Class 7: Machine Learning I

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

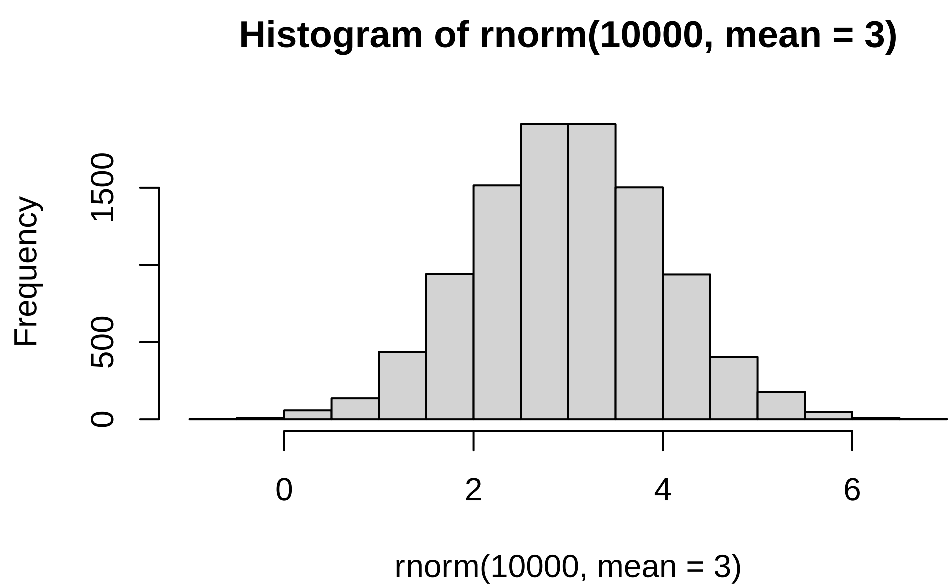
The goal here is to find cluster/groups in your input data.

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

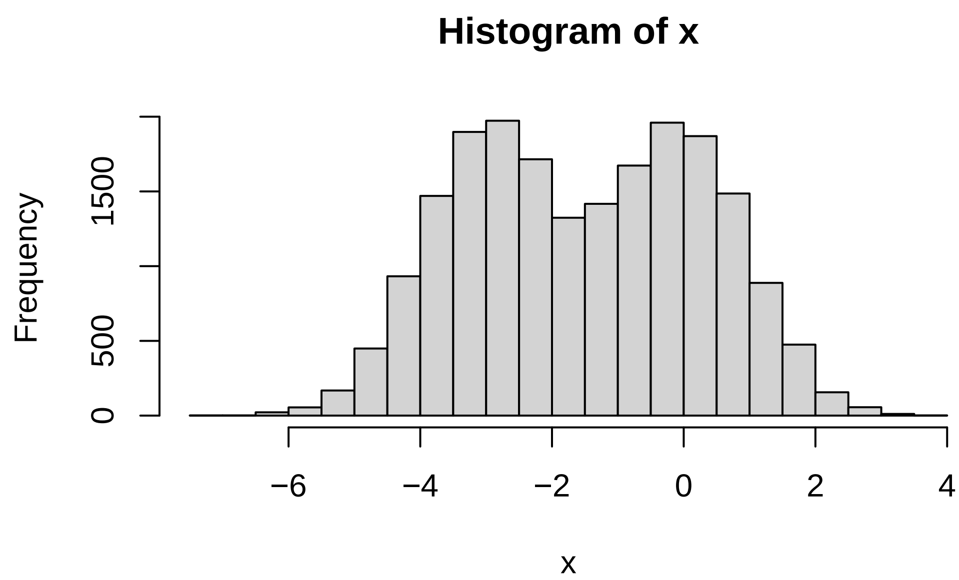
```
rnorm(10) #Give 10 random numbers from normal distribution
```

```
 [1]  0.38942456 -1.28573724  0.49745097  1.60649675 -0.02975181 -0.22809807
 [7] -1.30972086  0.13125049  0.37959831  1.84418140
```

```
hist(rnorm(10000, mean = 3))
```



```r
n <- 10000
x <- c(rnorm(n,-3), rnorm(n), +3) #Make a vector of normal distribution
hist(x)
```

