## SL RLab10: UNSUPERVISED LEARNING IN R

PRINCIPAL COMPONENTS (PCA)

Use the 'USArrests' dataset (in R). Arrests has much higher variance than other variables, and would dominate the principal components. Therefore, we standardize the variables for PCA; prcomp will do that for us if we set "scale=TRUE"

```
dimnames(USArrests)
```

```
## [[1]]
##  [1] "Alabama"        "Alaska"         "Arizona"        "Arkansas"
##  [5] "California"     "Colorado"       "Connecticut"    "Delaware"
##  [9] "Florida"        "Georgia"        "Hawaii"         "Idaho"
## [13] "Illinois"       "Indiana"        "Iowa"           "Kansas"
## [17] "Kentucky"       "Louisiana"      "Maine"          "Maryland"
## [21] "Massachusetts"  "Michigan"       "Minnesota"      "Mississippi"
## [25] "Missouri"       "Montana"        "Nebraska"       "Nevada"
## [29] "New Hampshire"  "New Jersey"     "New Mexico"     "New York"
## [33] "North Carolina" "North Dakota"   "Ohio"           "Oklahoma"
## [37] "Oregon"         "Pennsylvania"   "Rhode Island"   "South Carolina"
## [41] "South Dakota"   "Tennessee"      "Texas"          "Utah"
## [45] "Vermont"        "Virginia"       "Washington"     "West Virginia"
## [49] "Wisconsin"      "Wyoming"
##
## [[2]]
## [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
```

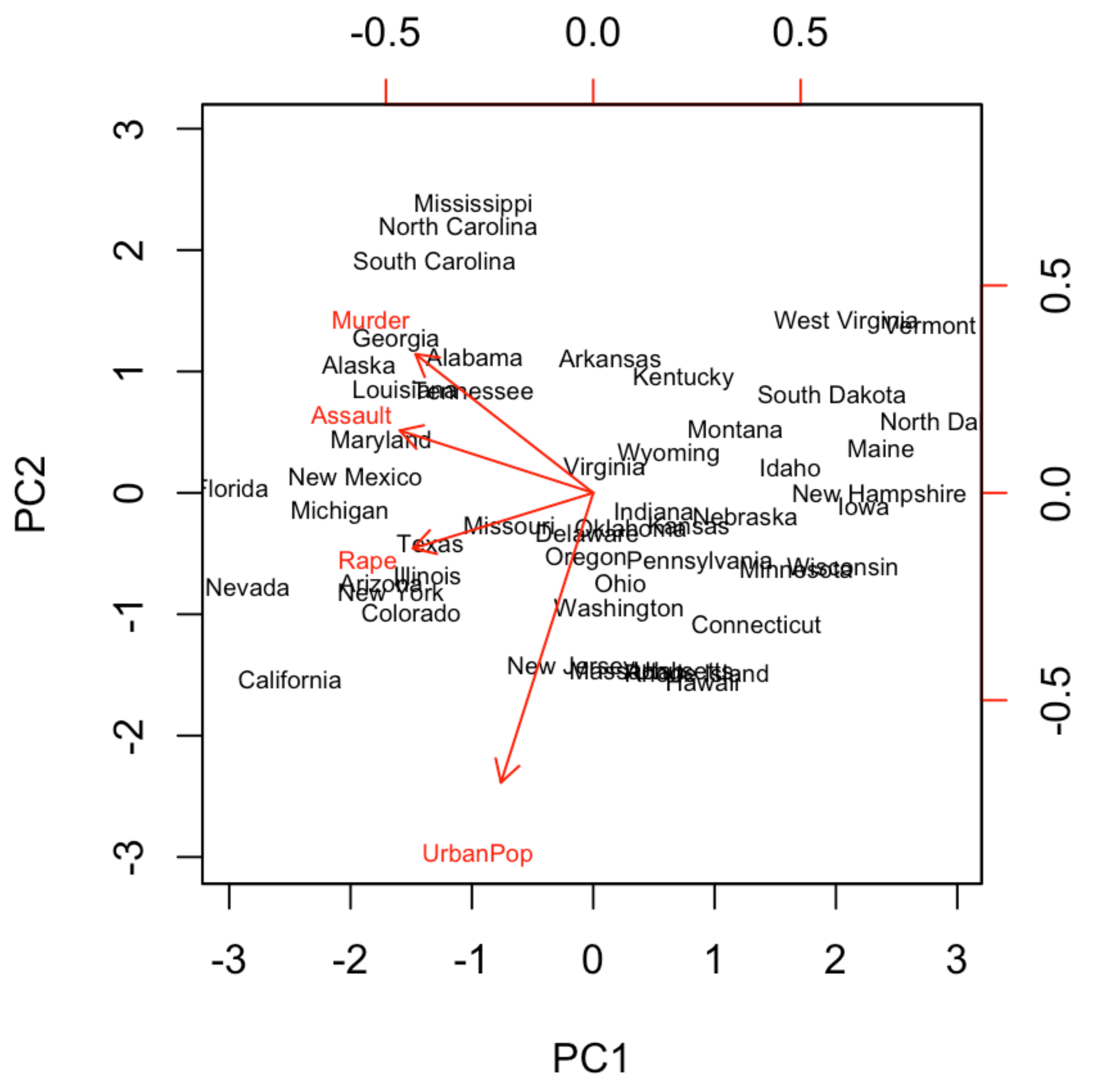
```
pca.out = prcomp(USArrests, scale=TRUE)
pca.out
```

```
## Standard deviations:
## [1] 1.5748783 0.9948694 0.5971291 0.4164494
##
## 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
```

```
names(pca.out)
```

```
## [1] "sdev"     "rotation" "center"   "scale"    "x"
```

