Class 7: Machine Learning

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Today we are going to learn how to apply different machine learning methods, beginning with clustering:

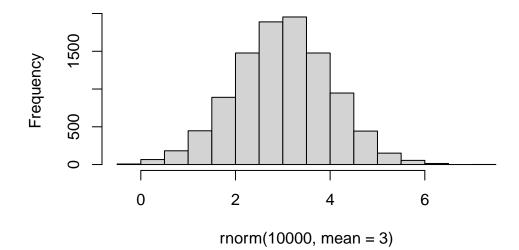
The goals here is to find groups/clusters in your input data.

First I will make up some data with clear groups. For this I will use the rnorm() function:

rnorm(10)

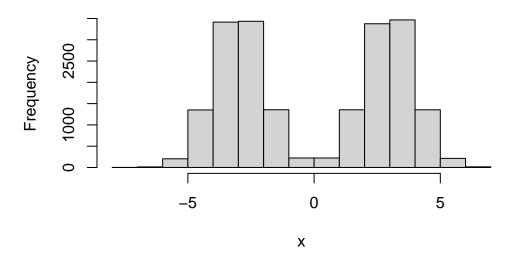
hist(rnorm(10000, mean=3))

Histogram of rnorm(10000, mean = 3)



```
n <-10000
x <- c(rnorm(n,-3), rnorm(n,+3))
hist(x)</pre>
```

Histogram of x

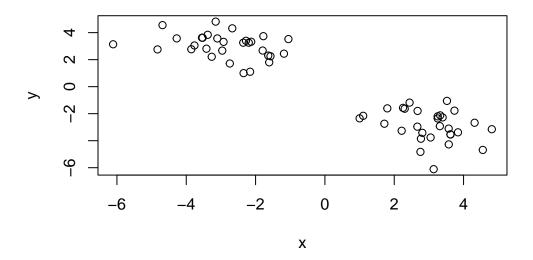


```
n <-30
x <- c(rnorm(n,-3), rnorm(n,+3))
y <- rev(x)

z<- cbind(x,y)
head(z)</pre>
```

```
x y
[1,] -1.795610 2.673960
[2,] -1.570300 2.253782
[3,] -3.417743 2.811161
[4,] -1.181336 2.442952
[5,] -3.527441 3.619961
[6,] -3.103558 3.570790
```

plot(z)



Use the kmeans() function setting k to 2 and nstart=20

Inspect/print the results

Q. How many points are in each cluster?

Q. What 'component' of your result object details -cluster size? -cluster assignment/member -cluster center? Q. Plot x colored by the k means closter assignment and add cluster centers as blue points

```
km <- kmeans(z, centers=2)
km</pre>
```

K-means clustering with 2 clusters of sizes 30, 30

Cluster means:

Clustering vector:

Within cluster sum of squares by cluster:

[1] 62.81326 62.81326

(between_SS / total_SS = 89.2 %)

Available components:

[1] "cluster" "centers" "totss" "withinss" "tot.withinss"

[6] "betweenss" "size" "iter" "ifault"

Results in kmeans object km

attributes(km)

\$names

[1] "cluster" "centers" "totss" "withinss" "tot.withinss"

[6] "betweenss" "size" "iter" "ifault"

\$class

[1] "kmeans"

cluster size?

km\$size

[1] 30 30

cluster assignment/membership?

km\$cluster

cluster center?

