Clustering and Principal Component Analysis

Data Analytics and Visualizqation (Spring 2019)

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NCI60 cancer cell line microarray data, which consists of 6,830 gene expression measurements on 64 cancer cell lines. Each cell line is labeled with a cancer type. The data has 64 rows and 6,830 columns.

```
library (ISLR)
nci.labs=NCI60$labs
nci.data=NCI60$data

dim(nci.data)
```

```
## [1]   64 6830
```

Examining the cancer types for the cell lines

```
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
```

We first perform PCA on the data after scaling the variables (genes) to have standard deviation one.

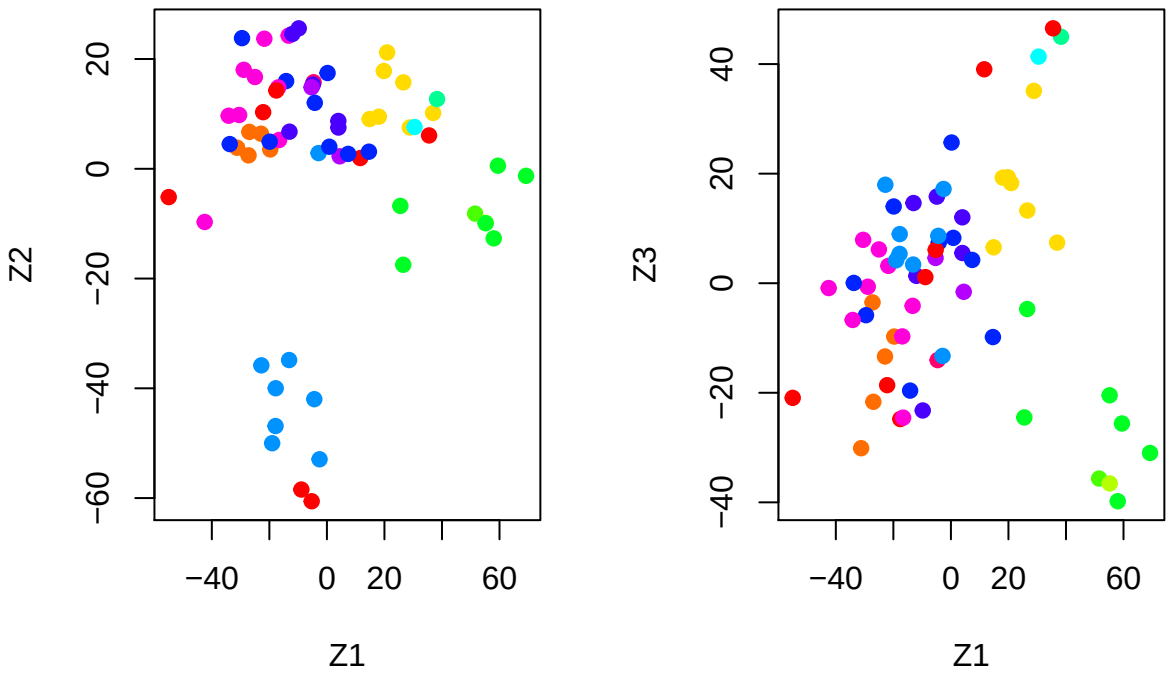
```
pr.out =prcomp (nci.data , scale=TRUE)
```

The function will be used to assign a color to each of the 64 cell lines, based on the cancer type to which it corresponds.

```
Cols=function (vec ){
  cols=rainbow (length (unique (vec )));
  return (cols[as.numeric (as.factor (vec))]);
}
```

Plot the principal component score vectors.

```
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")
```



obtain a summary of the proportion of variance explained (PVE) of the first few principal components using the summary() method for a prcomp object.