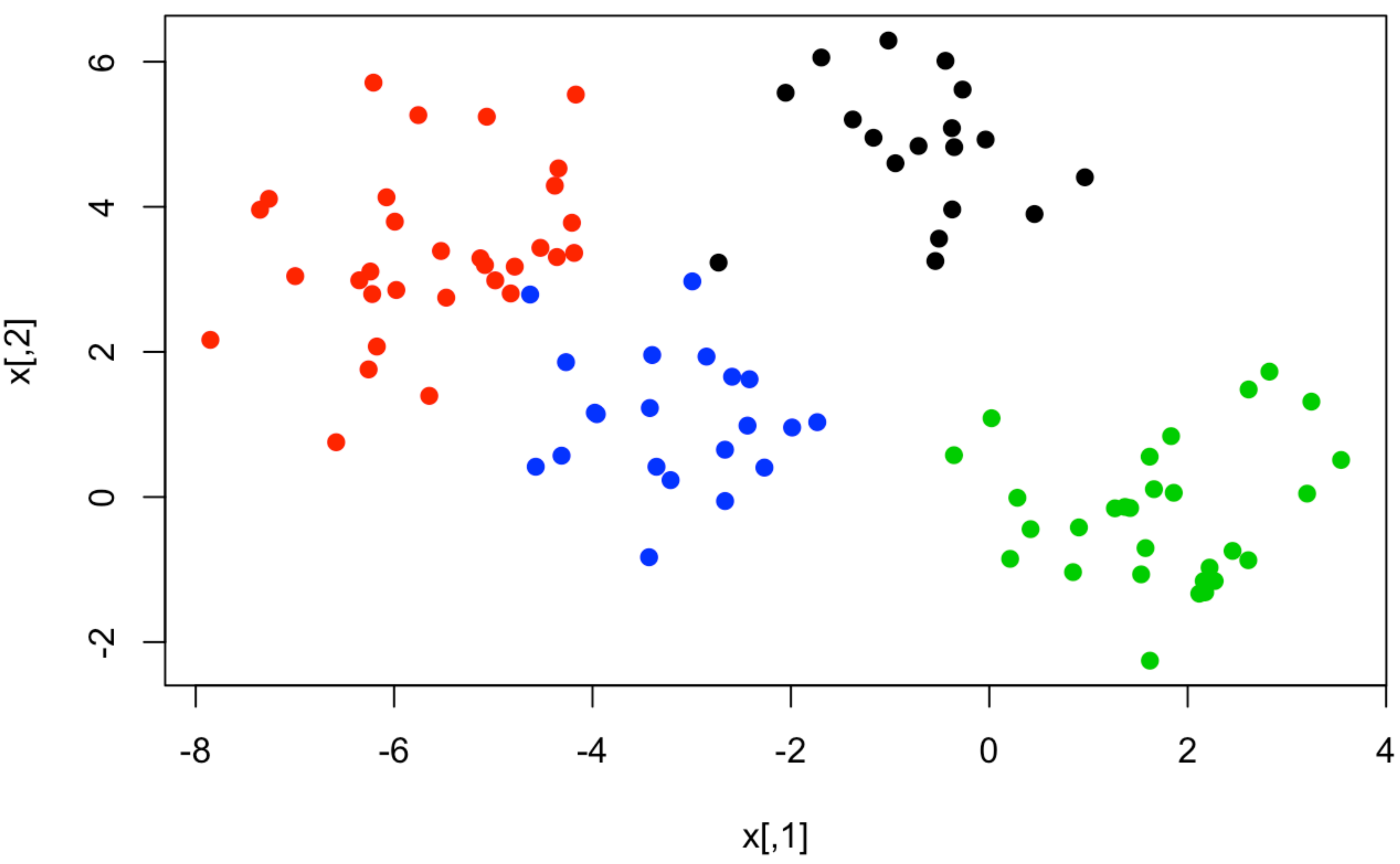
```
biplot(pca.out, scale=0, cex=.6)
```