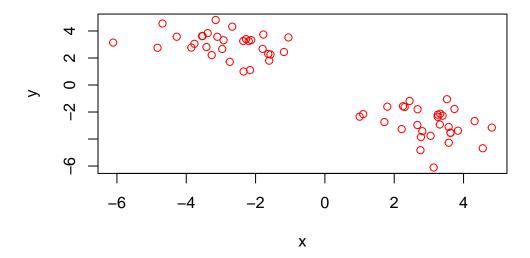
km\$centers

X

1 3.014153 -2.876144

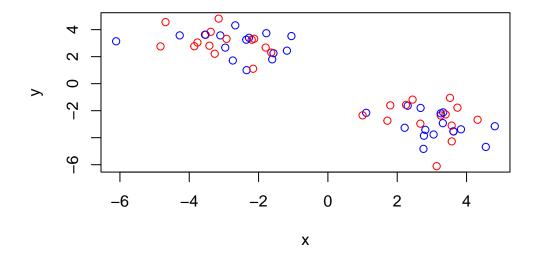
2 -2.876144 3.014153

Q. Plot **x** colored by the **k** means closter assignment and add cluster centers as blue points

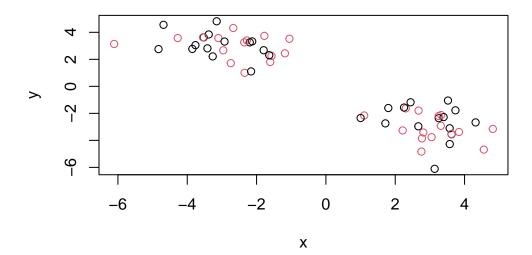


R will re-cycle the shorter color vector to be the same length as the longer (number of data points) in ${\bf z}$

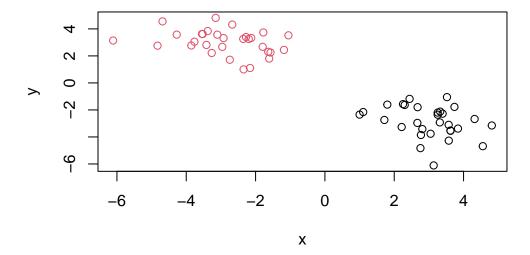
```
plot(z, col=c("red", "blue"))
```



plot(z, col=c(1,2))

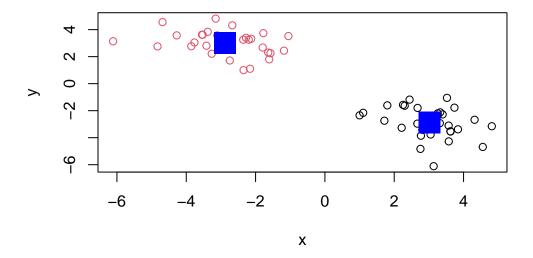


plot(z, col=km\$cluster)



We can use the points() function to add new points to an existing plot...like the cluster centers.

```
plot(z, col=km$cluster)
points(km$centers, col="blue", pch=15, cex=3)
```



Q. Can you run kmeans and ask for 4 clusters please and plot the results like we have done above?

```
km1 <- kmeans(z, centers=4)
km1</pre>
```

K-means clustering with 4 clusters of sizes 16, 14, 16, 14

Cluster means:

x y 1 -2.065397 2.541689 2 3.554113 -3.802713 3 2.541689 -2.065397 4 -3.802713 3.554113

Clustering vector:

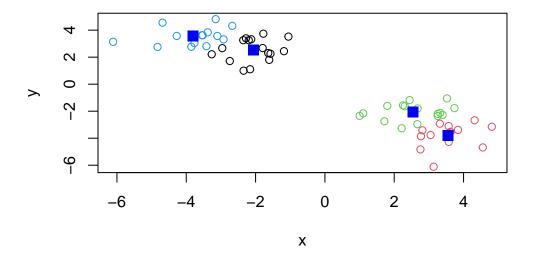
Within cluster sum of squares by cluster:

[1] 16.25584 16.36767 16.25584 16.36767 (between_SS / total_SS = 94.4 %)

Available components:

```
[1] "cluster" "centers" "totss" "withinss" "tot.withinss" [6] "betweenss" "size" "iter" "ifault"
```

```
plot(z, col=km1$cluster)
points(km1$centers, col="blue", pch=15, cex=1.5)
```



##Hierarchal Clustering

Let's take our same made-up data z and see how hierarchal clustering works.