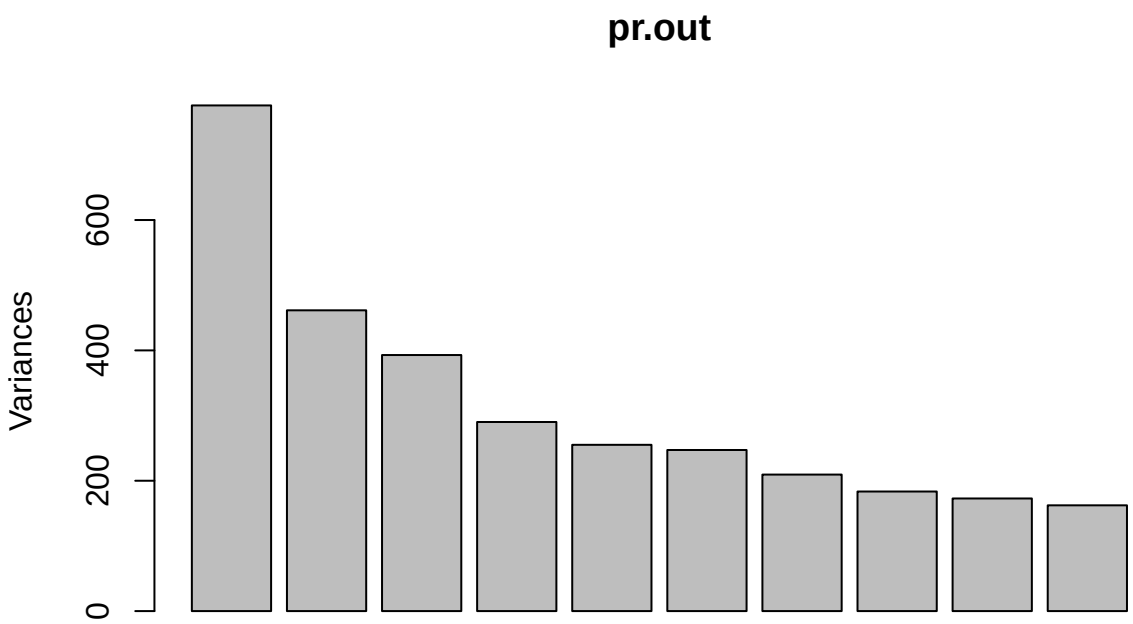
```
summary (pr.out)
```

```
## 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
```

Using the plot() function, we can also plot the variance explained by the first few principal components

```
plot(pr.out) # Note that the height of each bar in the bar plot is given by squaring the corresponding
```



Performing Hierarchical Clustering.

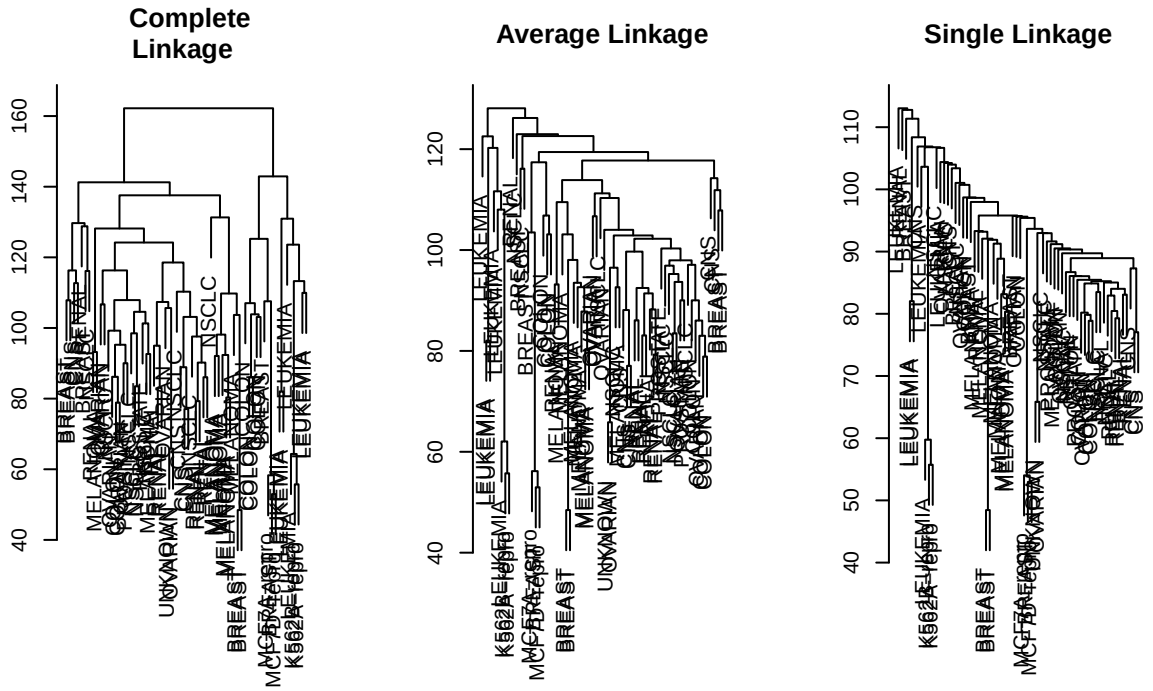
```
# Clustering the Observations of the NCI60 Data
sd.data=scale(nci.data)

par(mfrow =c(1,3))
data.dist=dist(sd.data)

# performing hierarchical clustering
# Complete linkage
plot(hclust (data.dist), labels =nci.labs , main=" Complete
Linkage ", xlab ="", sub ="", ylab ="")

#Average Linkage
plot(hclust (data.dist , method ="average"), labels =nci.labs ,
       main=" Average Linkage ", xlab ="", sub ="", ylab ="")

#Single Linkage
plot(hclust (data.dist , method ="single"), labels =nci.labs ,
       main=" Single Linkage ", xlab="", sub ="", ylab ="")
```



