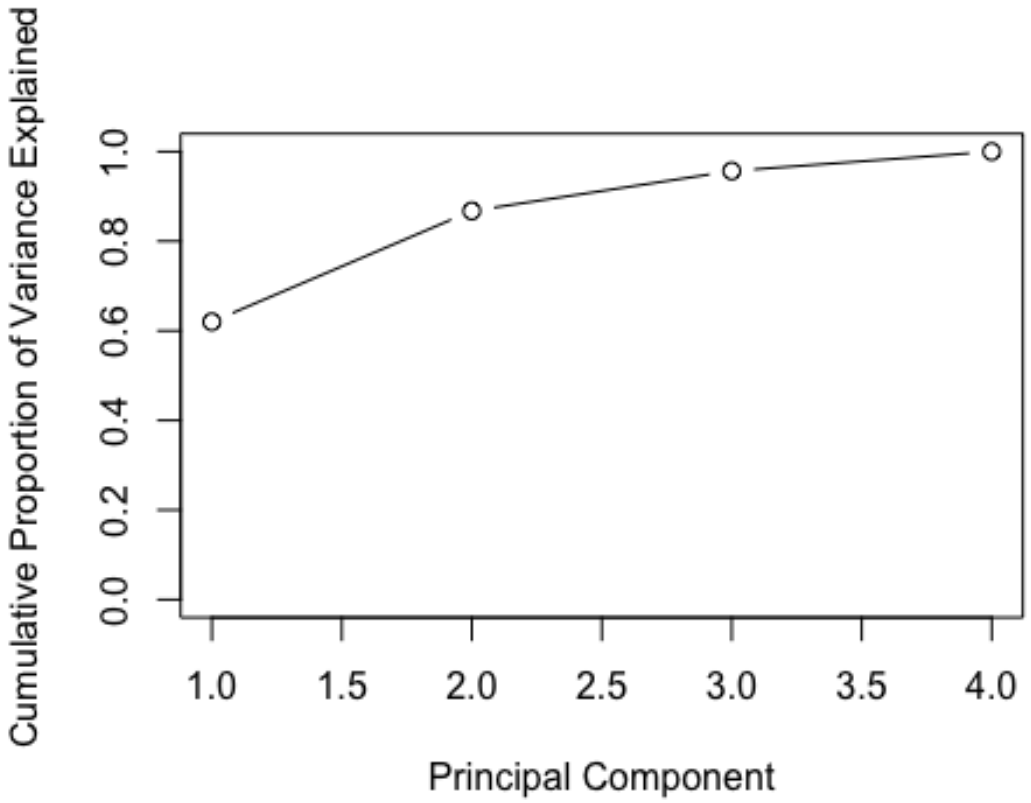

```
pr.out$rotation=-pr.out$rotation
pr.out$x=-pr.out$x
biplot(pr.out, scale=0)
```




```
pr.out$sdev
## [1] 1.5748783 0.9948694 0.5971291 0.4164494
pr.var=pr.out$sdev^2
pr.var
## [1] 2.4802416 0.9897652 0.3565632 0.1734301
pve=pr.var/sum(pr.var)
pve
## [1] 0.62006039 0.24744129 0.08914080 0.04335752
plot(pve, xlab="Principal Component", ylab="Proportion of Variance
Explained", ylim=c(0,1),type='b')
```




```
plot(cumsum(pve), xlab="Principal Component", ylab="Cumulative Proportion of
Variance Explained", ylim=c(0,1),type='b')
```

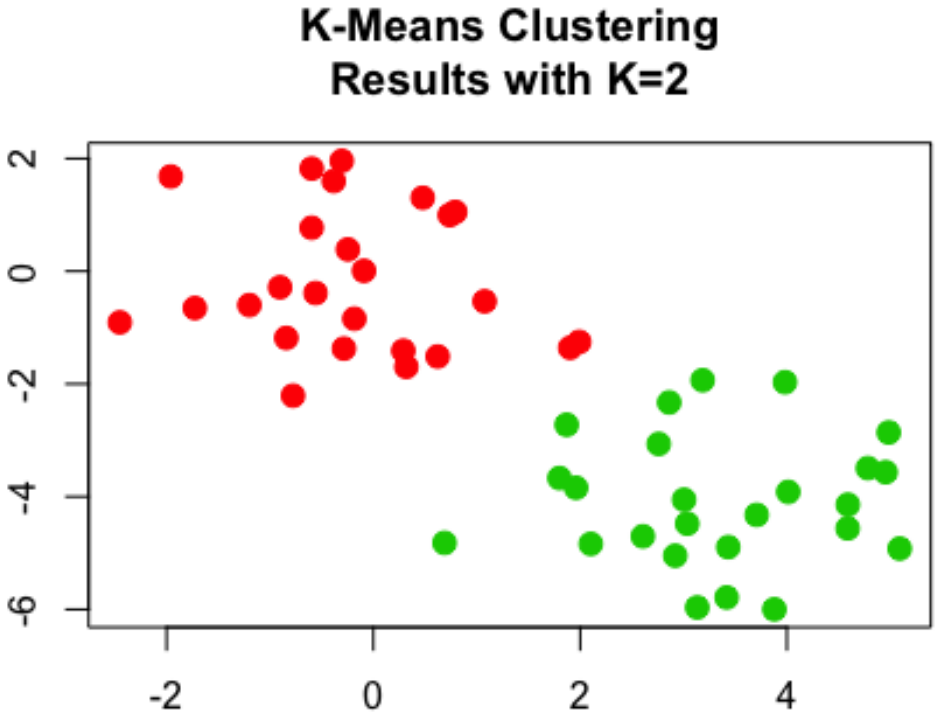



```
a=c(1,2,8,-3)
cumsum(a)
## [1]  1  3 11  8
```

