

# Machine Learning 1

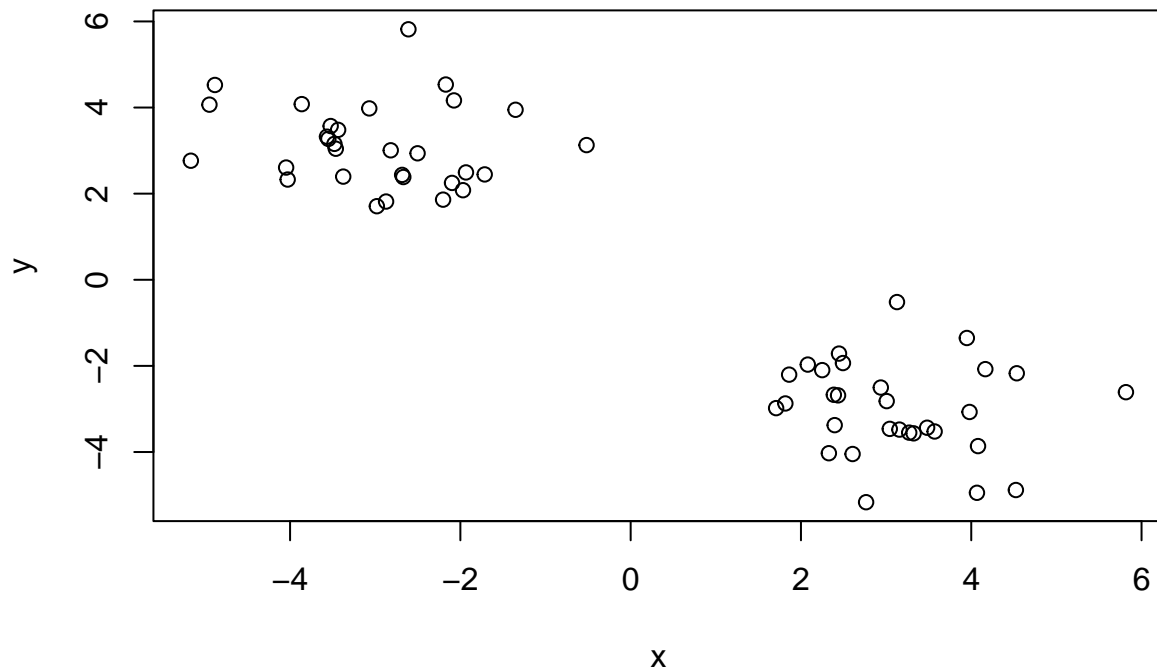
Kiley Hooker (PID: A15441609)

2/8/2022

## First up kmeans()

Demo of using kmeans() function in base R. First make up some data with a known structure.

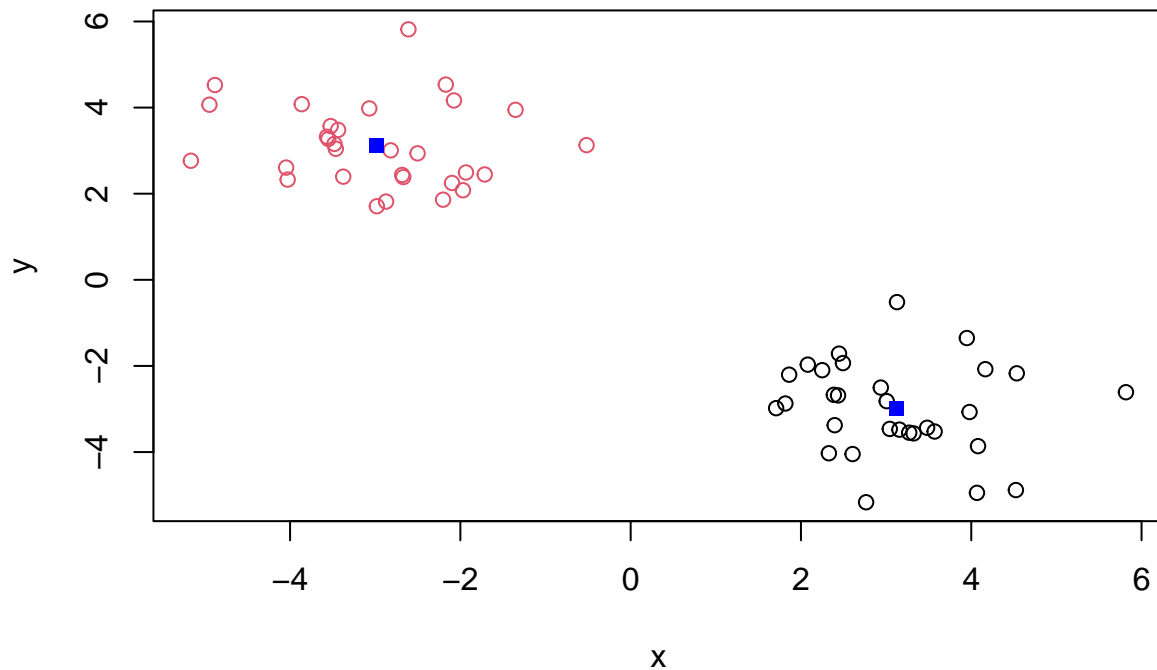
```
tmp <- c(rnorm(30, -3), rnorm(30, 3))  
x <- cbind(x=tmp, y=rev(tmp))  
plot(x)
```



