Statistics 452: Statistical Learning and Prediction

Chapter 10, part 3: Hierarchical Clustering

Brad McNeney

2018-11-21

Hierarchical Clustering

- Instead of setting the number of clusters in advance, as in K-means/medoids, we create a tree drawing (dendrogram) that represents a hierarchy of nested partitions of the objects into clusters.
  - See the example on the next slide.
- We can create the hierarchy in a top-down or bottom-up fashion.
- Bottom-up, or agglomerative clustering is the most common and will be described.
  - Given a measure of dissimilarity between clusters, we successively fuse, or merge clusters, starting with n clusters of size one and ending with a single cluster of size n.

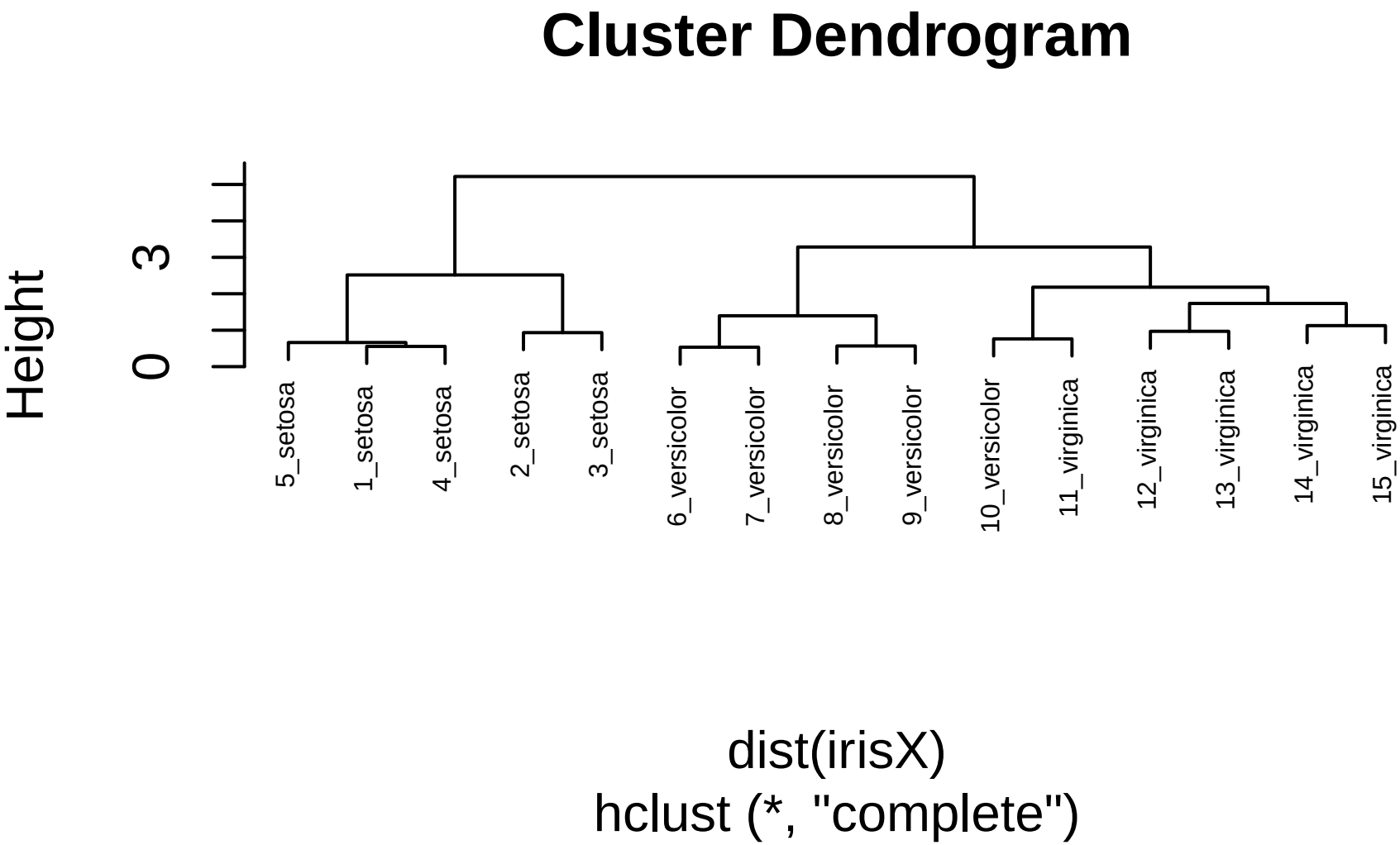
Example: Hierarchical Clustering of Irises

- First select a subsample of 5 irises from each species, then remove the species information.
- We use the function `hclust()` to generate the hierarchical clustering.

```
data(iris)
set.seed(1)
library(dplyr)
iris <- iris %>%
  group_by(Species) %>%
  sample_n(size=5) %>%
  ungroup()
irisX <- iris %>%
  select(-Species) %>%
  scale()
rownames(irisX) <- paste(rownames(iris),iris$Species,sep="_")
ic <- hclust(dist(irisX))
```