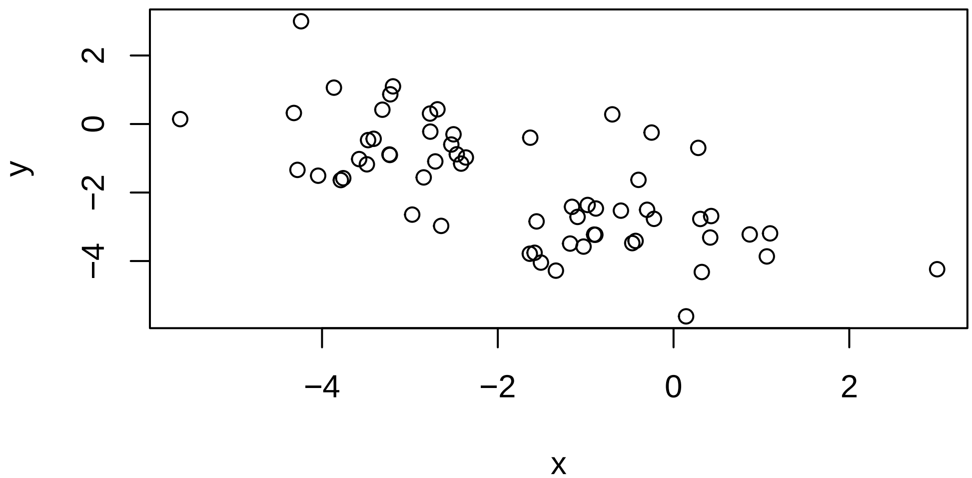



```r
n <- 30
x <- c(rnorm(n,-3), rnorm(n), +3)
y <- rev(x)

z <- cbind(x,y)
head(z)
```

```
              x          y
[1,] -4.2386906  3.0000000
[2,] -0.6970244  0.2811774
[3,] -3.7866359 -1.6358185
[4,] -2.9739680 -2.6444166
[5,] -3.2327851 -0.8898777
[6,] -3.4127389 -0.4318250
```

```r
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/membership? - cluster center?

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

```
K-means clustering with 2 clusters of sizes 31, 30

Cluster means:
           x          y
1 -0.4232245 -3.0860075
2 -3.1805521 -0.4290097

Clustering vector:
 [1] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 1 1 1 1 1 1 1 1
[39] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Within cluster sum of squares by cluster:
```

```
[1] 67.66121 59.31711
 (between_SS / total_SS =  63.8 %)

Available components:

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

Results in kmeans object `km`

```r
attributes(km)
```

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

$class
[1] "kmeans"
```

cluster size?

```r
km$size
```

```
[1] 31 30
```

cluster assignment/membership?

```r
km$cluster
```

```
 [1] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 1 1 1 1 1 1 1 1
[39] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
```

cluster center?

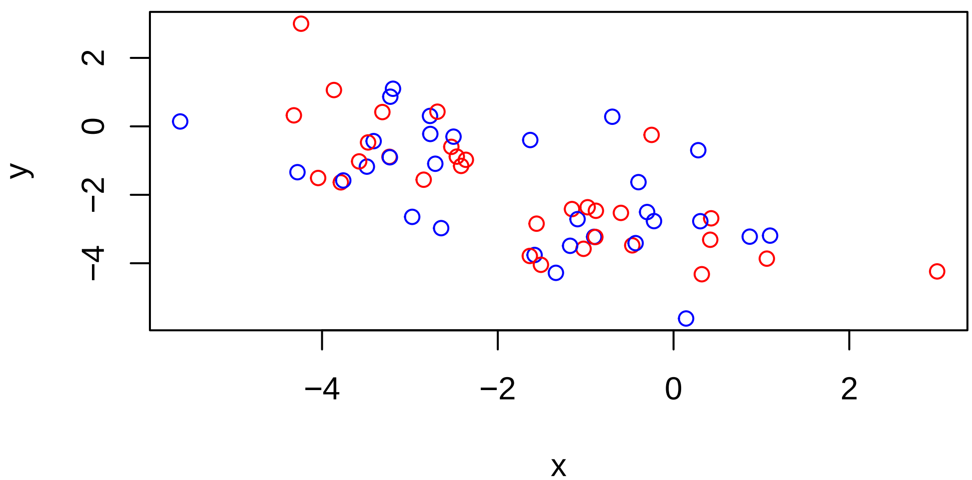
```r
km$centers
```