TASK 2 Chapter 10 Lab 2: Clustering

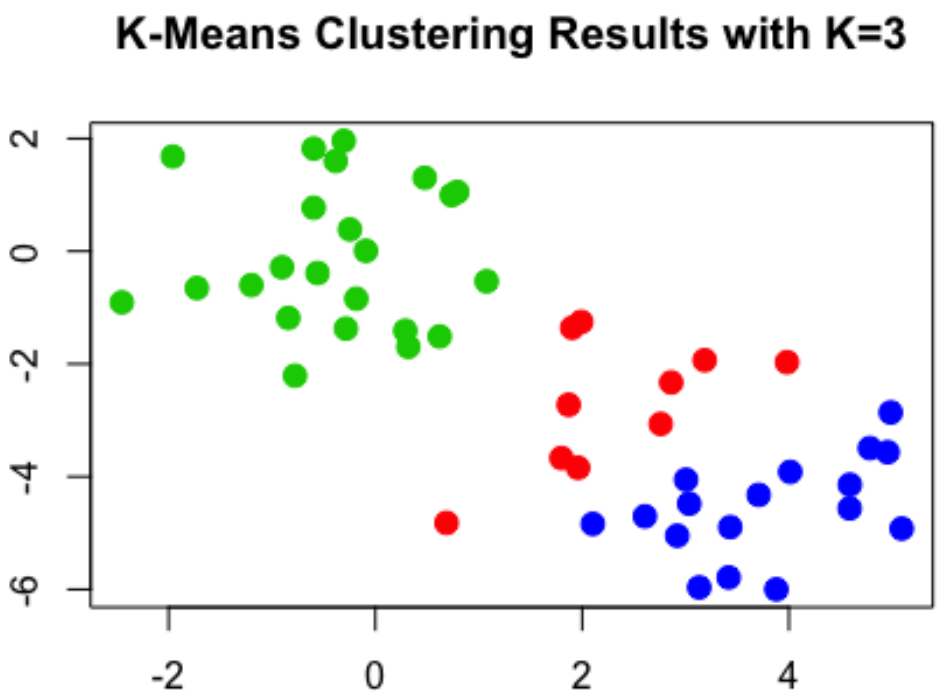
K-Means Clustering

```
set.seed(2)
x=matrix(rnorm(50*2), ncol=2)
x[1:25,1]=x[1:25,1]+3
x[1:25,2]=x[1:25,2]-4
km.out=kmeans(x,2,nstart=20)
km.out$cluster
##  [1] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 1 1 1 1 1 1 1 1 1 1
## [36] 1 1 1 1 1 1 1 1 1 1 1 1 1 1
plot(x, col=(km.out$cluster +1), main="K-Means Clustering
Results with K=2", xlab="", ylab="", pch=20, cex=2)
```




```
set.seed(4)
km.out=kmeans(x,3,nstart=20)
km.out
## K-means clustering with 3 clusters of sizes 10, 23, 17
##
## Cluster means:
##         [,1]        [,2]
## 1  2.3001545 -2.69622023
```

```
## 2 -0.3820397 -0.08740753
## 3  3.7789567 -4.56200798
##
## Clustering vector:
##  [1] 3 1 3 1 3 3 3 1 3 1 3 1 3 1 3 1 3 3 3 3 3 1 3 3 3 2 2 2 2 2 2 2 2 2
## [36] 2 2 2 2 2 2 2 2 1 2 1 2 2 2 2
##
## Within cluster sum of squares by cluster:
## [1] 19.56137 52.67700 25.74089
##  (between_SS / total_SS =  79.3 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
## [5] "tot.withinss" "betweenss"    "size"         "iter"
## [9] "ifault"
plot(x, col=(km.out$cluster+1), main="K-Means Clustering Results with K=3",
xlab="", ylab="", pch=20, cex=2)
```