Now we have some made up data in x let's see how kmeans works with this data

```
k <- kmeans(x, centers = 2, nstart = 20)  
k
```





### Now for `hclust()`

We will cluster the same data `x` with the `hclust()`. In this case `hclust()` requires a distance matrix as output.

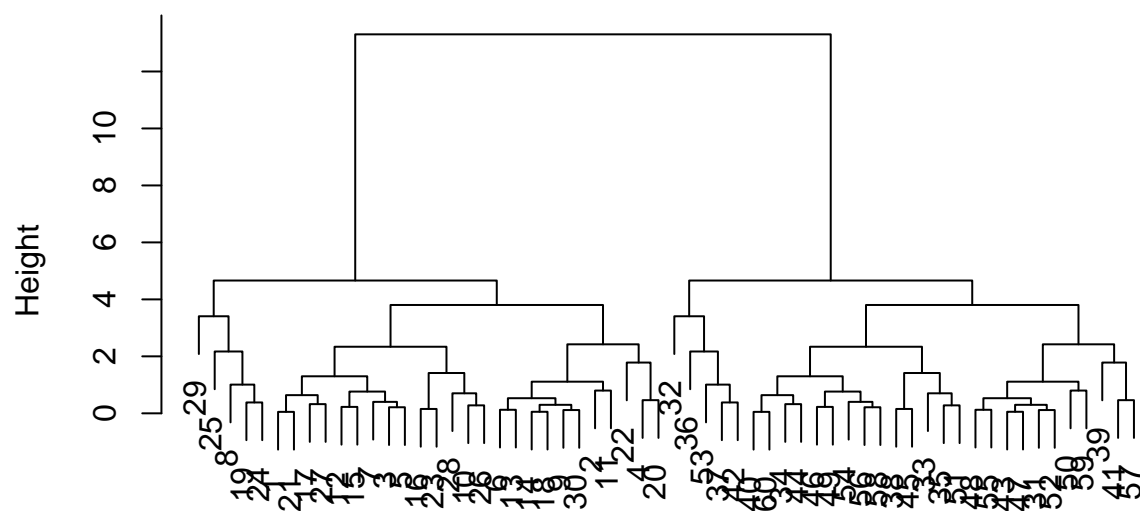
```
hc <- hclust(dist(x))
hc
```

```
##
## Call:
## hclust(d = dist(x))
##
## Cluster method   : complete
## Distance        : euclidean
## Number of objects: 60
```