First we need a distance matrix of our data to be clustered.

```
d<- dist(z)
hc<- hclust(d)
hc</pre>
```

Call:
hclust(d = d)

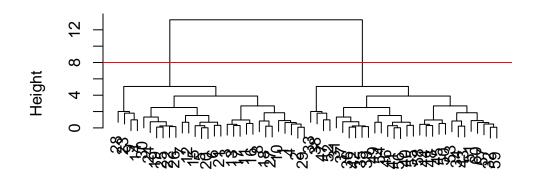
Cluster method : complete

Distance : euclidean

Number of objects: 60

```
plot(hc)
abline(h=8, col="red")
```

Cluster Dendrogram



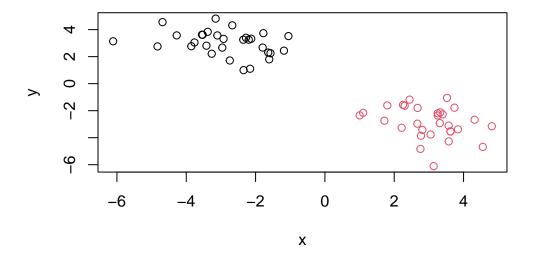
d hclust (*, "complete")

I can get my cluster membership vector by "cutting the tree" with the ${\tt cutree}$ () function like so:

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

Can you plot ${\tt z}$ colored by our hclust results:

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



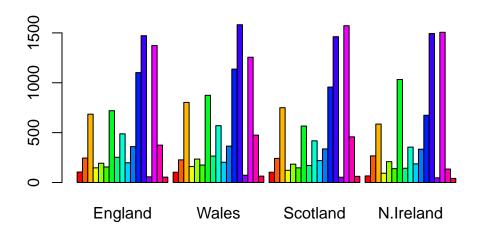
PCA of UK food data

Read data from the UK on food consumption in different parts of the UK

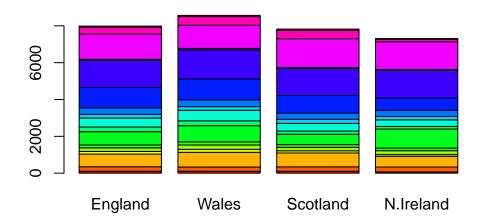
```
url <- "https://tinyurl.com/UK-foods"
x <- read.csv(url,row.names=1)
head(x)</pre>
```

	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

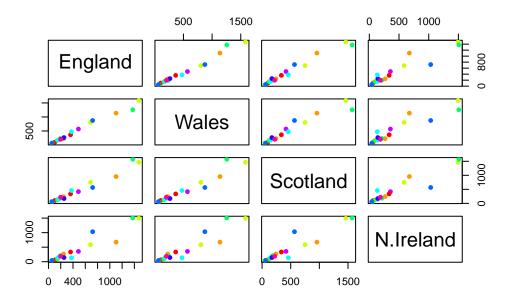
```
barplot(as.matrix(x), beside=T, col=rainbow(nrow(x)))
```



barplot(as.matrix(x), beside=F, col=rainbow(nrow(x)))



A so-called "Pairs" plot can be useful for small datasets like this one



It is hard to see structure and trends in even this small data-set. How will we ever do this when we have big datasets with 1,000s or 10s of thousands of this we are measuring...

PCA to the rescue

Let's see how PCA deals with this dataset. So main function in base R to do PCA is called prcomp()

```
pca<- prcomp( t(x))
summary(pca)</pre>
```

Importance of components:

	PC1	PC2	PC3	PC4
Standard deviation	324.1502	212.7478	73.87622	2.921e-14
Proportion of Variance	0.6744	0.2905	0.03503	0.000e+00
Cumulative Proportion	0.6744	0.9650	1.00000	1.000e+00

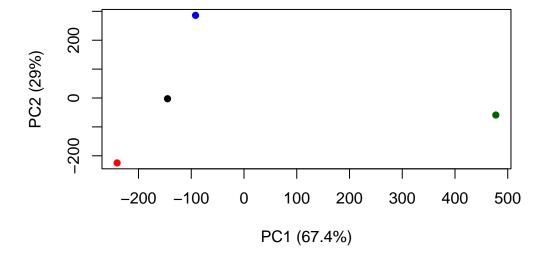
Let's see what is inside this pca object that we created from running prcomp()

attributes(pca)

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

pca\$x

```
PC1 PC2 PC3 PC4
England -144.99315 -2.532999 105.768945 -9.152022e-15
Wales -240.52915 -224.646925 -56.475555 5.560040e-13
Scotland -91.86934 286.081786 -44.415495 -6.638419e-13
N.Ireland 477.39164 -58.901862 -4.877895 1.329771e-13
```



```
par(mar=c(10, 3, 0.35, 0))
barplot( pca$rotation[,1], las=2 )
```