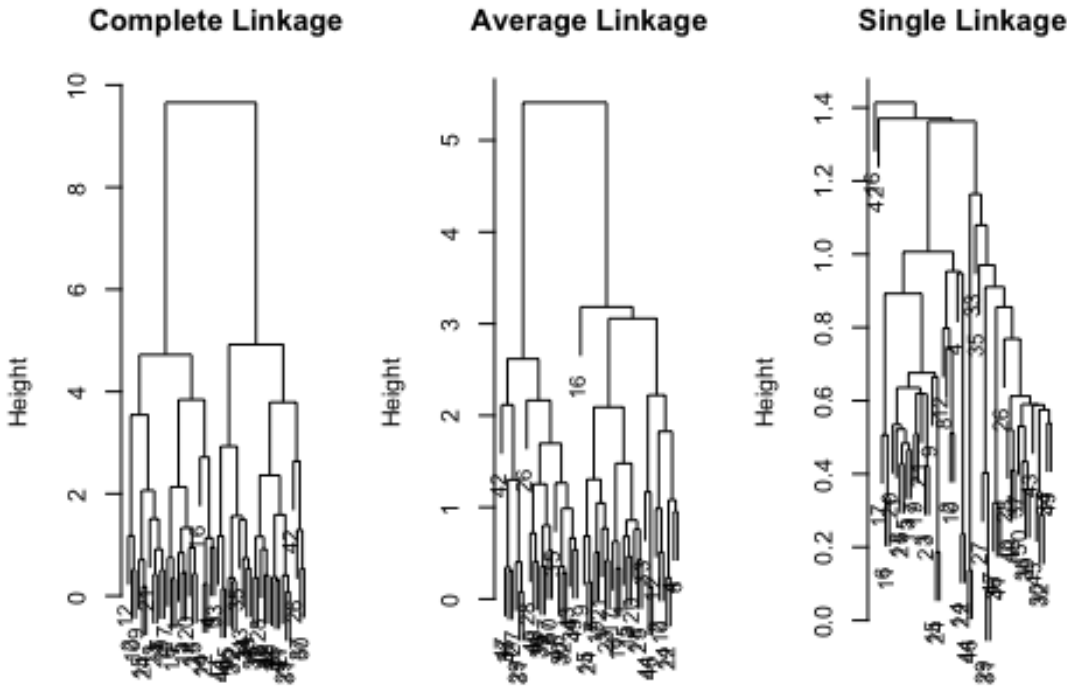



```
set.seed(3)
km.out=kmeans(x,3,nstart=1)
km.out$tot.withinss
## [1] 104.3319
```

```
km.out=kmeans(x,3,nstart=20)
km.out$tot.withinss
## [1] 97.97927
```

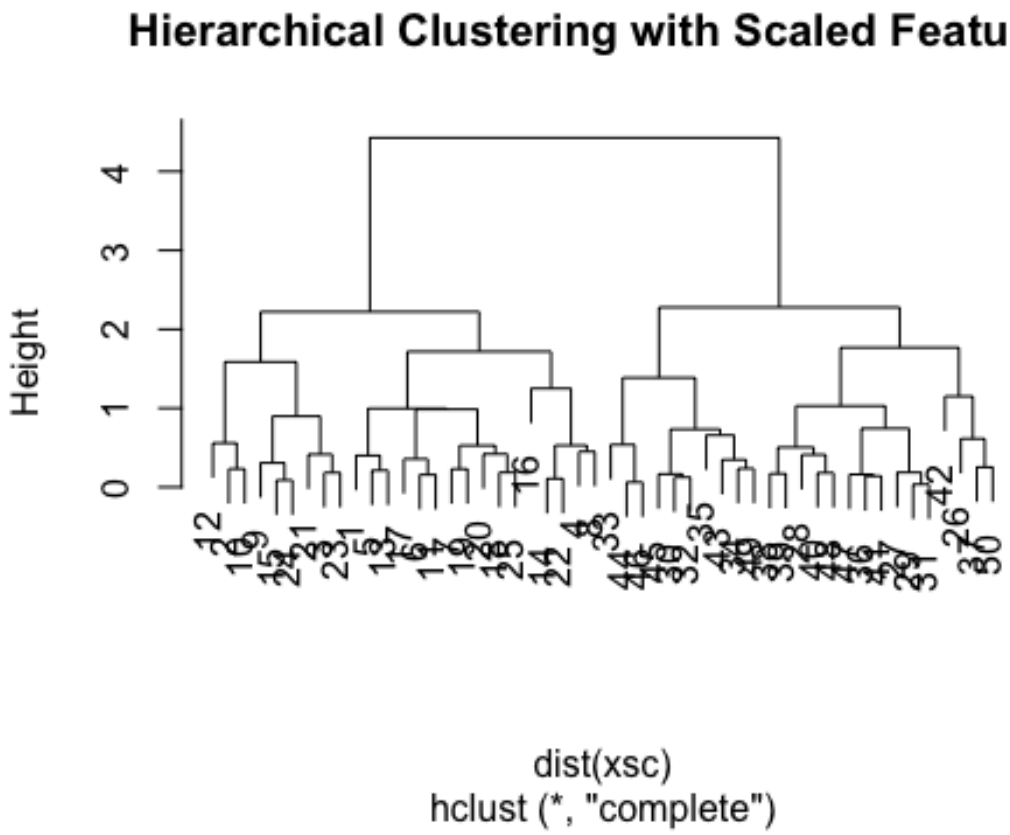
Hierarchical Clustering

```
hc.complete=hclust(dist(x), method="complete")
hc.average=hclust(dist(x), method="average")
hc.single=hclust(dist(x), method="single")
par(mfrow=c(1,3))
plot(hc.complete,main="Complete Linkage", xlab="", sub="", cex=.9)
plot(hc.average, main="Average Linkage", xlab="", sub="", cex=.9)
plot(hc.single, main="Single Linkage", xlab="", sub="", cex=.9)
```