Let's plot our `hclust` result

```
plot(hc)
```

## Cluster Dendrogram



```
dist(x)
hclust (*, "complete")
```

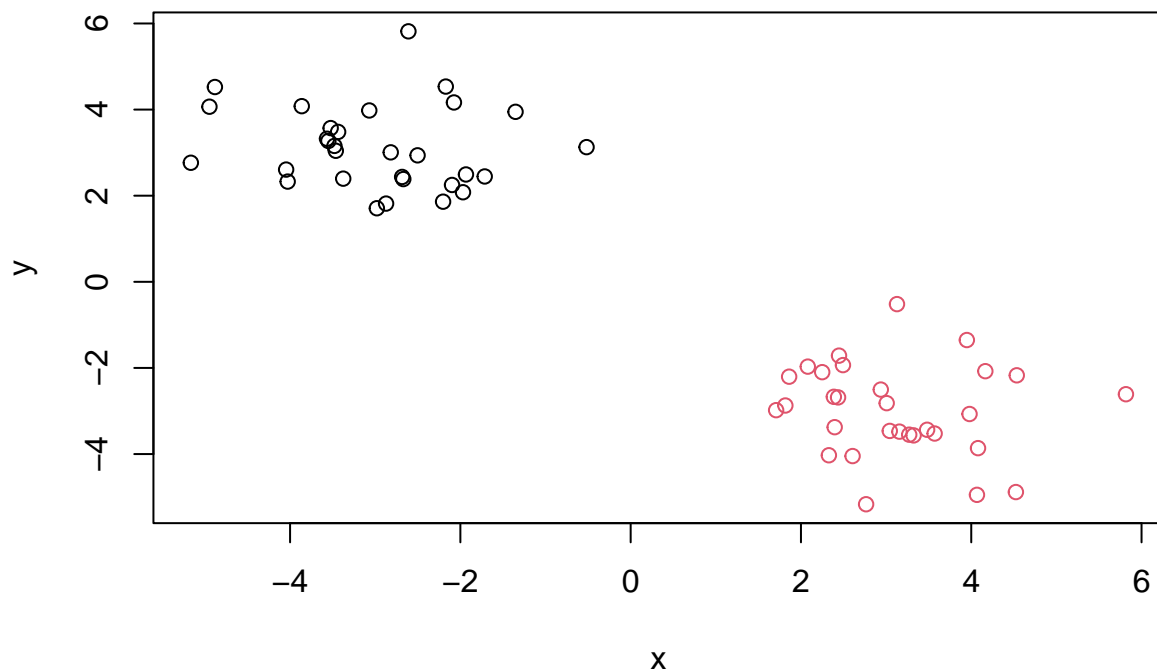
To get our cluster membership vector we need to “cut” the tree with the `cutree()`

```
grps <- cutree(hc, h=8)
grps
```

[illegible]

Now plot our data with the `hclust()` results.

```
plot(x, col=grps)
```



## Principal Component Analysis (PCA)

### PCA of UK food data

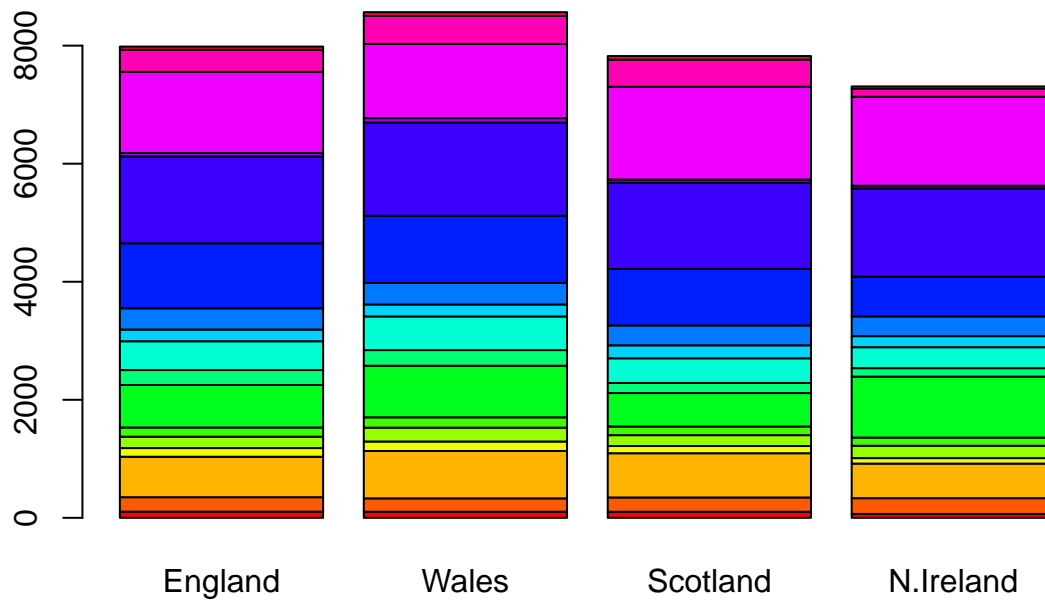
Read data from website and try a few visualizations.

```
url <- "https://tinyurl.com/UK-foods"
x <- read.csv(url, row.names=1)
x
```

