class07

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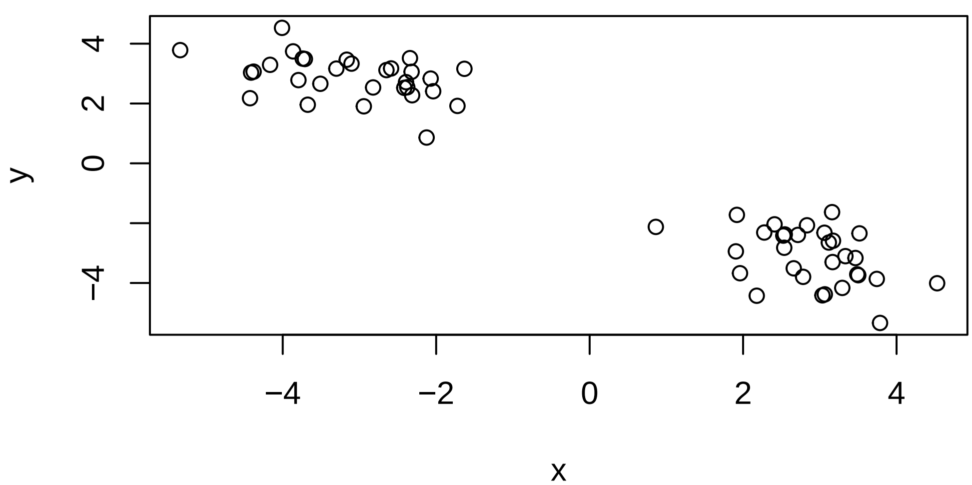
Today we are going to learn how to apply dif machine learning methods, Clustering:

Goal: find groups/clusters in your input data.

Make up some data with clear groups, for clustering. For this we use 'rnorm()' function

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




```
km <- kmeans(x,centers =4)
km
```

```
K-means clustering with 4 clusters of sizes 5, 14, 30, 11

Cluster means:
          x         y
1 -3.669552  2.296998
2 -2.272097  2.617362
3  2.884265 -3.111482
4 -3.926122  3.490898

Clustering vector:
 [1] 4 2 1 1 4 4 2 2 1 2 4 2 1 4 4 2 1 4 2 2 4 2 2 4 4 4 2 2 2 2 3 3 3 3 3 3 3 3
[39] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3

Within cluster sum of squares by cluster:
[1]  1.789530  7.085897 40.380021  6.013642
 (between_SS / total_SS =  95.2 %)

Available components:

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

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

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

Cluster means:
          x         y
1 -3.111482  2.884265
2  2.884265 -3.111482

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

Within cluster sum of squares by cluster:
[1] 40.38002 40.38002
 (between_SS / total_SS =  93.0 %)

Available components:
```

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

> Q. How many points are in each cluster?

```r
k$size
```

```
[1] 30 30
```

> Q. How do we go to the cluster membership/assingment?

```r
k$cluster
```

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

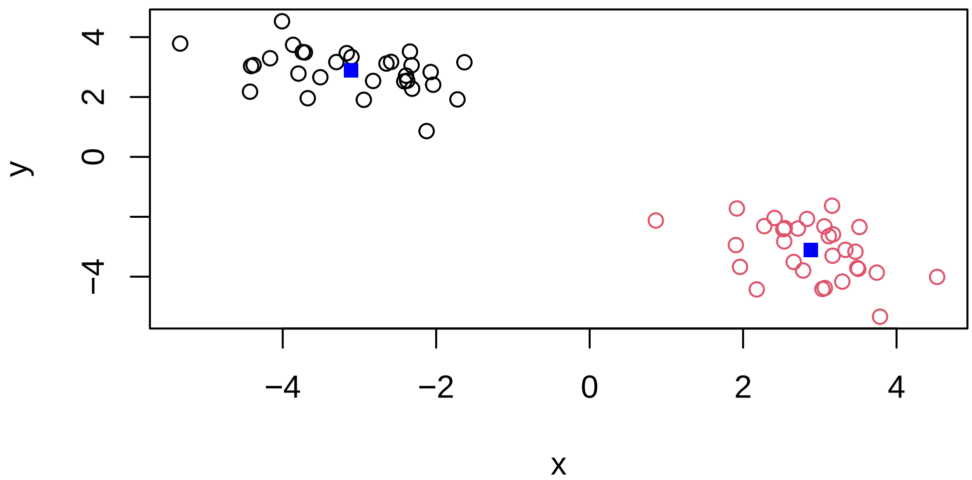
> Q. What 'component' of your result object details - cluster sixe? - cluster assignment/membership? - cluster center?

```r
k$centers
```

```
          x         y
1 -3.111482  2.884265
2  2.884265 -3.111482
```