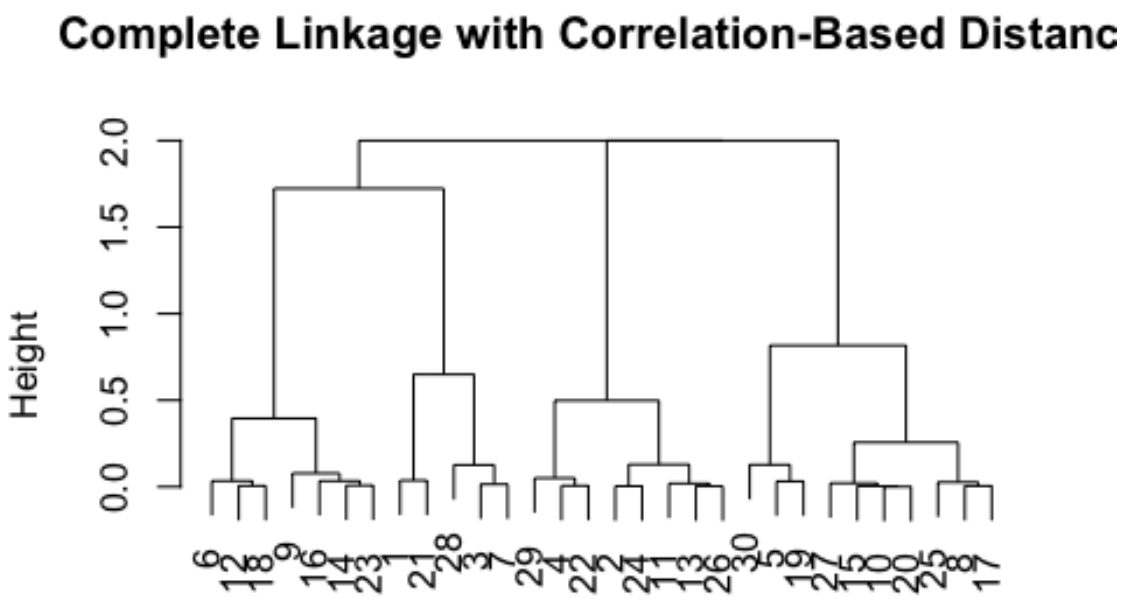



```
cutree(hc.complete, 2)
##  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2
## [36] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
cutree(hc.average, 2)
##  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 1 2 2
## [36] 2 2 2 2 2 2 2 2 1 2 1 2 2 2 2
cutree(hc.single, 2)
##  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [36] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
cutree(hc.single, 4)
```

```
##  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 3 3 3 3 3 3 3 3 3
## [36] 3 3 3 3 3 3 4 3 3 3 3 3 3 3 3
xsc=scale(x)
plot(hclust(dist(xsc), method="complete"), main="Hierarchical Clustering with
Scaled Features")
```




```
x=matrix(rnorm(30*3), ncol=3)
dd=as.dist(1-cor(t(x)))
plot(hclust(dd, method="complete"), main="Complete Linkage with Correlation-
Based Distance", xlab="", sub="")
```


Complete Linkage with Correlation-Based Distanc
Height
0.0
0.5
1.0
1.5
2.0
6
12
18
9
16
14
23
1
21
28
3
7
29
4
22
2
24
11
13
26
30
5
19
27
15
10
20
25
8
17

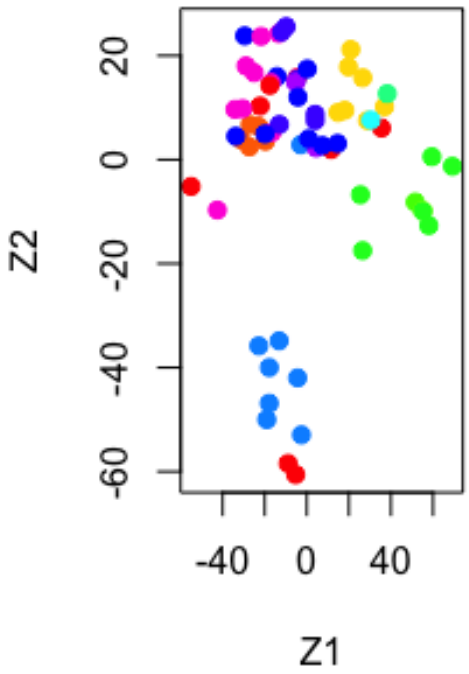
TASK 3 Chapter 10 Lab 3: NCI60 Data Example

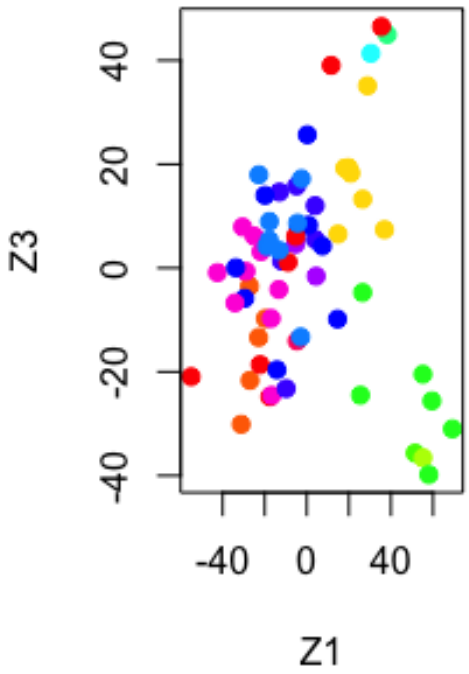
The NCI60 data

```
library(ISLR)
nci.labs=NCI60$labs
nci.data=NCI60$data
dim(nci.data)
## [1]   64 6830
nci.labs[1:4]
## [1] "CNS"   "CNS"   "CNS"   "RENAL"
table(nci.labs)
## nci.labs
##      BREAST         CNS       COLON K562A-repro K562B-repro    LEUKEMIA
##           7           5           7           1           1           6
## MCF7A-repro MCF7D-repro    MELANOMA       NSCLC     OVARIAN    PROSTATE
##           1           1           8           9           6           2
##       RENAL     UNKNOWN
##           9           1
```