```
           x          y
1 -0.4232245 -3.0860075
2 -3.1805521 -0.4290097
```

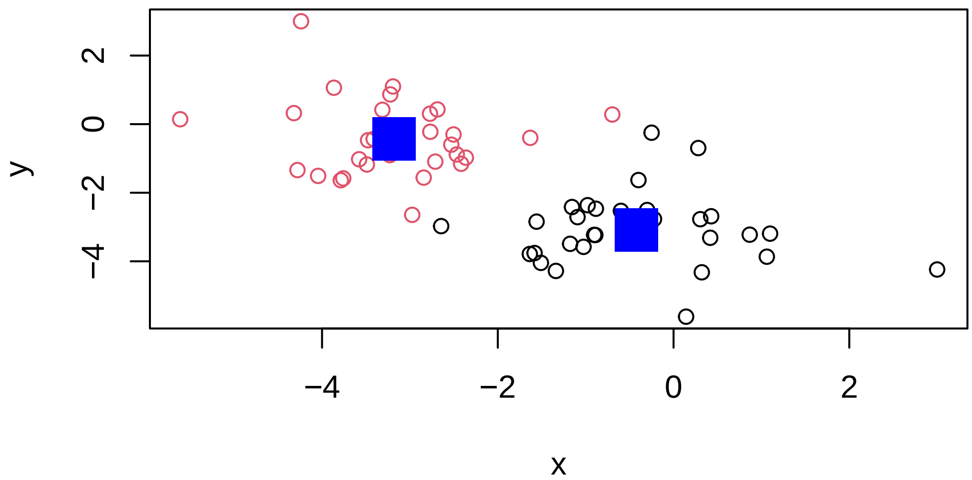
> Q. Plot x colored by the kmeans cluster assignment and add cluster centers as blue points

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

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

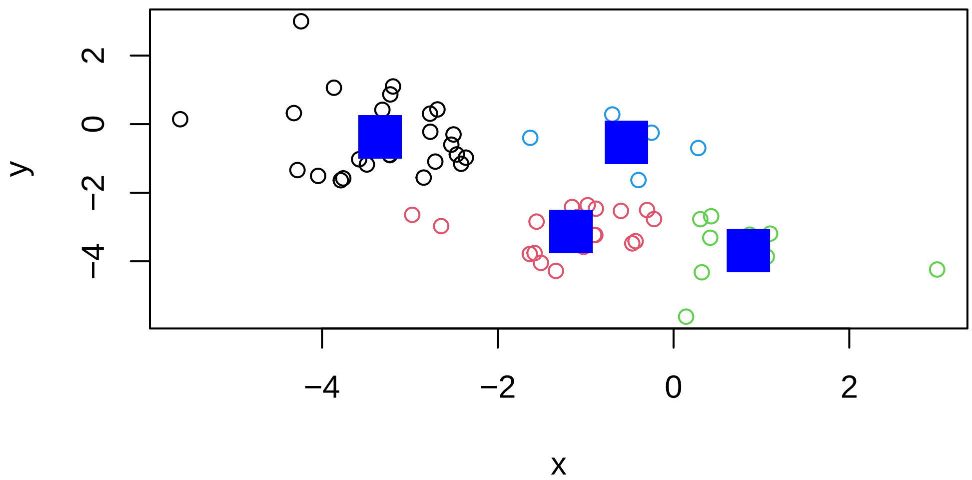



```
plot(z, col = km$cluster)
points(km$centers, col = "blue",pch = 15, cex=3) #Make mean shown on plot.
```



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

```
km4 <- kmeans(z,centers = 4)
plot(z, col = km4$cluster)
points(km4$centers, col = "blue",pch = 15, cex=3)
```