Plotting the Dendrogram

```
plot(ic,cex=.5)
```

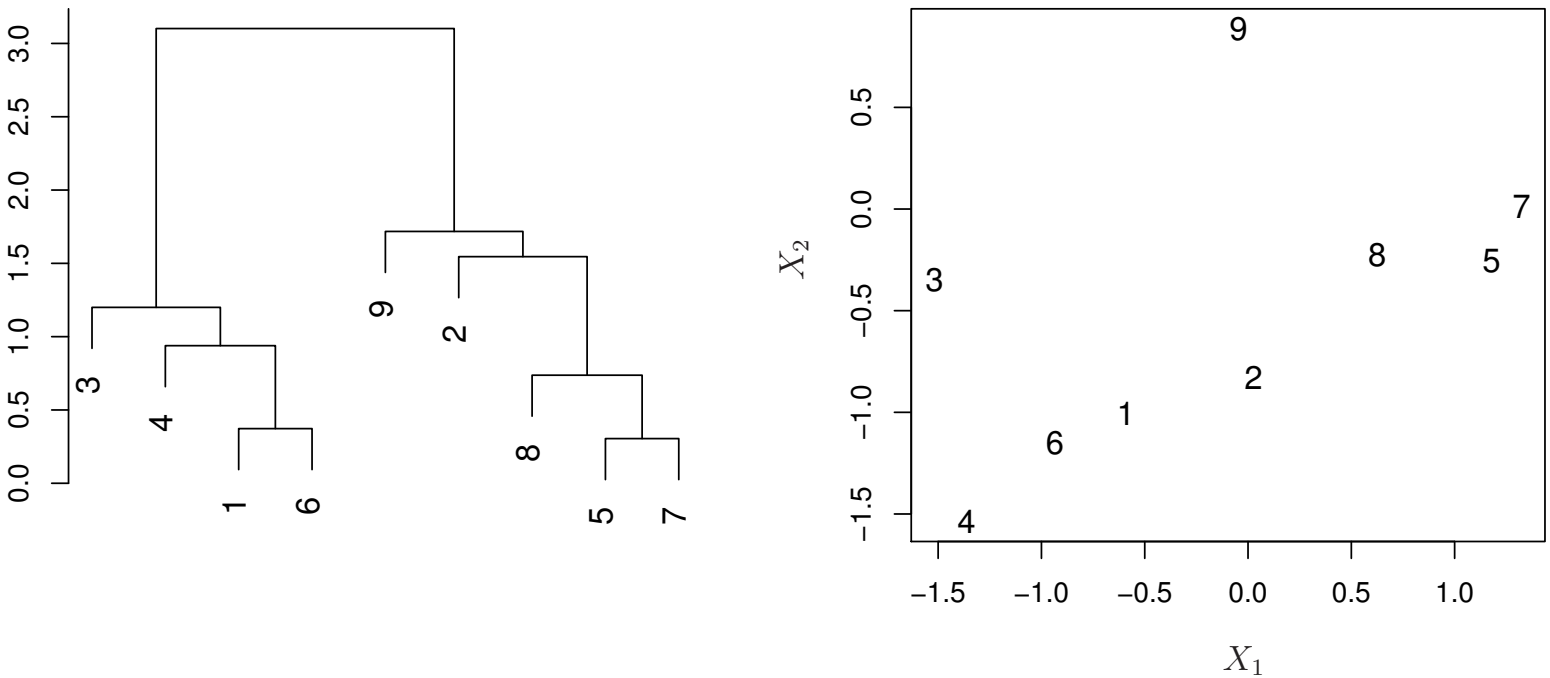


Interpretation of the Dendrogram

- The height of a node reflects the dissimilarity of its two descendant clusters.
  - Branch lengths are not generally informative.
- The first node on the dendrogram partitions the data in to two clear clusters.
  - Knowing the species we can see this reflects the separation between the *setosa* and other species.
- The second node roughly separates the *versicolor* and *virginica* species, though there is one *versicolor* in the *virginica* cluster.
  - Note: The subtrees can be rotated without changing the structure of the dendrogram, so we should not interpret the horizontal placement of the leaves and/or branches.

Simulated Data Example

- Figure 10.10 from the text:



- The height of the node that merges $\{9\}$ with $\{2, 8, 5, 7\}$ reflects the dissimilarity. Branch lengths separating, say, 9 and 2 are not meaningful.

Cutting Dendrograms to Obtain Clusters

- Cutting the dendrogram at a given dissimilarity value leads to clusters.
  - For example, on the iris dendrogram, cutting at about 4 gives two clusters (*setosa vs* others) and cutting at about 3 gives three clusters (*setosa* and roughly *vesicolor* and *virginica*.)
- The `cutree()` function allows us to cut at either a height `h` or where there are `k` clusters.

```
cutree(ic,k=3)
```

```
##      1_setosa      2_setosa      3_setosa      4_setosa      5_setosa
##             1             1             1             1             1
##  6_versicolor  7_versicolor  8_versicolor  9_versicolor 10_versicolor
##             2             2             2             2             3
##  11_virginica  12_virginica  13_virginica  14_virginica  15_virginica
##             3             3             3             3             3
```

```
table(cutree(ic,k=3))
```

```
##
## 1 2 3
## 5 4 6
```

Hierarchical Clustering Algorithm

1. Begin with n observations and a measure of the $n(n-1)/2$ pairwise dissimilarities. Treat each observation as its own cluster.
2. For $i = n, n-1, \ldots, 2$:
   - 2.1 Identify the pair of clusters that are least dissimilar and merge them. The dissimilarity between merged clusters is the height of the new node on the dendrogram.
   - 2.2 Compute the pairwise inter-cluster dissimilarities among the $i-1$ remaining clusters.

- To be determined: How do we measure dissimilarity between objects and between **clusters**?

Dissimilarity Between Objects

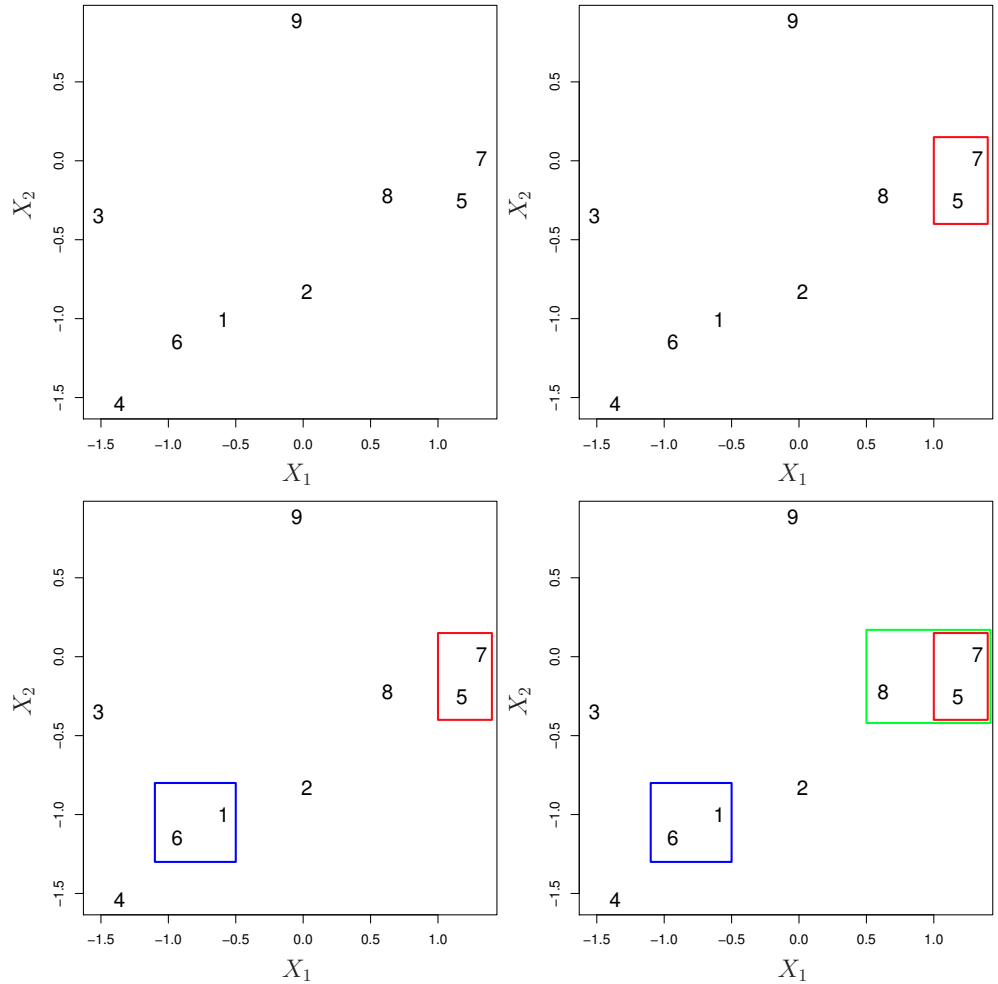
- Several possibilities:
  - Euclidean (ℓ_2) distance, $d(a,b) = \sqrt{\sum_{i=1}^{p}(a_i - b_i)^2}$.
  - Squared Euclidean (ℓ_2^2) distance, $d(a,b) = \sum_{i=1}^{p}(a_i - b_i)^2$.
  - Manhattan (ℓ_1) distance, $d(a,b) = \sum_{i=1}^{p}|a_i - b_i|^2$
  - Maximum (ℓ_∞) distance, $d(a,b) = \max_i |a_i - b_i|$.
- Euclidean, manhattan and maximum distances are implemented in the `dist()` function in R, and squared Euclidean can be computed with `dist(x,method="euclidean")^2`.