PCA on the NCI60 Data

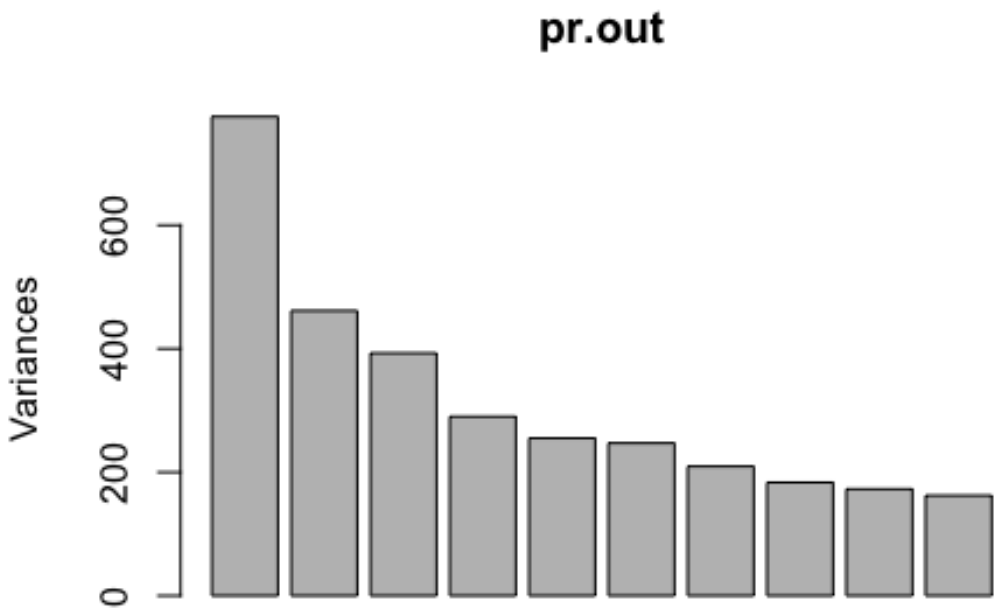
```
pr.out=prcomp(nci.data, scale=TRUE)
Cols=function(vec){
    cols=rainbow(length(unique(vec)))
    return(cols[as.numeric(as.factor(vec))])
  }
par(mfrow=c(1,2))
plot(pr.out$x[,1:2], col=Cols(nci.labs), pch=19,xlab="Z1",ylab="Z2")
plot(pr.out$x[,c(1,3)], col=Cols(nci.labs), pch=19,xlab="Z1",ylab="Z3")
```