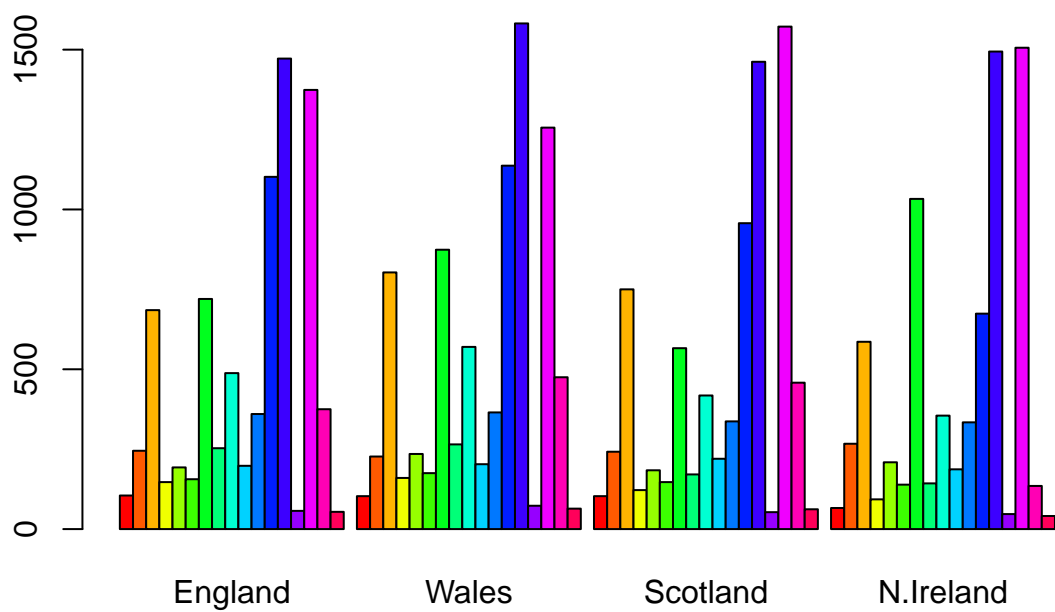
##	England	Wales	Scotland	N.Ireland
## Cheese	105	103	103	66
## Carcass_meat	245	227	242	267
## Other_meat	685	803	750	586
## Fish	147	160	122	93
## Fats_and_oils	193	235	184	209
## Sugars	156	175	147	139
## Fresh_potatoes	720	874	566	1033
## Fresh_Veg	253	265	171	143
## Other_Veg	488	570	418	355
## Processed_potatoes	198	203	220	187
## Processed_Veg	360	365	337	334
## Fresh_fruit	1102	1137	957	674
## Cereals	1472	1582	1462	1494

```
## Beverages          57    73    53    47
## Soft_drinks       1374  1256  1572  1506
## Alcoholic_drinks   375   475   458   135
## Confectionery      54    64    62    41
```