Linkage: Dissimilarity Between Clusters

- The four most common linkages are:
  - Complete: $\max\{\, d(a,b) : a \in A,\ b \in B \,\}$.
  - Average: $\frac{1}{|A||B|} \sum_{a \in A} \sum_{b \in B} d(a,b)$.
  - Centroid: $||c_s - c_t||$ where c_s and c_t are the centroids of clusters s and t, respectively.
  - Single: $\min\{\, d(a,b) : a \in A,\ b \in B \,\}$.
- According to the text, average, complete and single linkage are the most popular among statisticians, and average and complete are preferred because they produce more balanced dendrograms than single.
- In `hclust()`, complete is the default, and the three others are options.

Example: Clustering of the Simulated Data Example

- Figure 10.11 from the text: The first three steps of clustering using Euclidean distance and complete linkage.



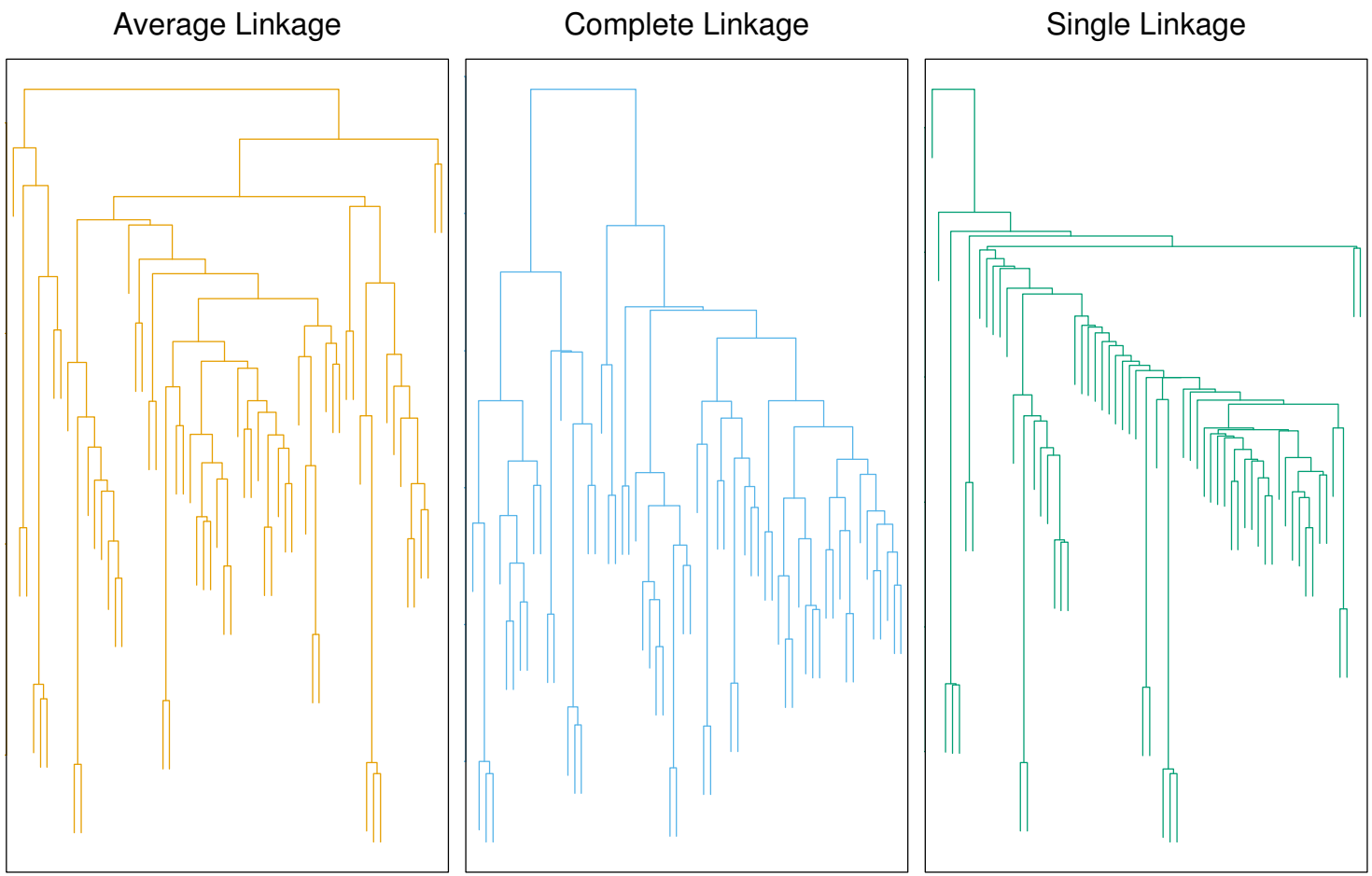
- Read top-left, top-right, bottom-left, bottom-right.

The Choice of Dissimilarity, Linkage and Scaling Affect the Dendrogram

- Each choice will influence the dendrogram.
- Illustrate sensitivity to linkage and scaling.

Sensitivity to Linkage

- Figure 10.12 from the text. Note the imbalance in the dendrogram under single linkage:



Sensitivity to Scaling

- Whether to scale or not is problem dependent.
- The amount of variation in a variable will determine how much it influences the dissimilarities, and therefore the linkages between clusters.
- Example: In the decathlon data from the week 12 exercises, the 1500m had by far the greatest variance.