### K-MEANS CLUSTERING

K-means works in any dimenion, but is most fun in 2-dim, because we can plot pictures. We generate some data with clusters (100 rows, 2 columns using rnorm function), and then shifting the means of the points around.

```
set.seed(101)
x = matrix(rnorm(100*2), 100, 2)
xmean = matrix(rnorm(8, sd=4), 4, 2)
which = sample(1:4, 100, replace=TRUE)
x = x+xmean[which,]
plot(x, col=which, pch=19)
```

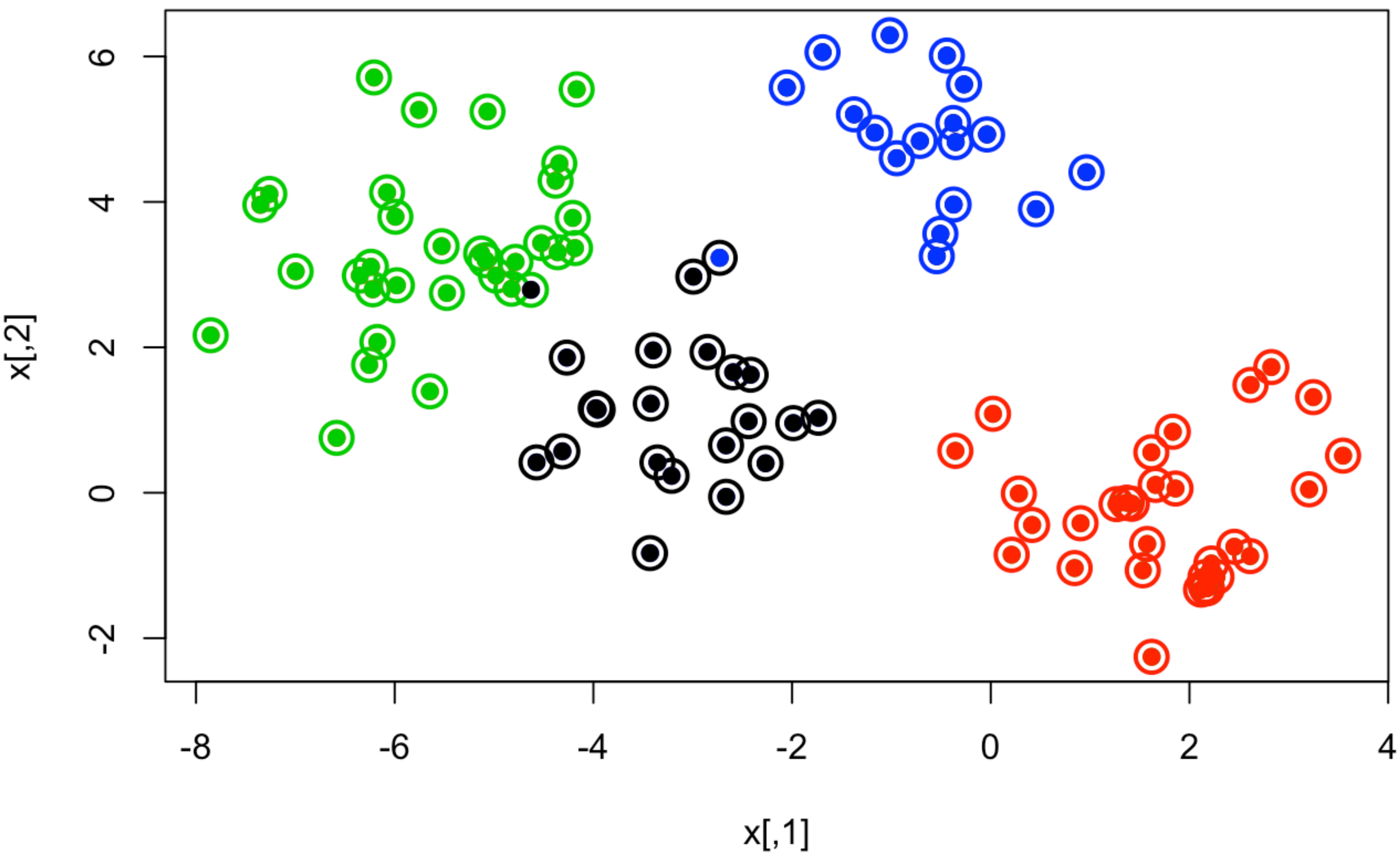


We know the ‘true’ cluster IDs, but we won’t tell that to the kmeans algorithm. We tell it to do 15 random starts We can print out the result and create a plot, with the cluster assigned points, and the original points created.

```
km.out = kmeans(x, 4, nstart=15)
km.out
```

```