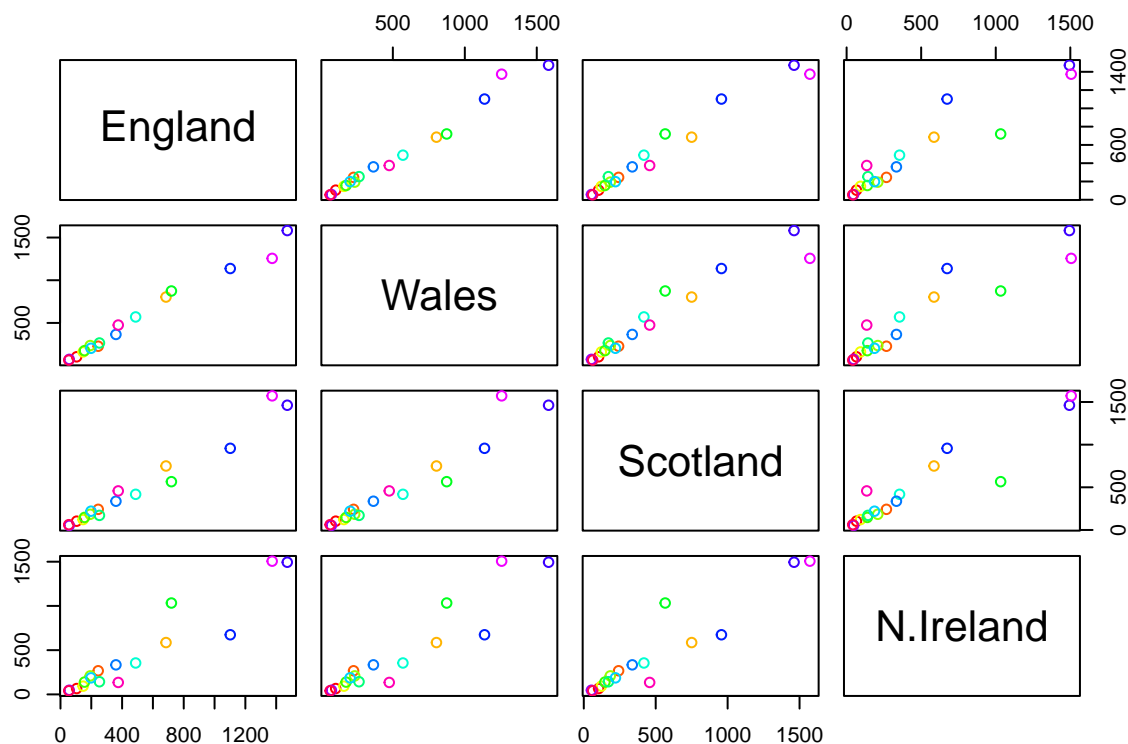
```
cols <- rainbow(nrow(x))
barplot(as.matrix(x), col=cols)
```



```
barplot(as.matrix(x), col=cols, beside=TRUE)
```



```
pairs(x, col=cols)
```



PCA to the rescue!! The main base R PCA function is called `prcomp()` and we will need to give it the transpose of our input data!

```
pca <- prcomp(t(x))
```

There is a nice summary of how well PCA is doing

```
summary(pca)
```

```
## Importance of components:
##               PC1      PC2      PC3      PC4
## Standard deviation  324.1502 212.7478 73.87622 4.189e-14
## Proportion of Variance  0.6744  0.2905  0.03503 0.000e+00
## Cumulative Proportion  0.6744  0.9650  1.00000 1.000e+00
```

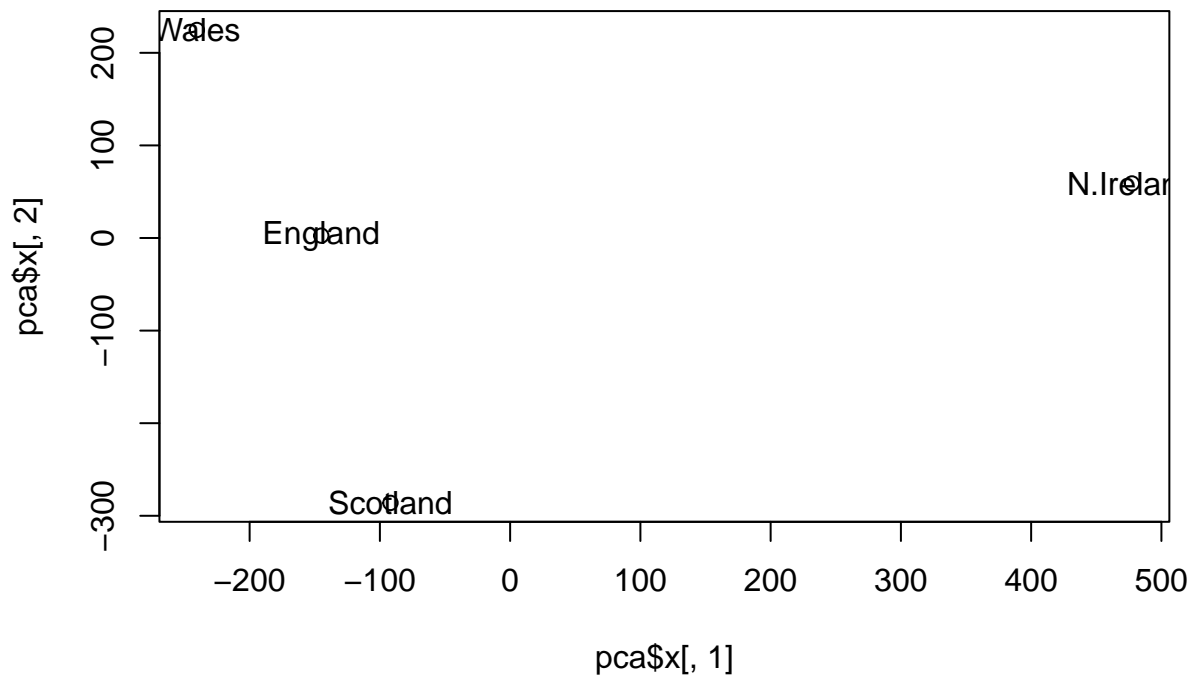
```
attributes(pca)
```

```
## $names
## [1] "sdev"      "rotation" "center"    "scale"     "x"
##
## $class
## [1] "prcomp"
```