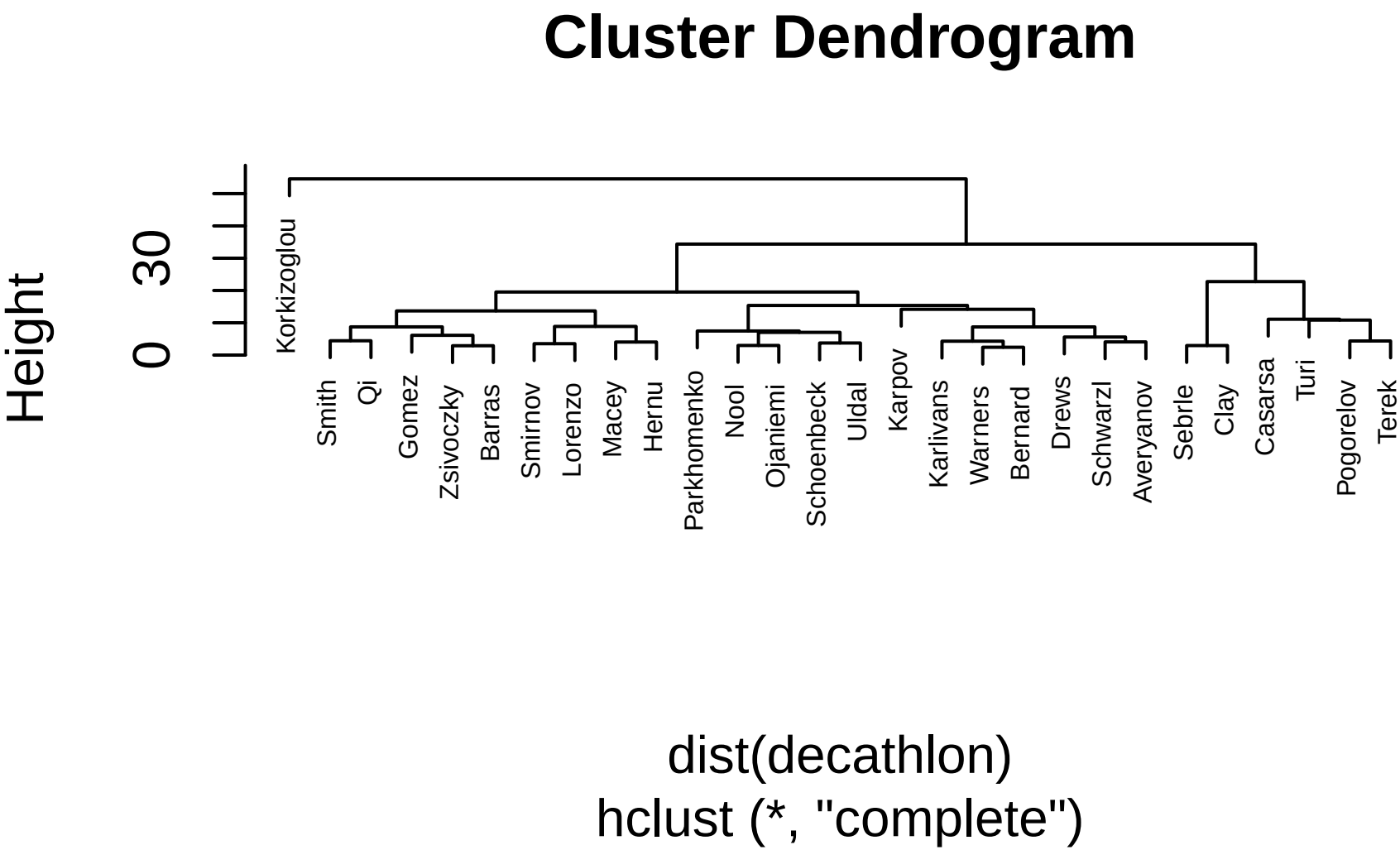
```
round(diag(var(decathlon)),3)
```

```
##        100m   Long.jump    Shot.put   High.jump        400m 110m.hurdle
##       0.053       0.116       0.733       0.008       1.609       0.196
##      Discus  Pole.vault    Javeline       1500m
##      10.887       0.084      24.759     128.184
```

Clustering of the Decathlon Data Without Scaling

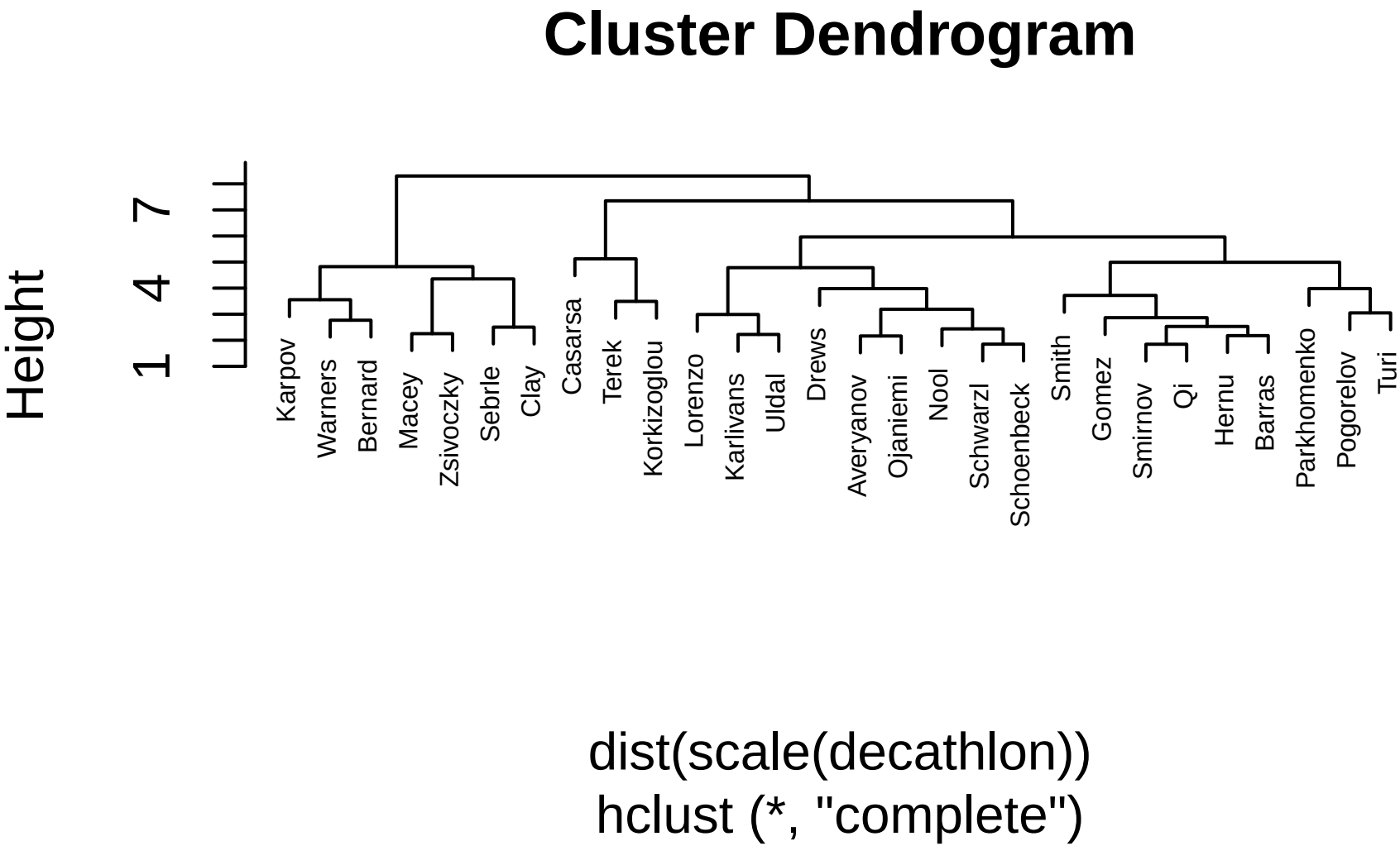
- Korkizoglou stands apart, because he beat the rest of the field by more than 20 seconds in the 1500m.

```
plot(hclust(dist(decathlon)),cex=.5)
```



Clustering of the Decathlon Data With Scaling

```
plot(hclust(dist(scale(decathlon))),cex=.5)
```