```
#It will be different every time you run it.
```

##Hierarchical Clustering

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

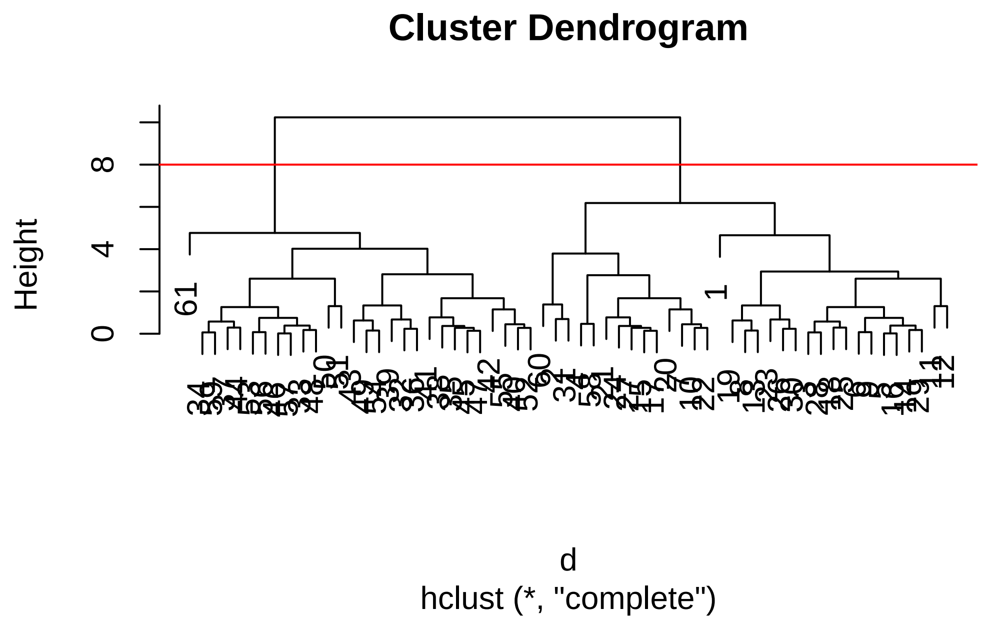
First we need a distance matrix of our data to be clustered.

```
d <- dist(z)
hc <- hclust(d)
hc
```

```
Call:
hclust(d = d)

Cluster method   : complete
Distance         : euclidean
Number of objects: 61
```

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



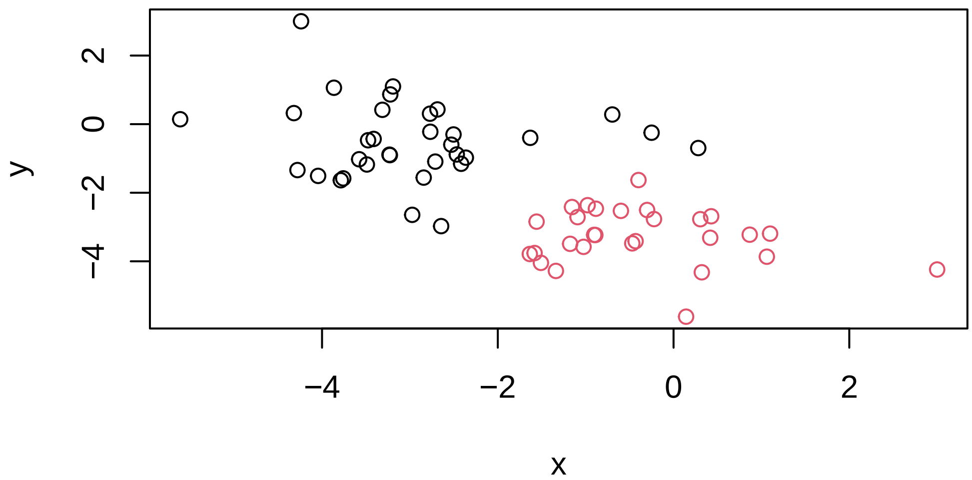
I can gget my cluster membership vector by "cutting the tree" with the `cutree()` function like so:

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

```
 [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2
[39] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 1 2 1 2
```

Can you plot `z` colored by our hclust results:

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



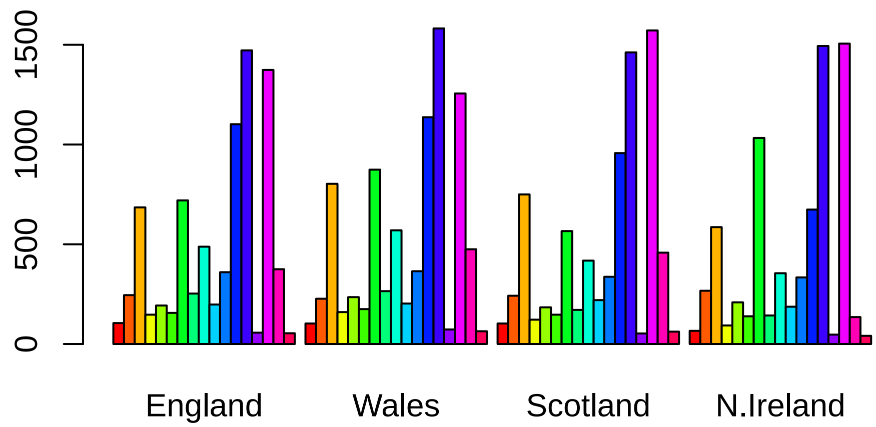
##PCA of UK food data

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)
```