## K-means clustering with 4 clusters of sizes 21, 30, 32, 17
##
## Cluster means:
##         [,1]       [,2]
## 1 -3.1068542  1.1213302
## 2  1.7226318 -0.2584919
## 3 -5.5818142  3.3684991
## 4 -0.6148368  4.8861032
##
## Clustering vector:
##   [1] 2 3 3 4 1 1 4 3 2 3 2 1 1 3 1 1 2 3 3 2 2 3 1 3 1 1 2 2 3 1 1 4 3 1 3
##  [36] 3 1 2 2 3 2 2 3 3 1 3 1 3 4 2 1 2 2 4 3 3 2 2 3 2 1 2 3 4 2 4 3 4 4 2
##  [71] 2 4 3 2 3 4 4 2 2 1 2 4 4 3 3 2 3 3 1 2 3 2 4 4 4 2 3 3 1 1
##
## Within cluster sum of squares by cluster:
## [1] 30.82790 54.48008 71.98228 21.04952
##  (between_SS / total_SS =  87.6 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
## [5] "tot.withinss" "betweenss"    "size"         "iter"
## [9] "ifault"
```

```
plot(x, col=km.out$cluster, cex=2, pch=1, lwd=2)
points(x, col=which, pch=19)
points(x, col=c(4, 3, 2, 1)[which], pch=19)
```