NCI60 data

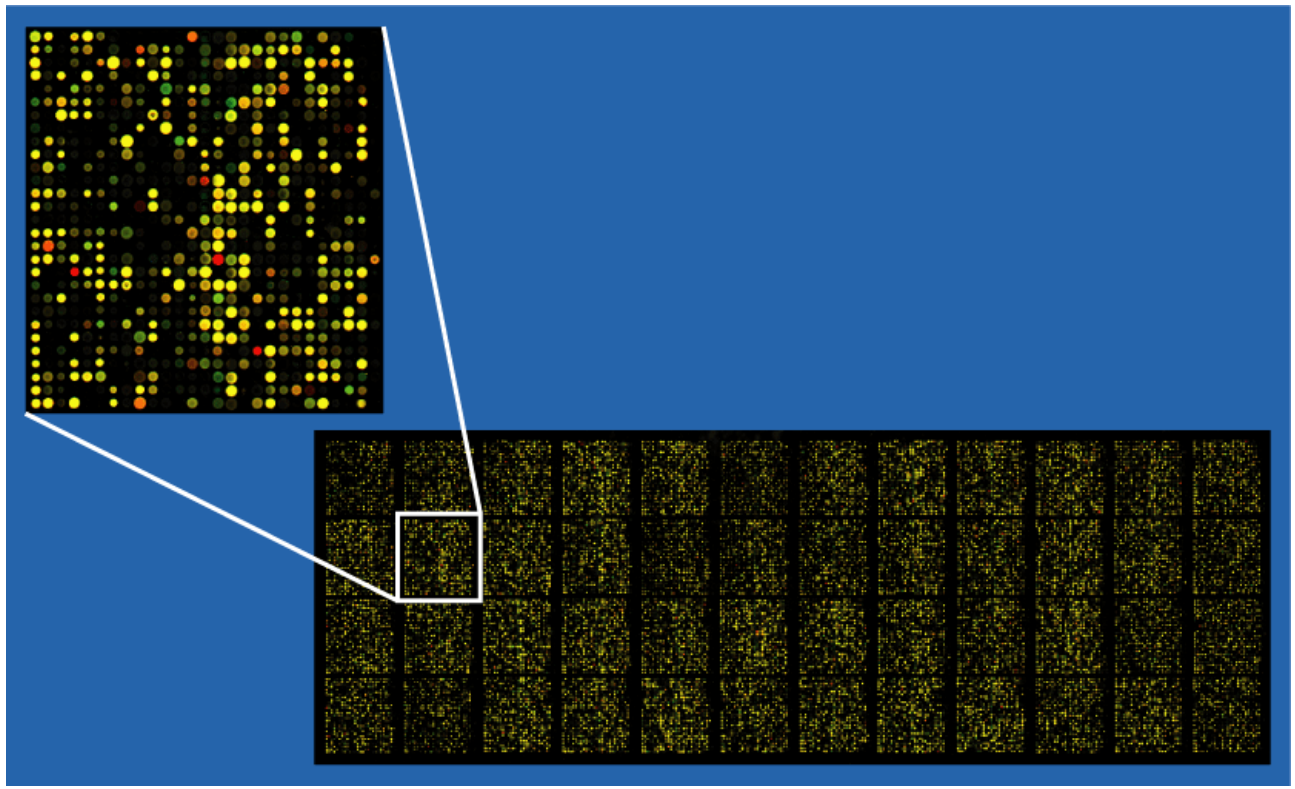
- We follow the lab on clustering of the NCI60 data set, which contains the results of a DNA microarray study of 64 cancer cells.
- Cancer cells are labelled by location of the cancer.
  - However, recent research suggests that classification based on location of the cancer may not be as useful as classification based on the cancer-causing mutation (e.g., a mutation in a gene responsible for DNA repair).

DNA Microarray Experiments

- See the Wikipedia page on microarrays (https://en.wikipedia.org/wiki/DNA_microarray) for a description.
- Briefly:
  - Genes in a cell are transcribed to produce messenger RNA, which is extracted and copied into DNA.
  - The DNA is fragmented, flourescently labelled, and then exposed to an ordered array of complementary DNA molecules called probes that identify specific genes.
  - The array "lights up" where the labelled DNA has bound to the probes. The flourescence intensity at each probe is a measure of how much of the corresponding gene was being expressed in the cell.

Microarray Picture

- Example micorarray with about 40,000 probes



Source: Wikimedia Commons

The NCI Data

- Rows are cancer cells, labelled by the type of cancer, and columns are the probes (genes).
- Entries of the data matrix are the flourescence intensities after quality control has been applied.

```
library(ISLR)
data(NCI60)
nciX <- NCI60$data
dim(nciX)
```

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

```
nciL <- NCI60$labs
rownames(nciX) <- nciL
nciX[1:5,1:5]
```

```
##                1         2         3         4         5
## CNS     0.300000  1.180000  0.550000  1.140000 -0.265000
## CNS     0.679961  1.289961  0.169961  0.379961  0.464961
## CNS     0.940000 -0.040000 -0.170000 -0.040000 -0.605000
## RENAL   0.280000 -0.310000  0.680000 -0.810000  0.625000
## BREAST  0.485000 -0.465000  0.395000  0.905000  0.200000
```

PCA on the NCI60 Data

- One could argue that highly expressed genes **should** drive the PCs, but we scale.

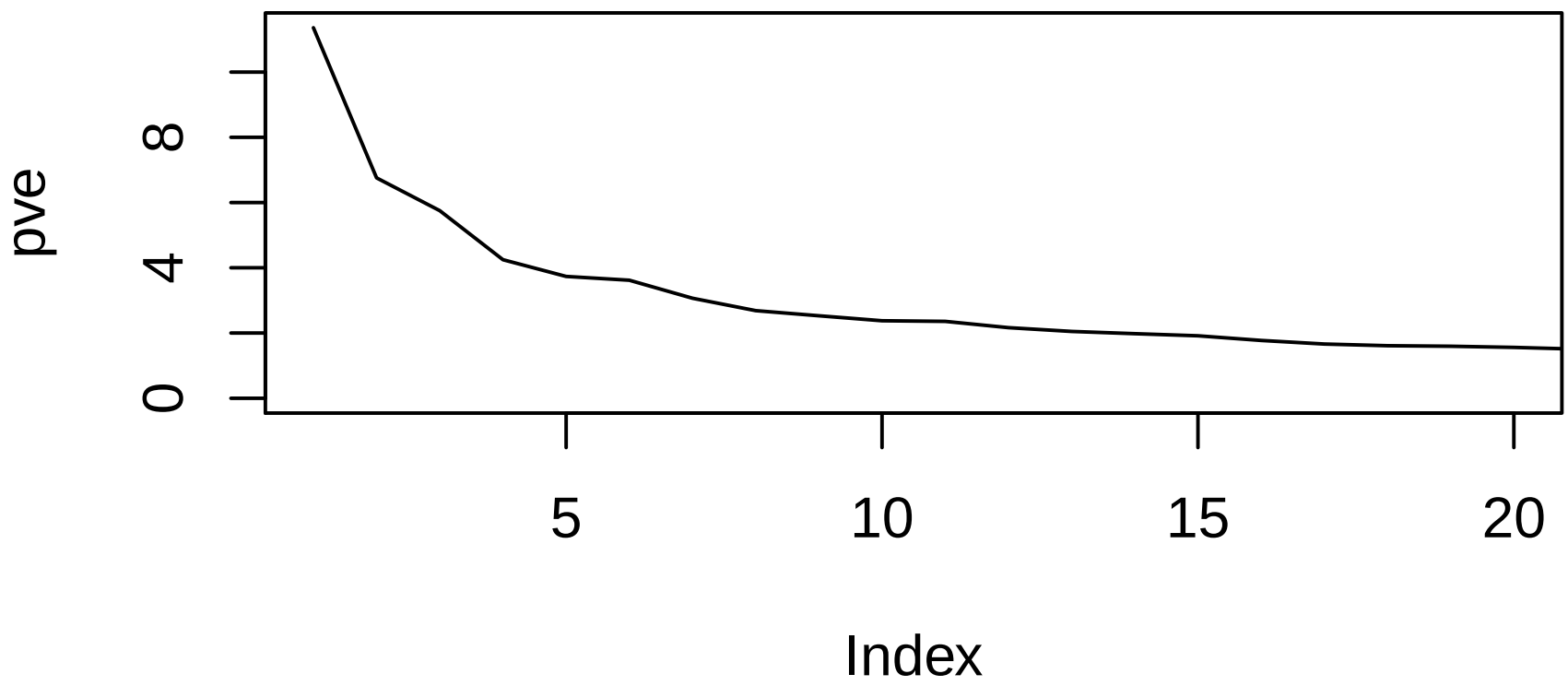
```
nciX <- scale(nciX)
pcout <- prcomp(nciX)
summary(pcout)
```

```
## 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
```