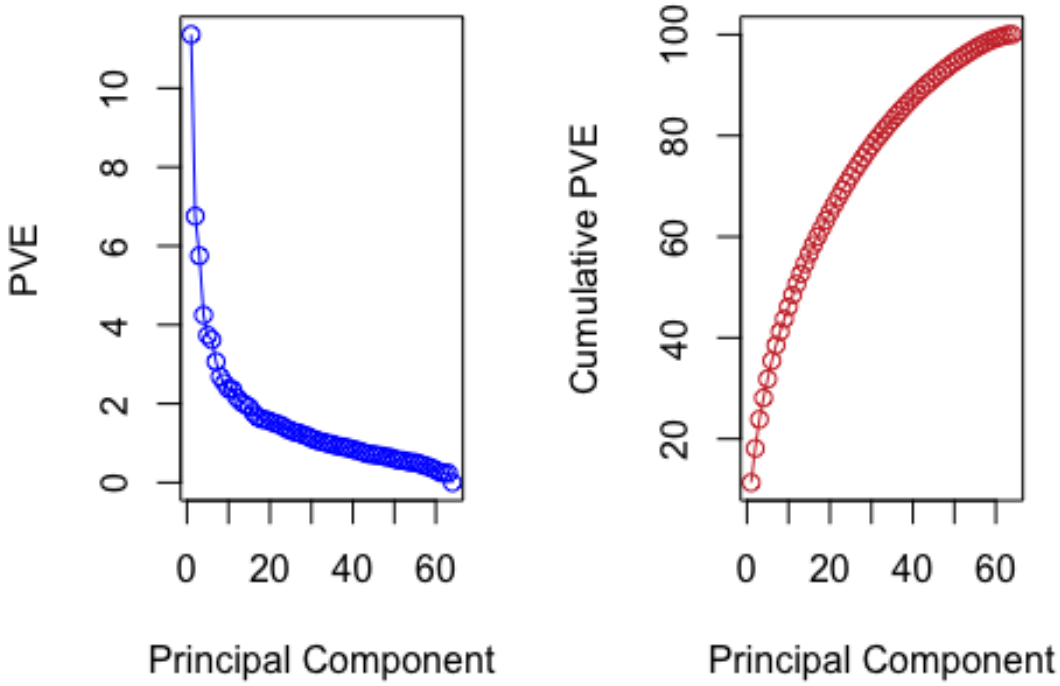



```
summary(pr.out)
## Importance of components:
##                             PC1      PC2      PC3      PC4      PC5
## Standard deviation     27.8535 21.48136 19.82046 17.03256 15.97181
## Proportion of Variance  0.1136  0.06756  0.05752  0.04248  0.03735
## Cumulative Proportion   0.1136  0.18115  0.23867  0.28115  0.31850
##                             PC6      PC7      PC8      PC9     PC10
## Standard deviation     15.72108 14.47145 13.54427 13.14400 12.73860
## Proportion of Variance  0.03619  0.03066  0.02686  0.02529  0.02376
## Cumulative Proportion   0.35468  0.38534  0.41220  0.43750  0.46126
##                            PC11     PC12     PC13     PC14     PC15
## Standard deviation     12.68672 12.15769 11.83019 11.62554 11.43779
## Proportion of Variance  0.02357  0.02164  0.02049  0.01979  0.01915
## Cumulative Proportion   0.48482  0.50646  0.52695  0.54674  0.56590
##                            PC16     PC17     PC18     PC19    PC20
## Standard deviation     11.00051 10.65666 10.48880 10.43518 10.3219
## Proportion of Variance  0.01772  0.01663  0.01611  0.01594  0.0156
## Cumulative Proportion   0.58361  0.60024  0.61635  0.63229  0.6479
##                            PC21    PC22    PC23    PC24    PC25    PC26
## Standard deviation     10.14608 10.0544 9.90265 9.64766 9.50764 9.33253
## Proportion of Variance  0.01507  0.0148 0.01436 0.01363 0.01324 0.01275
## Cumulative Proportion   0.66296  0.6778 0.69212 0.70575 0.71899 0.73174
##                            PC27   PC28    PC29    PC30    PC31    PC32
```

```
## Standard deviation     9.27320 9.0900 8.98117 8.75003 8.59962 8.44738
## Proportion of Variance 0.01259 0.0121 0.01181 0.01121 0.01083 0.01045
## Cumulative Proportion  0.74433 0.7564 0.76824 0.77945 0.79027 0.80072
##                           PC33    PC34    PC35    PC36    PC37    PC38
## Standard deviation     8.37305 8.21579 8.15731 7.97465 7.90446 7.82127
## Proportion of Variance 0.01026 0.00988 0.00974 0.00931 0.00915 0.00896
## Cumulative Proportion  0.81099 0.82087 0.83061 0.83992 0.84907 0.85803
##                           PC39    PC40    PC41   PC42    PC43   PC44
## Standard deviation     7.72156 7.58603 7.45619 7.3444 7.10449 7.0131
## Proportion of Variance 0.00873 0.00843 0.00814 0.0079 0.00739 0.0072
## Cumulative Proportion  0.86676 0.87518 0.88332 0.8912 0.89861 0.9058
##                           PC45   PC46    PC47    PC48    PC49    PC50
## Standard deviation     6.95839 6.8663 6.80744 6.64763 6.61607 6.40793
## Proportion of Variance 0.00709 0.0069 0.00678 0.00647 0.00641 0.00601
## Cumulative Proportion  0.91290 0.9198 0.92659 0.93306 0.93947 0.94548
##                           PC51    PC52    PC53    PC54    PC55    PC56
## Standard deviation     6.21984 6.20326 6.06706 5.91805 5.91233 5.73539
## Proportion of Variance 0.00566 0.00563 0.00539 0.00513 0.00512 0.00482
## Cumulative Proportion  0.95114 0.95678 0.96216 0.96729 0.97241 0.97723
##                           PC57   PC58    PC59    PC60    PC61    PC62
## Standard deviation     5.47261 5.2921 5.02117 4.68398 4.17567 4.08212
## Proportion of Variance 0.00438 0.0041 0.00369 0.00321 0.00255 0.00244
## Cumulative Proportion  0.98161 0.9857 0.98940 0.99262 0.99517 0.99761
##                           PC63      PC64
## Standard deviation     4.04124 2.148e-14
## Proportion of Variance 0.00239 0.000e+00
## Cumulative Proportion  1.00000 1.000e+00
plot(pr.out)
```