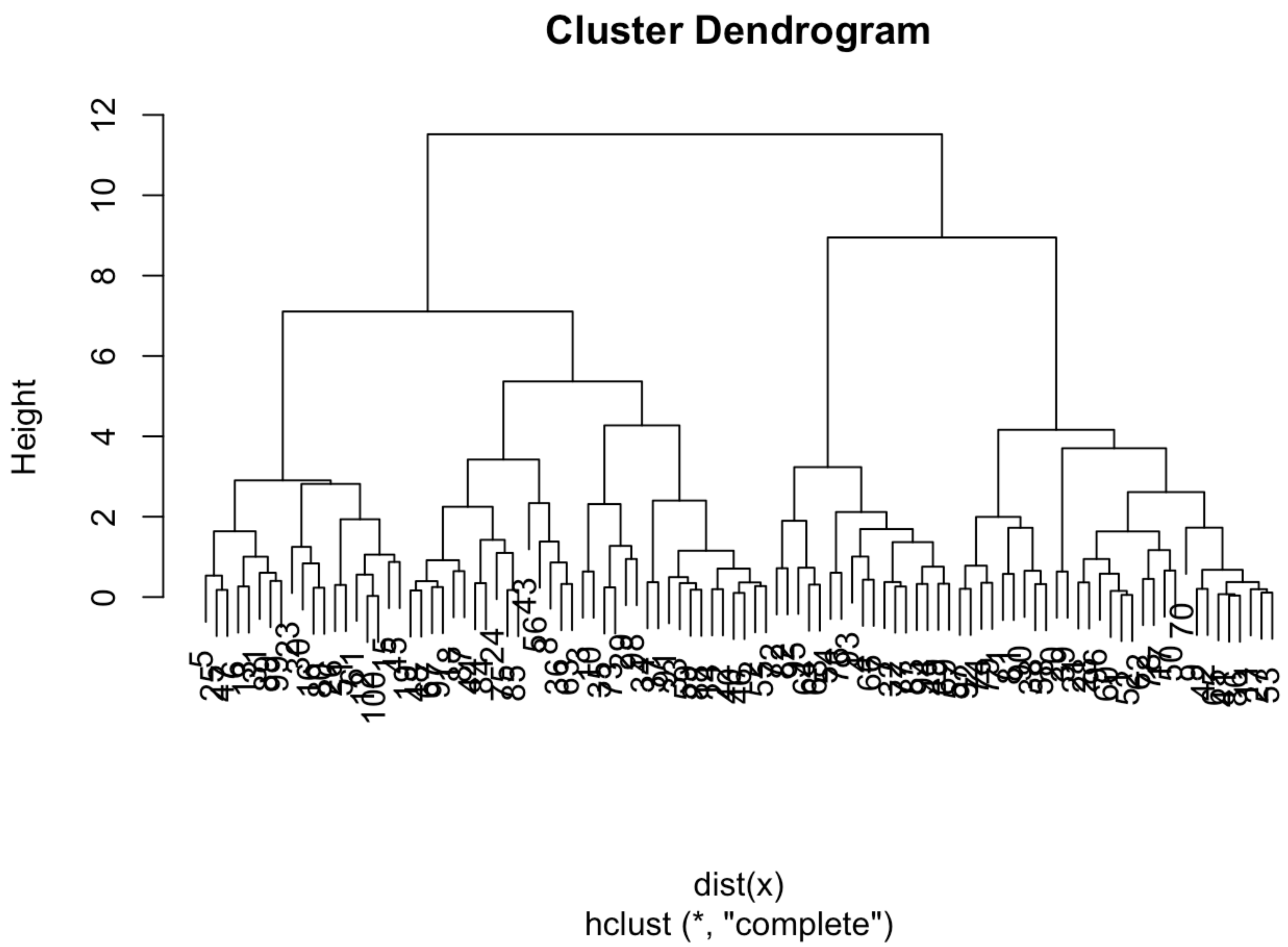
## HIERARCHICAL CLUSTERING

Use these same data for hierarchical clustering, which works off a distance matrix; we compute distance of x (100by100), using a call to hclust(), and then plot the data to show the dendrogram of the clustering.

```
hc.complete = hclust(dist(x), method="complete")
hc.complete
```