Scree Plot

- Express variances as percent total

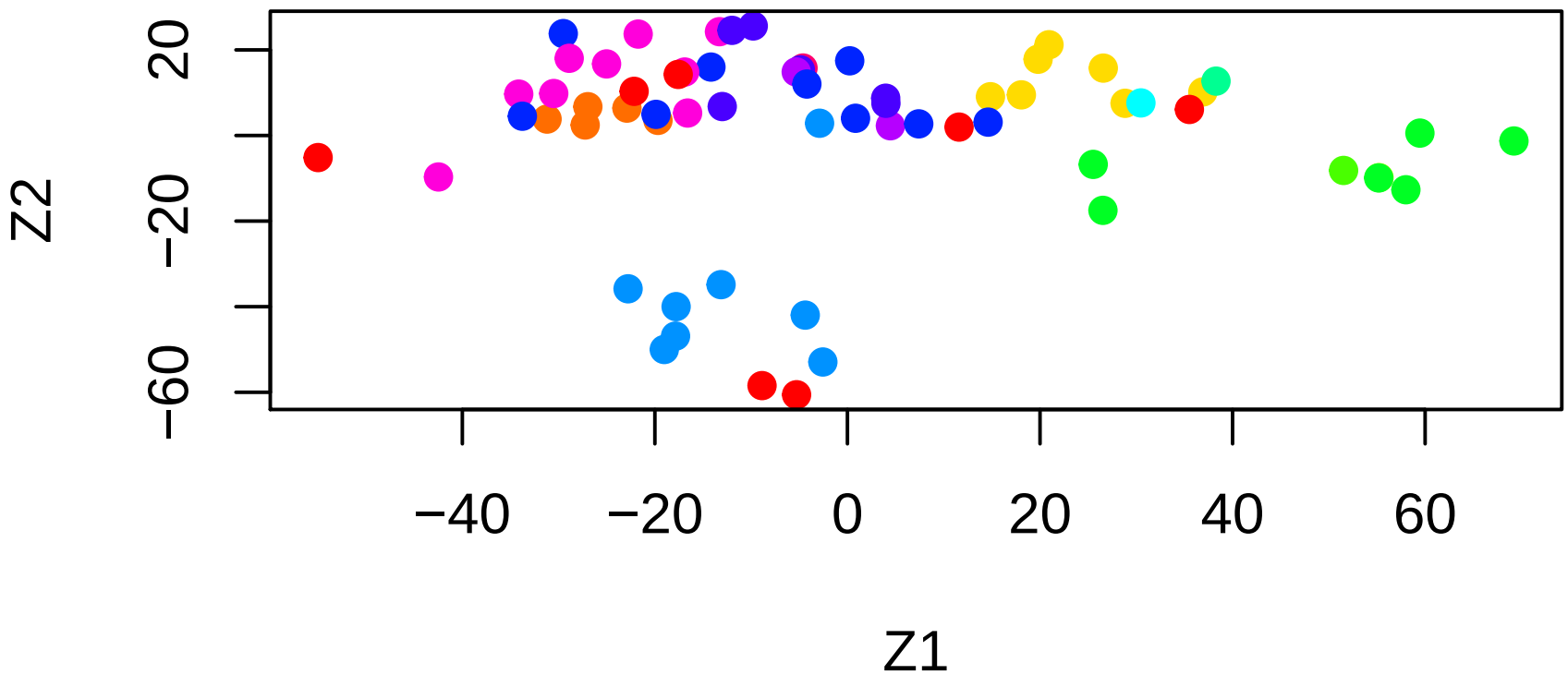
```
pve <- 100*pcout$sdev^2/sum(pcout$sdev^2)
plot(pve,xlim=c(1,20),type="l")
```



- Possible "elbow" at about 5 PCs

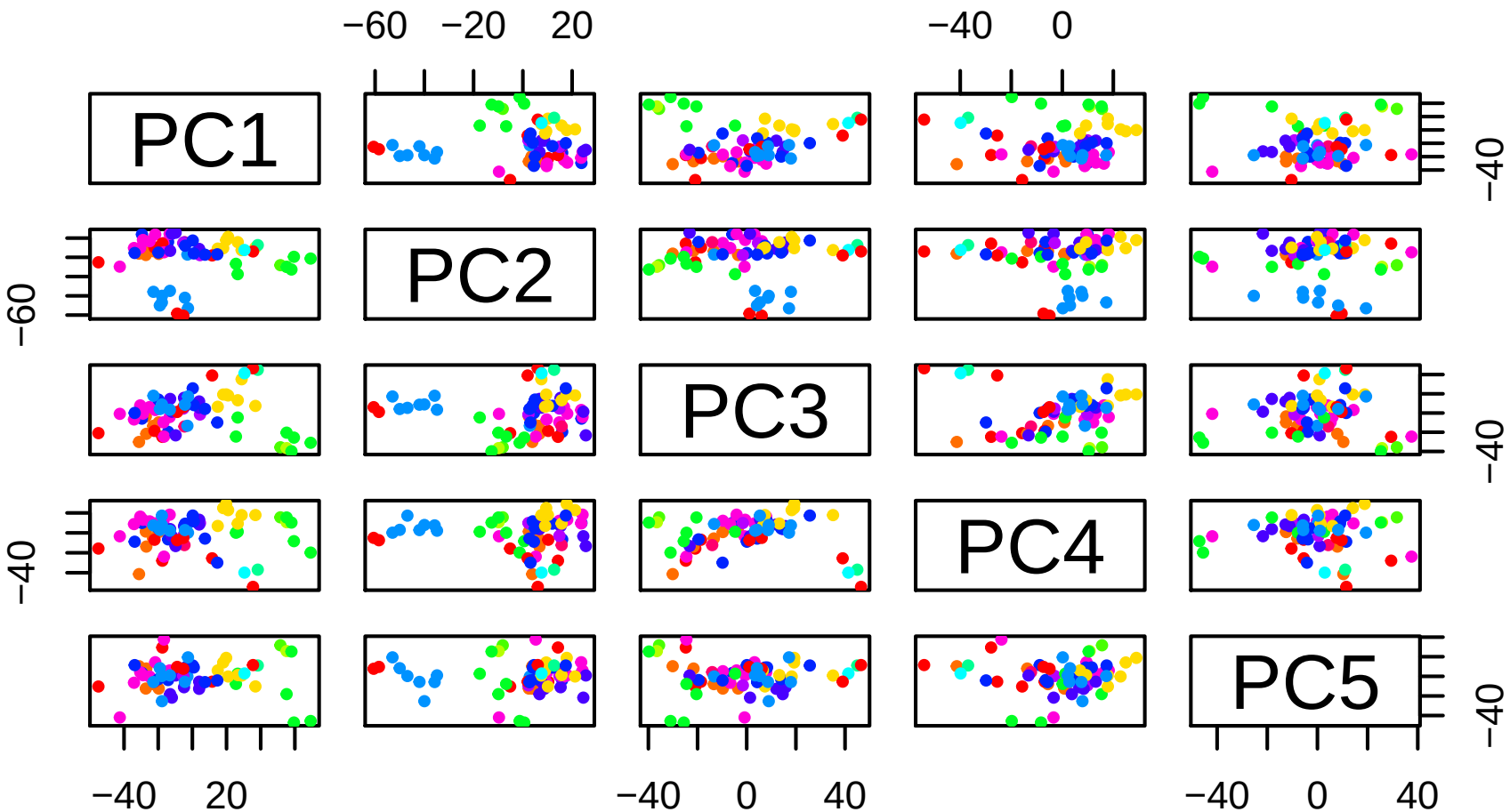
PC Plots

```
rcols <- rainbow(length(unique(nciL)))
ccols <- rcols[as.numeric(factor(nciL))]
plot(pcout$x[,1],pcout$x[,2],col=ccols,pch=19,xlab="Z1",ylab="Z2")
```