NOTE: the choice of linkage certainly does affect the results obtained. Typically, single linkage will tend to yield trailing clusters: very large clusters onto which individual observations attach one-by-one. On the other hand, complete and average linkage tend to yield more balanced, attractive clusters. For this reason, complete and average linkage are generally preferred to single linkage.

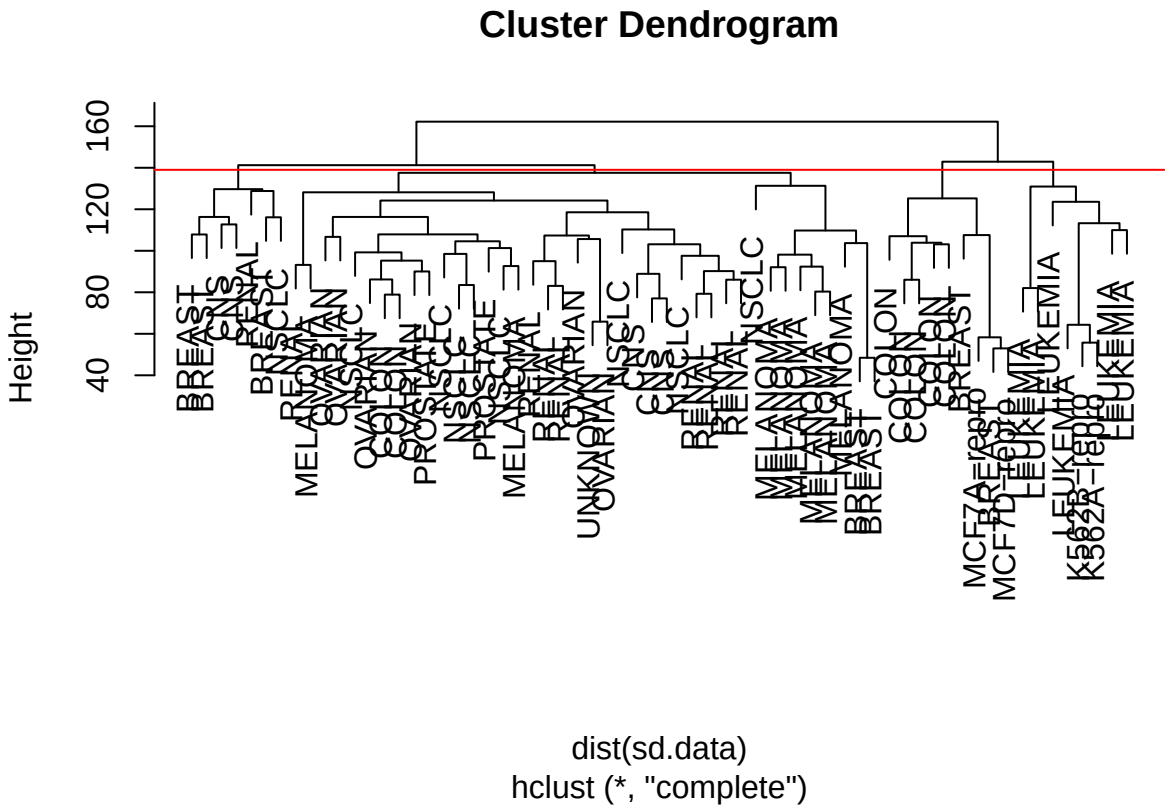
Inference: Clearly cell lines within a single cancer type do tend to cluster together, although the clustering is not perfect.

```
# We can cut the dendrogram at the height that will yield a particular number of clusters, k=4
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
```