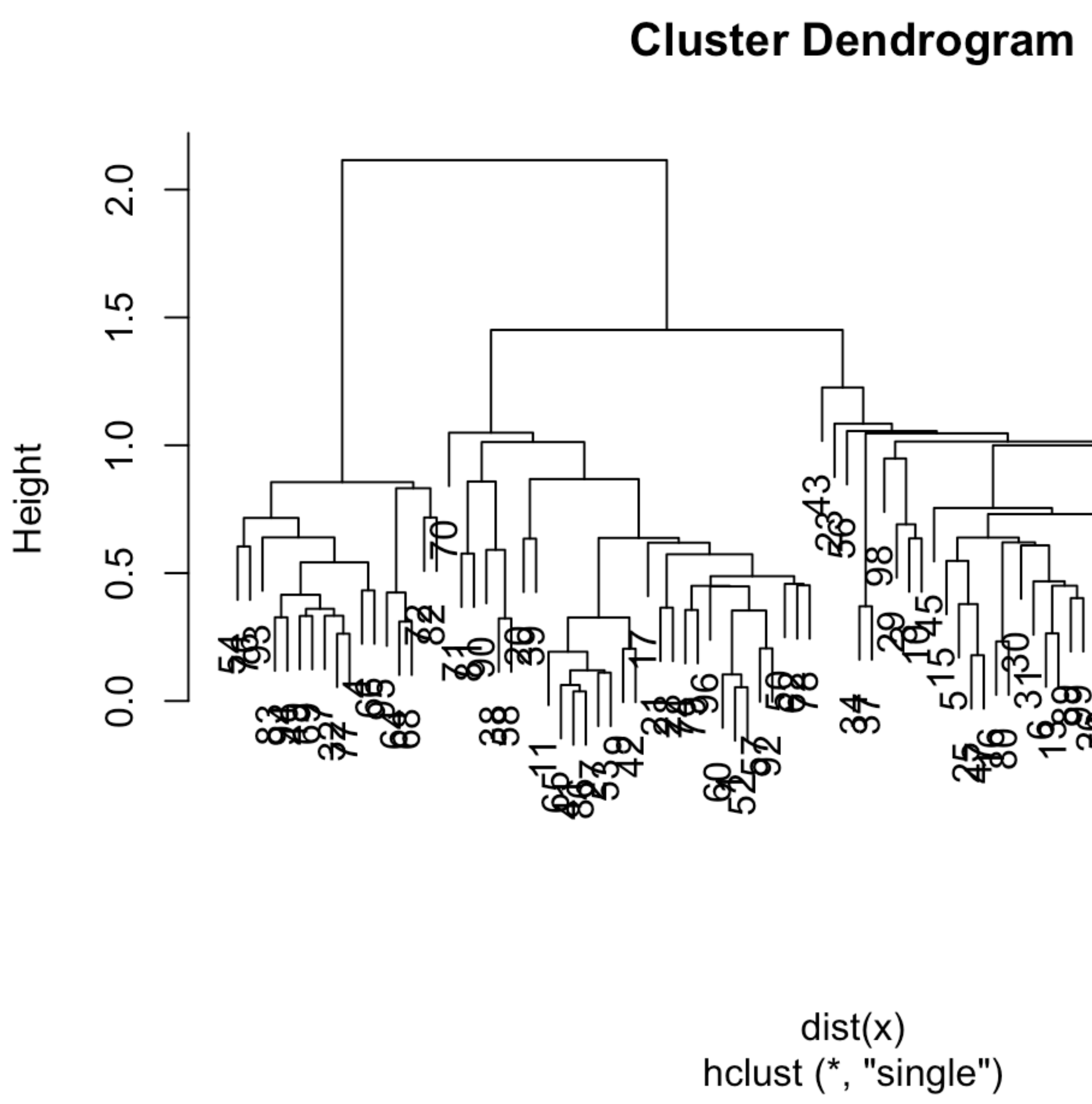
```
##
## Call:
## hclust(d = dist(x), method = "complete")
##
## Cluster method   : complete
## Distance         : euclidean
## Number of objects: 100
```

```
plot(hc.complete)
```