Pairwise PC plots

```
pairs(pcout$x[,1:5],col=ccols,pch=19,cex=.5)
```



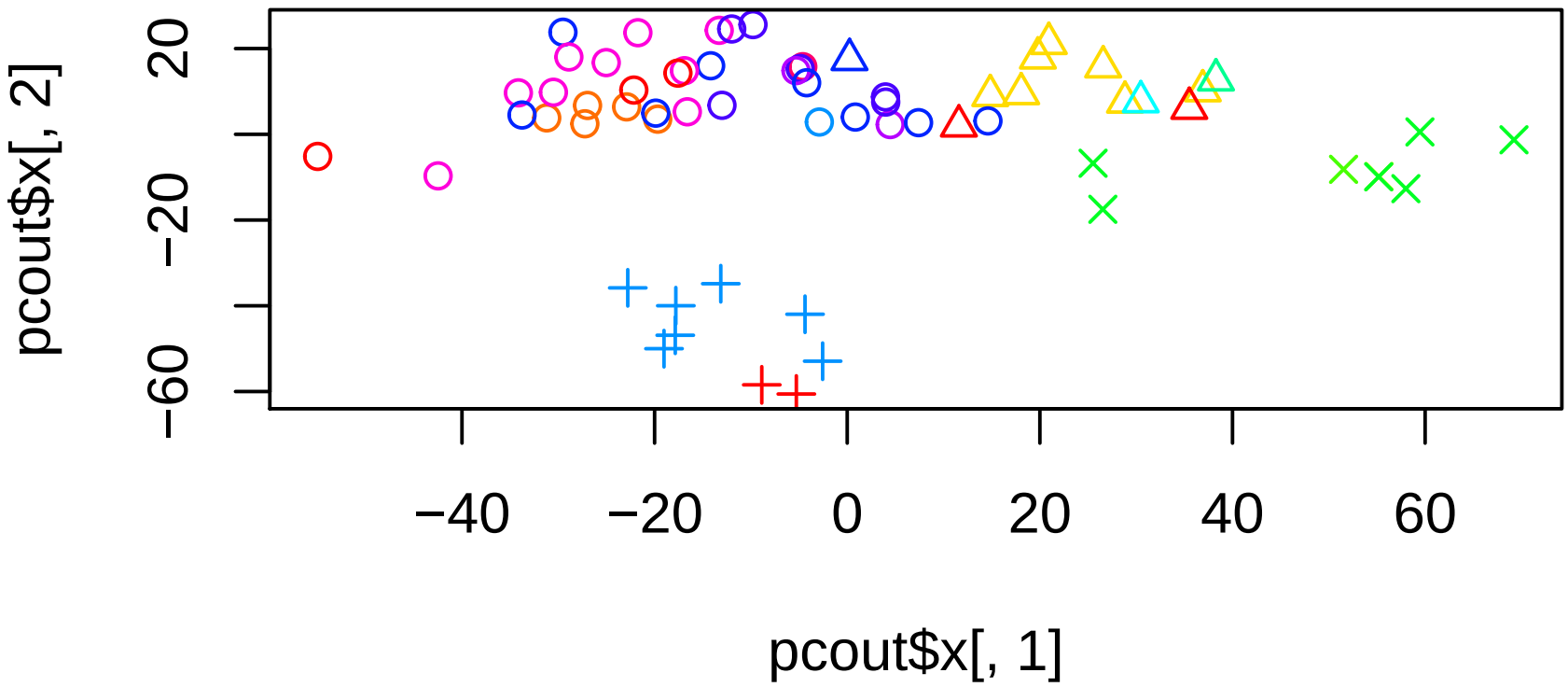
K-Means Clustering of NCI60 Data

- Remember that `nciX` has already been scaled.
- We know there are 16 different cancer types, but would not specify this many clusters in practice.
  - Try $K = 4$.

```
kout <- kmeans(nciX,centers=4)
table(kout$cluster,nciL)
```

```
##    nciL
##     BREAST CNS COLON K562A-repro K562B-repro LEUKEMIA MCF7A-repro
##   1      3   5     0           0           0        0           0
##   2      2   0     7           0           0        0           1
##   3      2   0     0           0           0        0           0
##   4      0   0     0           1           1        6           0
##    nciL
##     MCF7D-repro MELANOMA NSCLC OVARIAN PROSTATE RENAL UNKNOWN
##   1           0        1     8       6        2     9       1
##   2           1        0     1       0        0     0       0
##   3           0        7     0       0        0     0       0
##   4           0        0     0       0        0     0       0
```