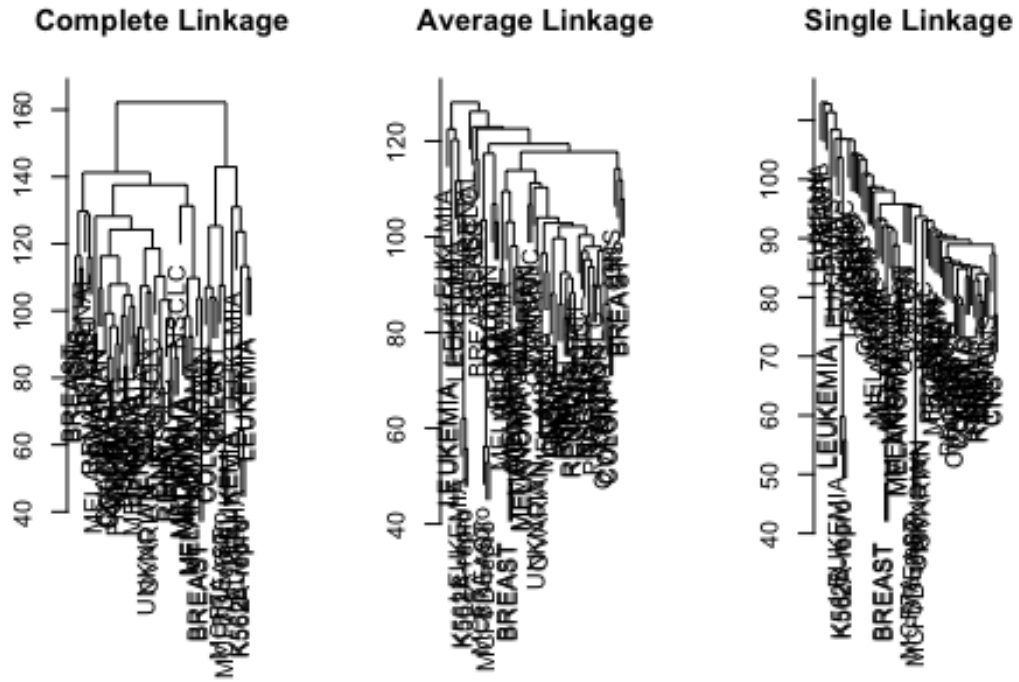



```r
pve=100*pr.out$sdev^2/sum(pr.out$sdev^2)
par(mfrow=c(1,2))
plot(pve,  type="o", ylab="PVE", xlab="Principal Component", col="blue")
plot(cumsum(pve), type="o", ylab="Cumulative PVE", xlab="Principal
Component", col="brown3")
```