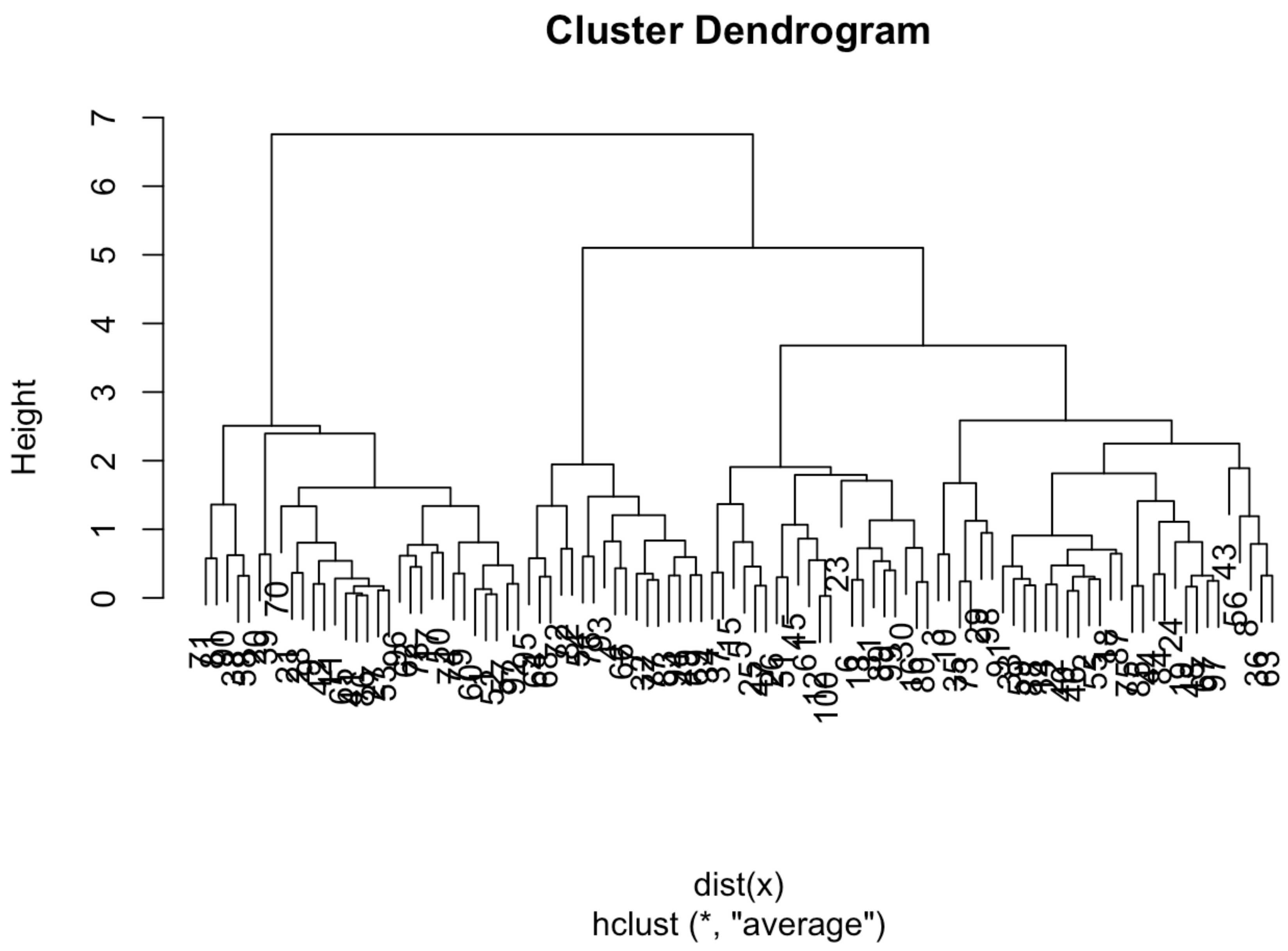


There are other clustering methods we can call, for example, ‘single-linkage’ clustering. Instead of using the largest distance, it uses the smallest distance. Average-linkage takes the average linkage of all pairs of points.

```
hc.single = hclust(dist(x), method="single")
plot(hc.single)
```



```
hc.average = hclust(dist(x), method="average")
plot(hc.average)
```



Let’s compare this withthe actual clusters in the data. We will use the function ‘cutree’, to cut the tree at level 4. This will produce a vector of numbers from 1 to 4, saying which branch each observation is on.