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

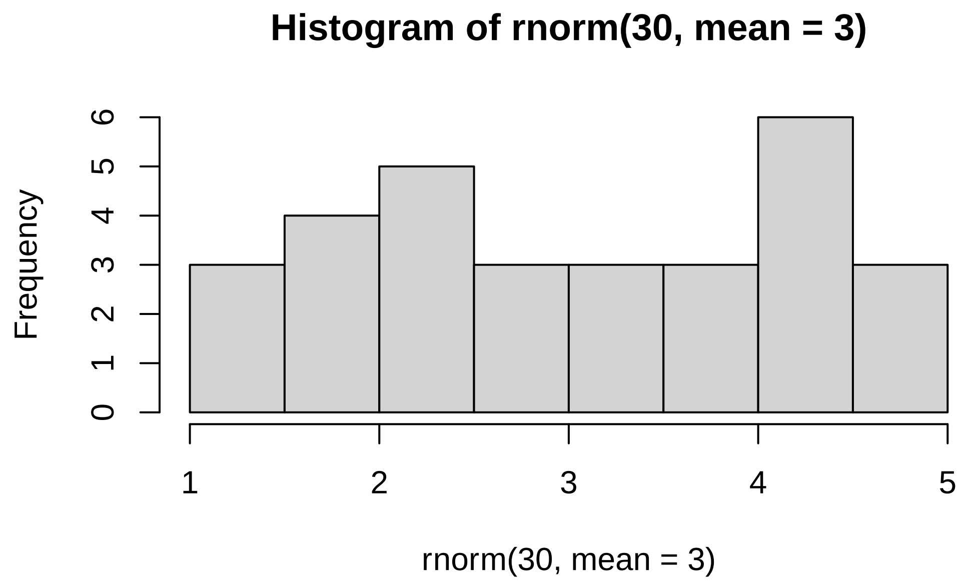
```r
plot(x, col =k$cluster)
points (k$centers, col ="blue", pch=15)
```



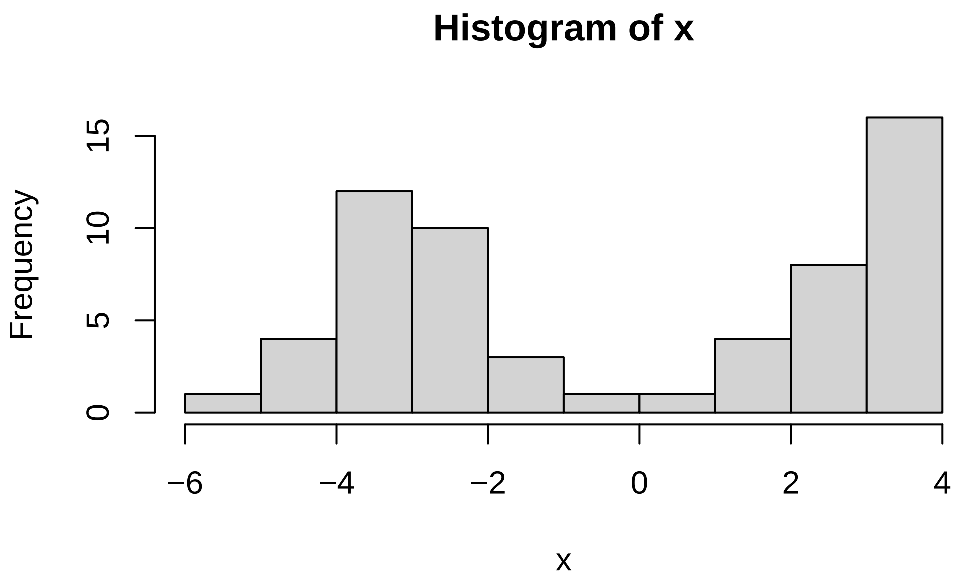

```
rnorm(10)
```

```
 [1]  0.8225387  0.5426470  1.4752785  0.1693167  0.5333468  0.6008524
 [7]  0.9434048 -0.8268720  2.5333351  1.0014656
```

```
hist( rnorm(30, mean=3))
```