There are some clear patterns. All the leukemia cell lines fall in cluster 3, while the breast cancer cell lines are spread out over three different clusters.

```
par(mfrow =c(1,1))
plot(hc.out , labels =nci.labs)
abline (h=139, col =" red ")
```



How do these NCI60 hierarchical clustering results compare to what we get if we perform K-means clustering with K = 4??

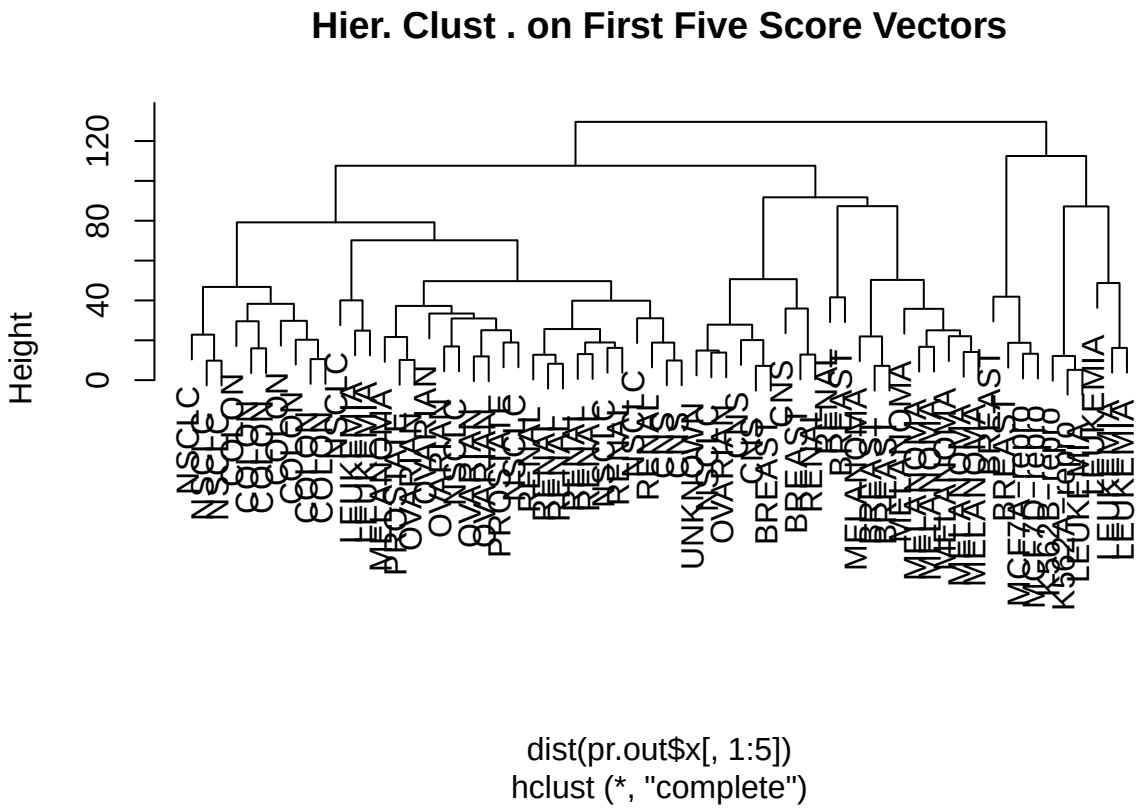
```
set.seed (2)
km.out =kmeans (sd.data , 4, nstart =20)
km.clusters =km.out$cluster
table(km.clusters ,hc.clusters )
```

```
##            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
```

We see that the four clusters obtained using hierarchical clustering and Kmeans clustering are somewhat different. Cluster 2 in K-means clustering is identical to cluster 3 in hierarchical clustering. However, the other clusters differ.

Rather than performing hierarchical clustering on the entire data matrix, we can simply perform hierarchical clustering on the first few principal component score vectors, as follows:

```
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
```