You sometimes see prety plots where the leaves of the dendrogram are colored, but is a bit too complicated for this demo. We can use a table to see how well they match.

```
hc.cut = cutree(hc.complete, 4)
table(hc.cut, which)
```

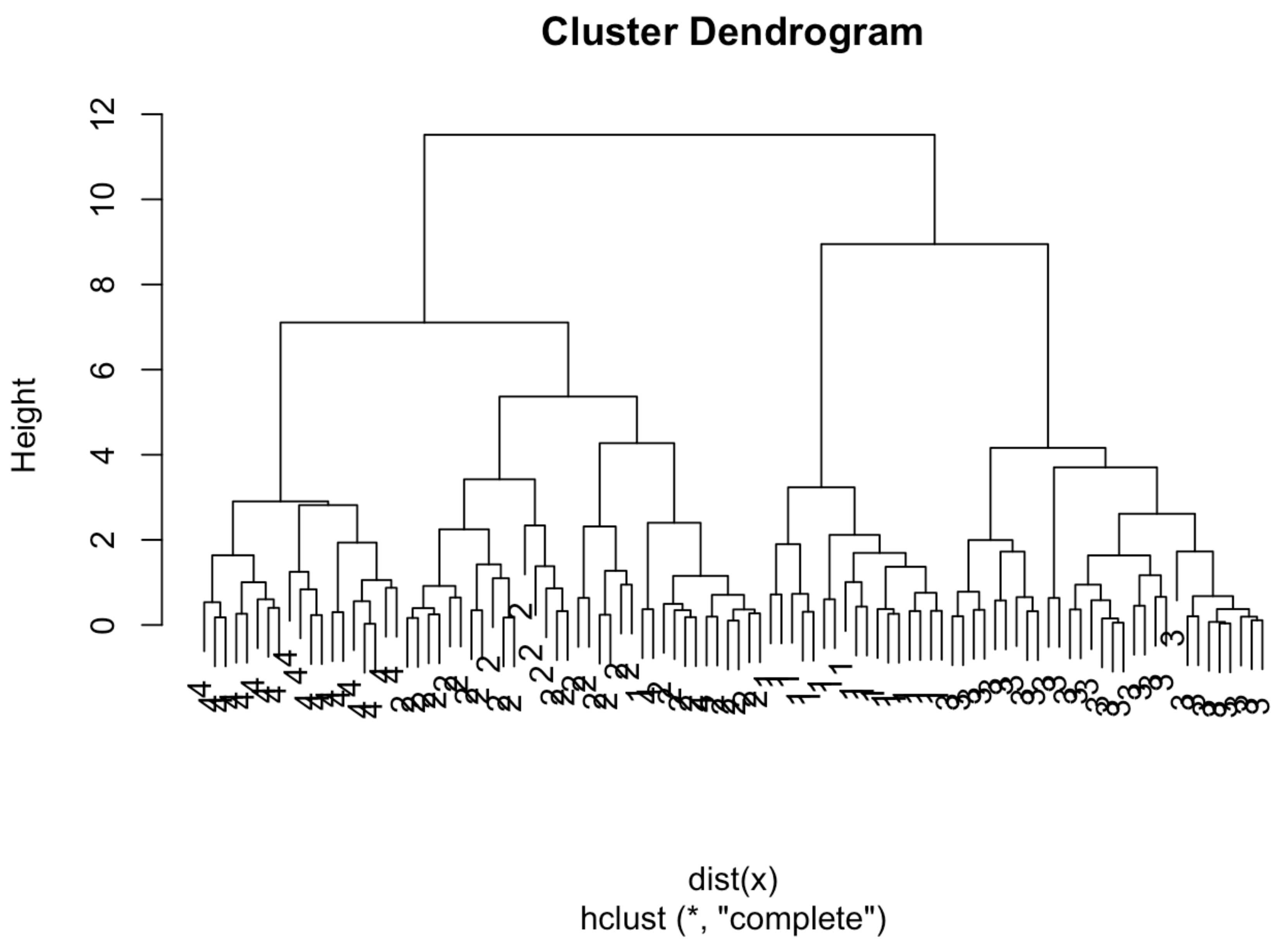
```
##       which
## hc.cut  1  2  3  4
##      1  0  0 30  0
##      2  1 31  0  2
##      3 17  0  0  0
##      4  0  0  0 19
```

```
table(hc.cut, km.out$cluster)
```

```
##
## hc.cut  1  2  3  4
##      1  0 30  0  0
##      2  2  0 32  0
##      3  0  0  0 17
##      4 19  0  0  0
```

or we can use our group membership as labels for the leaves of the dendrogram:

```
plot(hc.complete, labels=which)
```


Cluster Dendrogram
Height
dist(x)
hclust (*, "complete")