To make our new PCA plot(a.k.a PCA score plot) we access `pca$x`

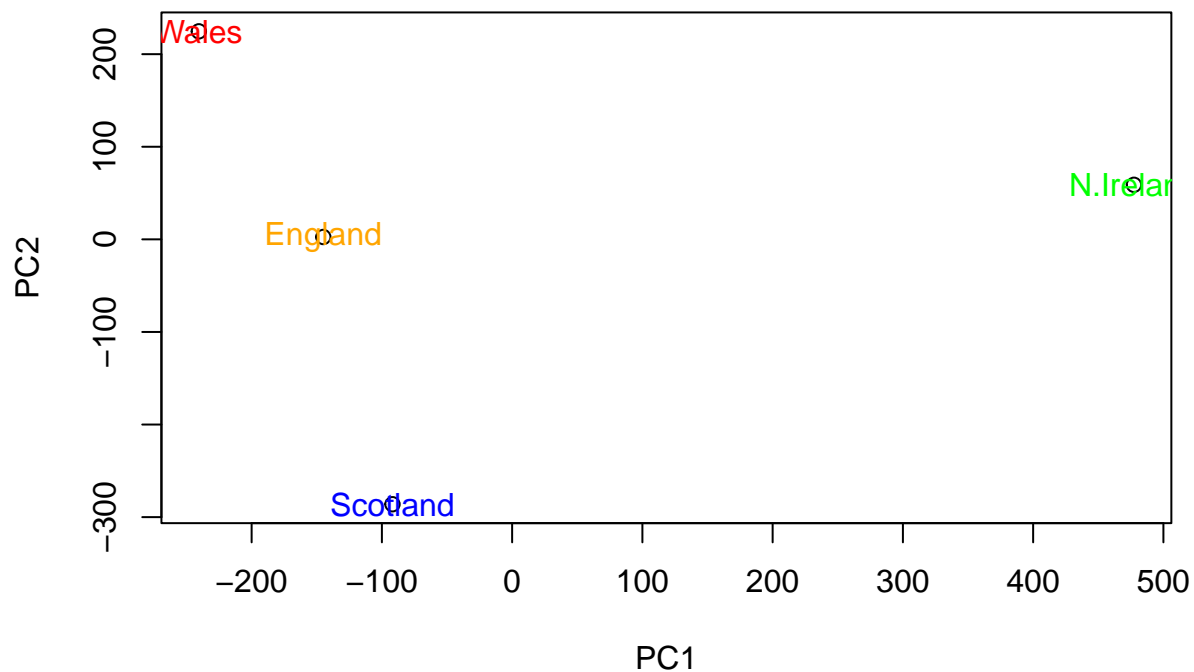


```
plot(pca$x[,1], pca$x[,2])
text(pca$x[,1], pca$x[,2], colnames(x))
```



color up the plot

```
country_cols <- c("orange", "red", "blue", "green")
plot(pca$x[,1], pca$x[,2], xlab="PC1", ylab="PC2")
text(pca$x[,1], pca$x[,2], colnames(x), col=country_cols)
```