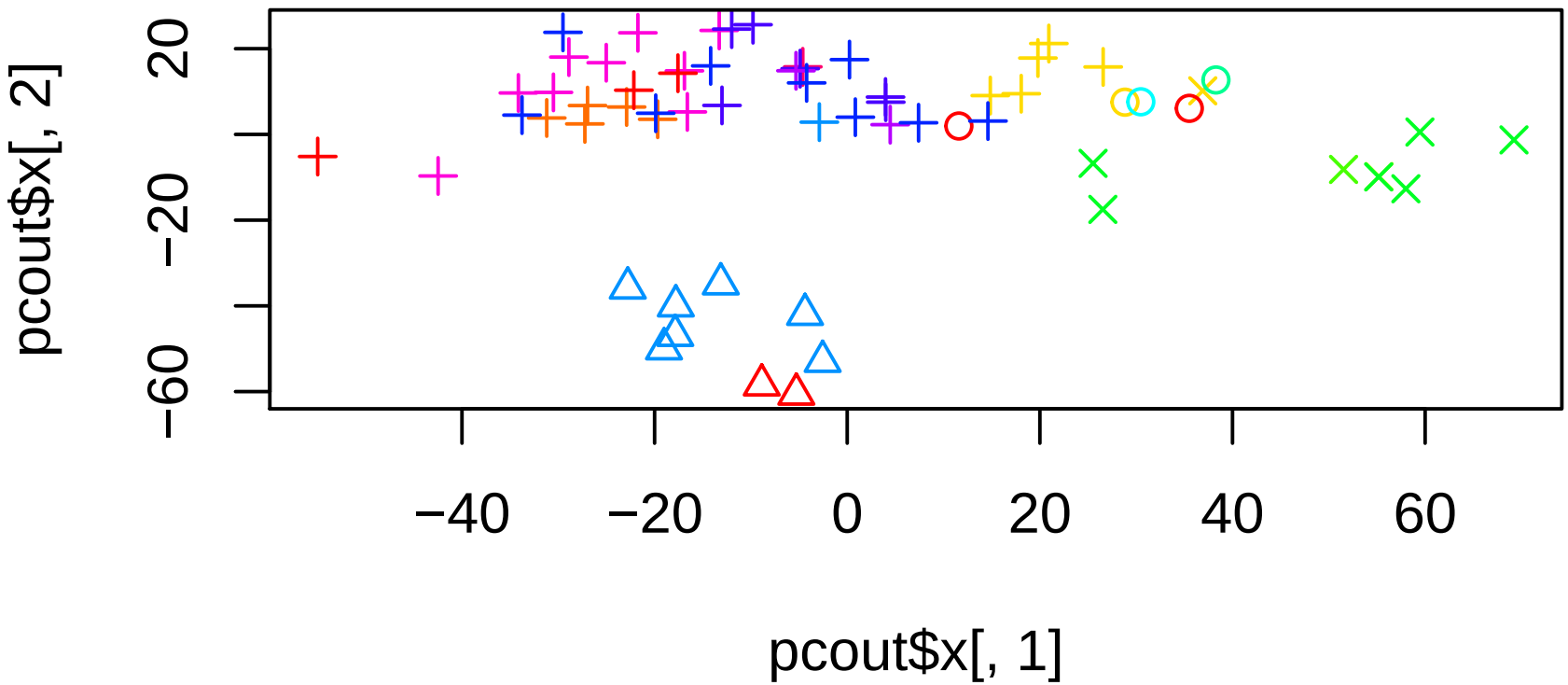
```
plot(pcout$x[,1],pcout$x[,2],col=ccols,pch=kout$cluster)
```



Clustering on PCs

- Can also use the PCs as the data.

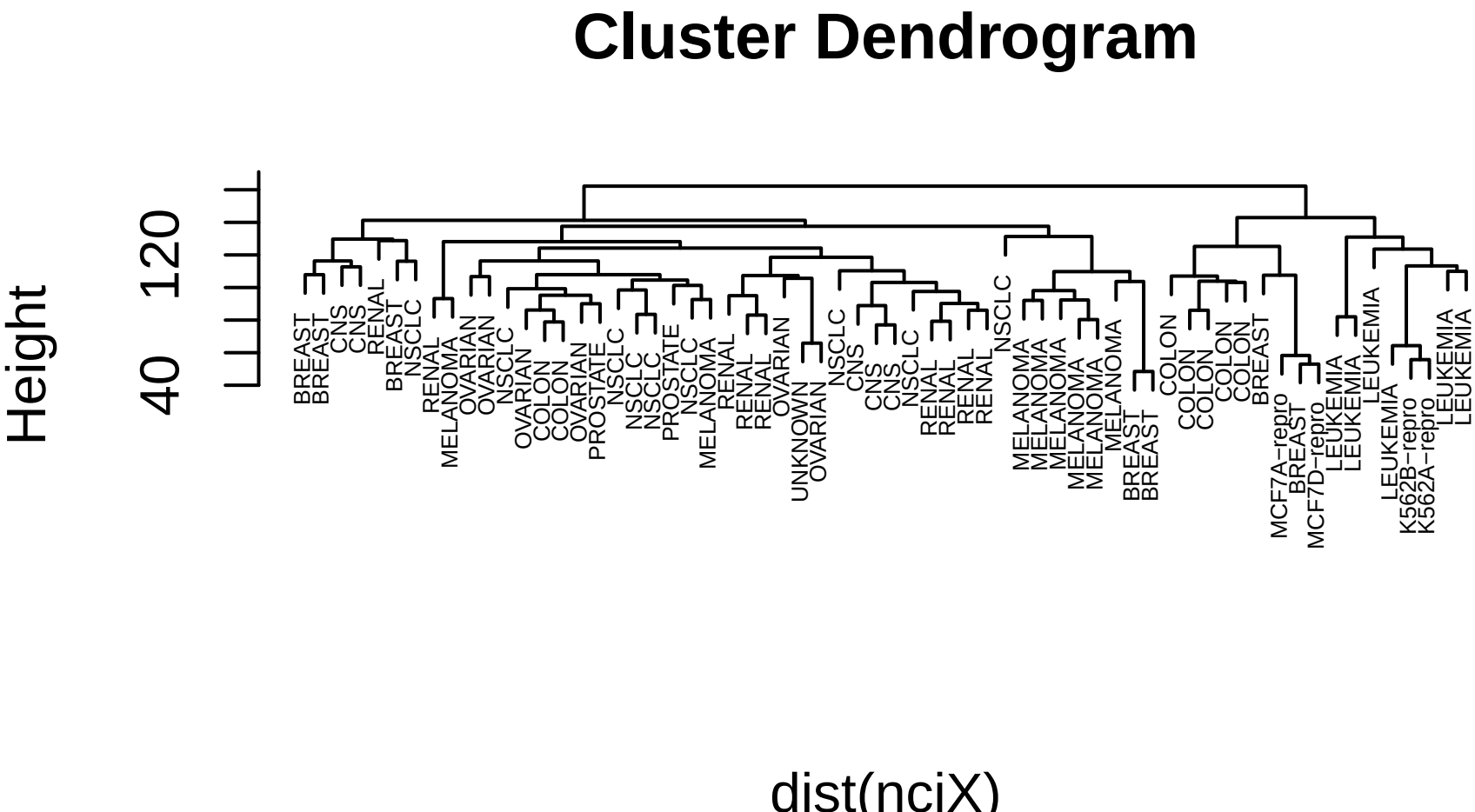
```
kout2 <- kmeans(pcout$x[,1:5],centers=4)
plot(pcout$x[,1],pcout$x[,2],col=ccols,pch=kout2$cluster)
```



Hierarchical Clustering of NCI60 Data

- Use Euclidean distance and complete linkage
  - See the text for a comparison of complete, average and single linkage

```
hcout <- hclust(dist(nciX))
plot(hcout,cex=.4)
```



```
plot(pcout$x[,1],pcout$x[,2],col=ccols,pch=cutree(hcout,k=4))
```