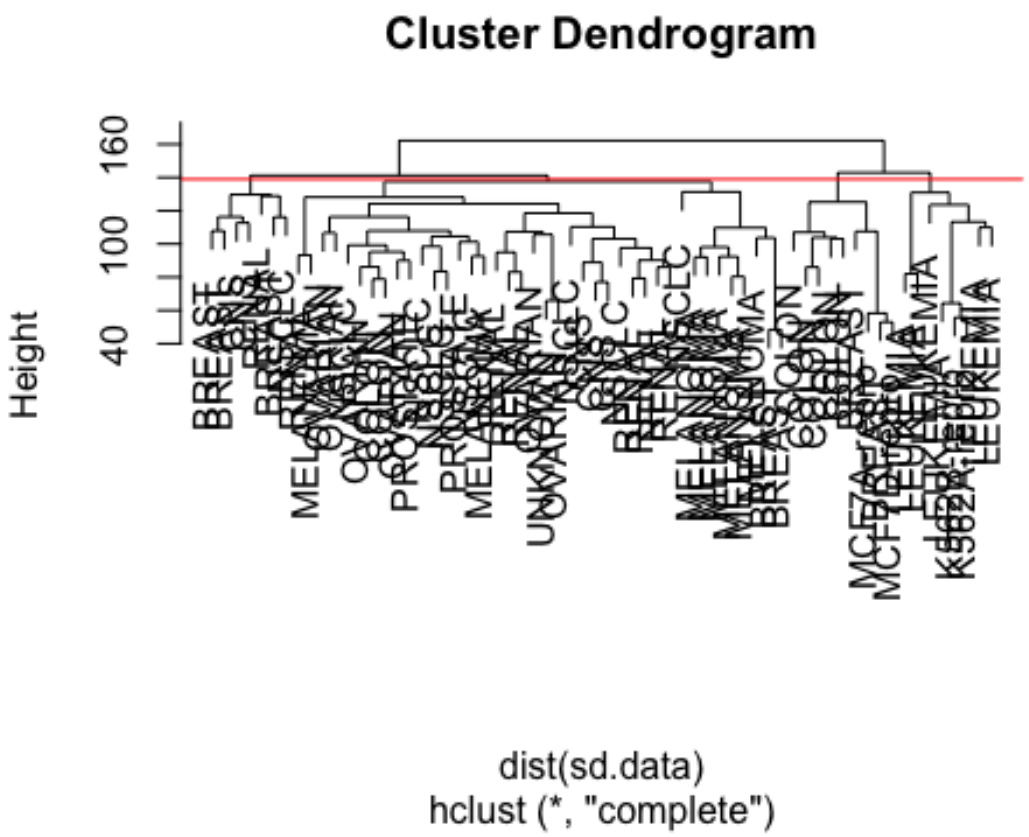


Clustering the Observations of the NCI60 Data

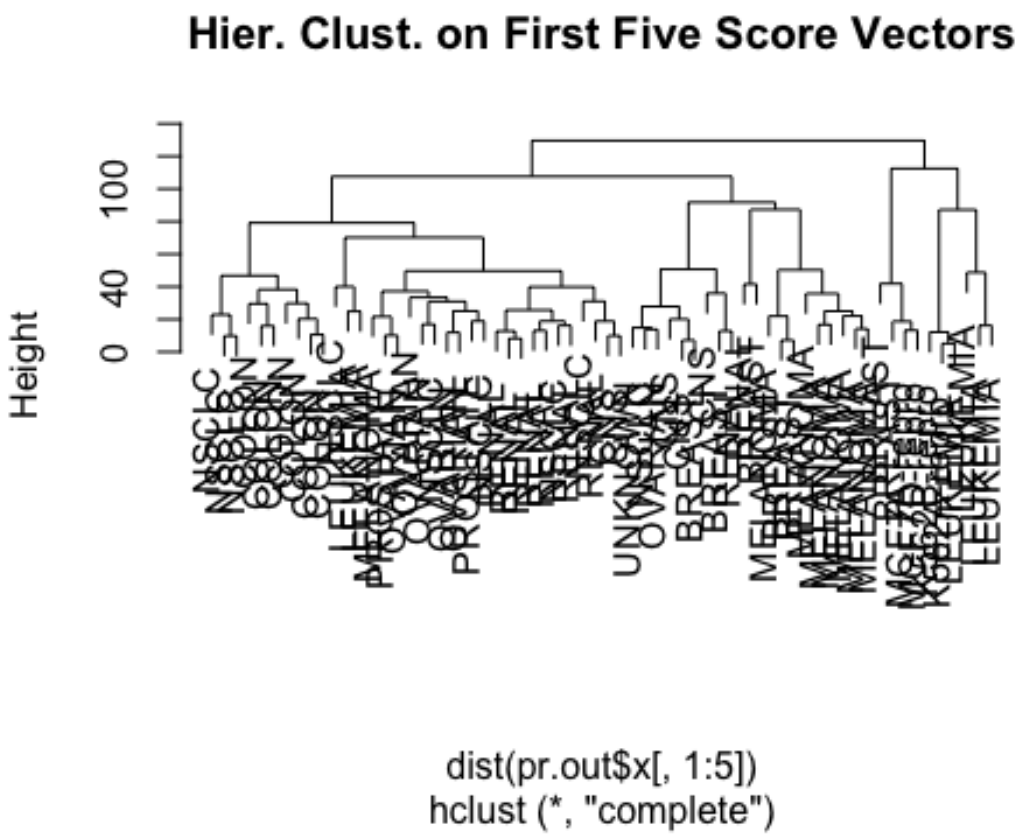
```
sd.data=scale(nci.data)
par(mfrow=c(1,3))
data.dist=dist(sd.data)
plot(hclust(data.dist), labels=nci.labs, main="Complete Linkage", xlab="",
sub="",ylab="")
plot(hclust(data.dist, method="average"), labels=nci.labs, main="Average
Linkage", xlab="", sub="",ylab="")
plot(hclust(data.dist, method="single"), labels=nci.labs,  main="Single
Linkage", xlab="", sub="",ylab="")
```




```
hc.out=hclust(dist(sd.data))
hc.clusters=cutree(hc.out,4)
table(hc.clusters,nci.labs)
##             nci.labs
## hc.clusters BREAST CNS COLON K562A-repro K562B-repro LEUKEMIA MCF7A-repro
##           1      2   3     2           0           0        0           0
##           2      3   2     0           0           0        0           0
##           3      0   0     0           1           1        6           0
##           4      2   0     5           0           0        0           1
##             nci.labs
## hc.clusters MCF7D-repro MELANOMA NSCLC OVARIAN PROSTATE RENAL UNKNOWN
##           1           0        8     8       6        2     8       1
##           2           0        0     1       0        0     1       0
##           3           0        0     0       0        0     0       0
##           4           1        0     0       0        0     0       0
par(mfrow=c(1,1))
plot(hc.out, labels=nci.labs)
abline(h=139, col="red")
```




```
hc.out
##
## Call:
## hclust(d = dist(sd.data))
##
## Cluster method   : complete
## Distance         : euclidean
## Number of objects: 64
set.seed(2)
km.out=kmeans(sd.data, 4, nstart=20)
km.clusters=km.out$cluster
table(km.clusters,hc.clusters)
##             hc.clusters
## km.clusters  1  2  3  4
##           1 11  0  0  9
##           2  0  0  8  0
##           3  9  0  0  0
##           4 20  7  0  0
hc.out=hclust(dist(pr.out$x[,1:5]))
plot(hc.out, labels=nci.labs, main="Hier. Clust. on First Five Score
Vectors")
```




```
table(cutree(hc.out,4), nci.labs)
##    nci.labs
##     BREAST CNS COLON K562A-repro K562B-repro LEUKEMIA MCF7A-repro
##   1      0   2     7           0           0        2           0
##   2      5   3     0           0           0        0           0
##   3      0   0     0           1           1        4           0
##   4      2   0     0           0           0        0           1
##    nci.labs
##     MCF7D-repro MELANOMA NSCLC OVARIAN PROSTATE RENAL UNKNOWN
##   1           0        1     8       5        2     7       0
##   2           0        7     1       1        0     2       1
##   3           0        0     0       0        0     0       0
##   4           1        0     0       0        0     0       0
```

TASK 4 Summary 10 points Report time required for homework, difficulties encountered, and collaborators.

Report time required for homework: The whole time taken for this project including the time spent on understanding the concepts and executing them along with the different variations possible was 10 days.

Difficulties Encountered: Working on R studio with R code has been relatively easy now given we have already done some projects on it.
However, the main challenge was to understand the project and the various aspects of it. Also, it is very important to understand the execution and the syntax of R to understand it for various ways different parts of a code could be altered and modified to get desired results.

Collaborators: Not required as the explanation in book is self sufficient.