## PCA of RNA-Seq data

Read in data from website

```
url2 <- "https://tinyurl.com/expression-CSV"
rna.data <- read.csv(url2, row.names=1)
head(rna.data)
```

```
##      wt1 wt2 wt3 wt4 wt5 ko1 ko2 ko3 ko4 ko5
## gene1 439 458 408 429 420 90  88  86  90  93
## gene2 219 200 204 210 187 427 423 434 433 426
## gene3 1006 989 1030 1017 973 252 237 238 226 210
## gene4 783 792 829 856 760 849 856 835 885 894
## gene5 181 249 204 244 225 277 305 272 270 279
## gene6 460 502 491 491 493 612 594 577 618 638
```

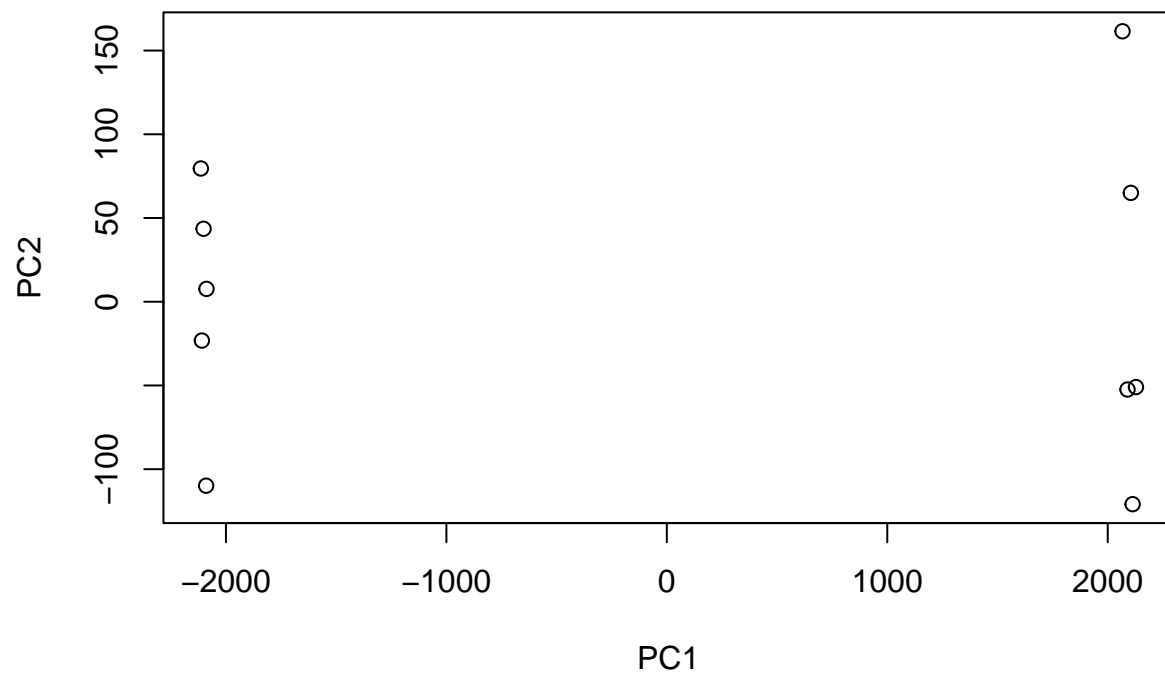
```
pca <- prcomp(t(rna.data))
summary(pca)
```

```
## Importance of components:
##              PC1      PC2      PC3      PC4      PC5      PC6
## Standard deviation    2214.2633  88.9209  84.33908  77.74094  69.66341  67.78516
## Proportion of Variance    0.9917  0.0016  0.00144  0.00122  0.00098  0.00093
## Cumulative Proportion    0.9917  0.9933  0.99471  0.99593  0.99691  0.99784
```

```
##
## Standard deviation      PC7      PC8      PC9      PC10
## Proportion of Variance 0.00086 0.00073 0.00057 0.000e+00
## Cumulative Proportion  0.99870 0.99943 1.00000 1.000e+00
```

Do our PCA plot of this RNA-Seq data

```
plot(pca$x[,1], pca$x[,2], xlab="PC1", ylab="PC2")
```



```
plot(pca$x[,1], pca$x[,2], xlab="PC1", ylab="PC2")
text(pca$x[,1], pca$x[,2], colnames(rna.data))
```