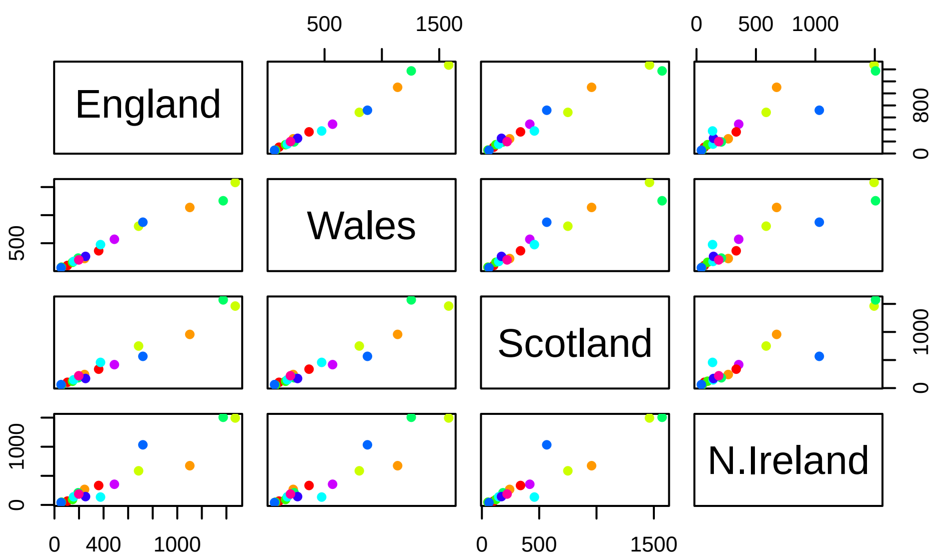
```
               England Wales Scotland N.Ireland
Cheese             105   103      103        66
Carcass_meat       245   227      242       267
Other_meat         685   803      750       586
Fish               147   160      122        93
Fats_and_oils      193   235      184       209
Sugars             156   175      147       139
```

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



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

```
pairs(x, col=rainbow(10), pch=16)
```



It is hard to see structure and treds in even this small data-set. How will we ever do this when we have big datasets with 10002 or 10s of thousands of things 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)
```

```
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's inside this `pca` object that we created from running `prcomp()`

```
attributes(pca)
```

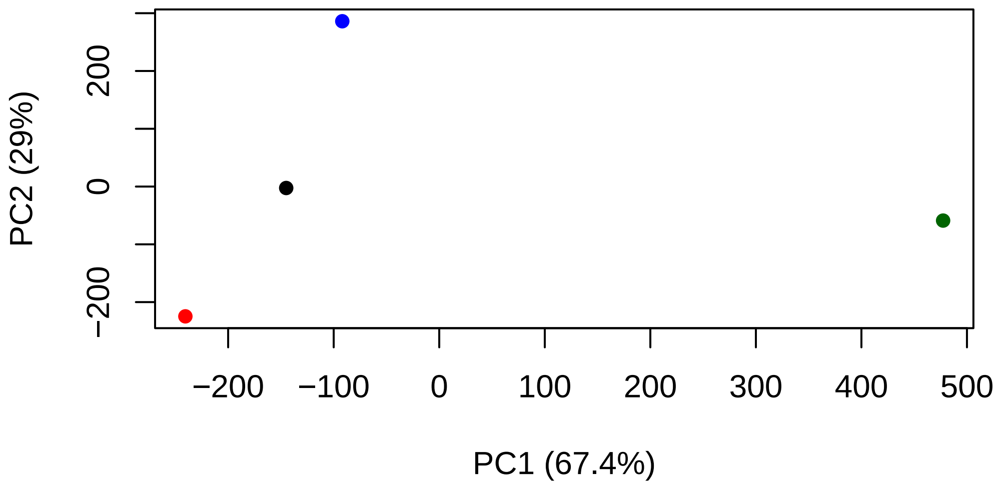
```
$names
[1] "sdev"     "rotation" "center"   "scale"    "x"

$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
```

```
plot(pca$x[,1], pca$x[,2],
     col = c("black", "red", "blue", "darkgreen"),
     pch=16,
     xlab="PC1 (67.4%)",
     ylab="PC2 (29%)")
```



PC2 (29%)
200
0
−200
−200
−100
0
100
200
300
400
500
PC1 (67.4%)