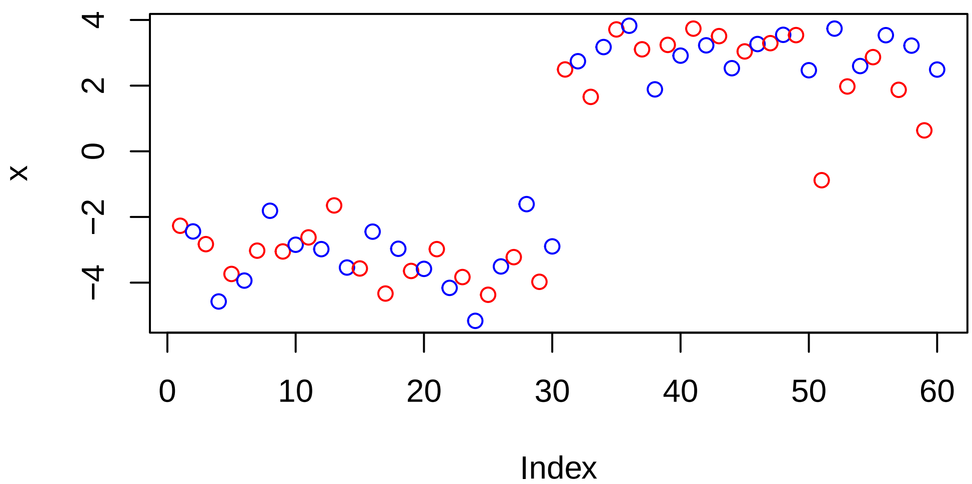



```
n<-30
x<-c(rnorm(n,-3), rnorm(n,+3))
#to get the y axis we reverse x with 'x'
y<-rev(x)
hist(x)
```

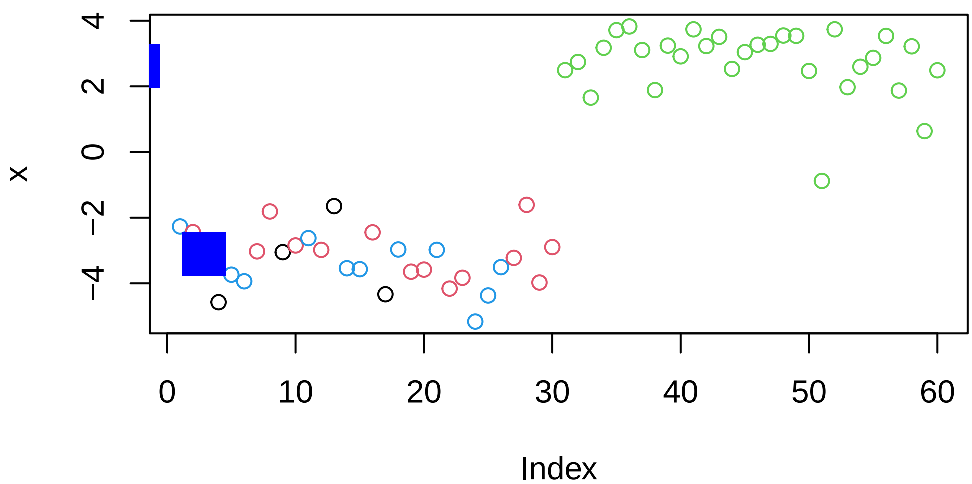


R will re-cycle the shorter color vector to be the same lenght as the longer (number of data points) in x >Plot x colored by the kmeans cluster assignment and add cluster centers as blue points

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

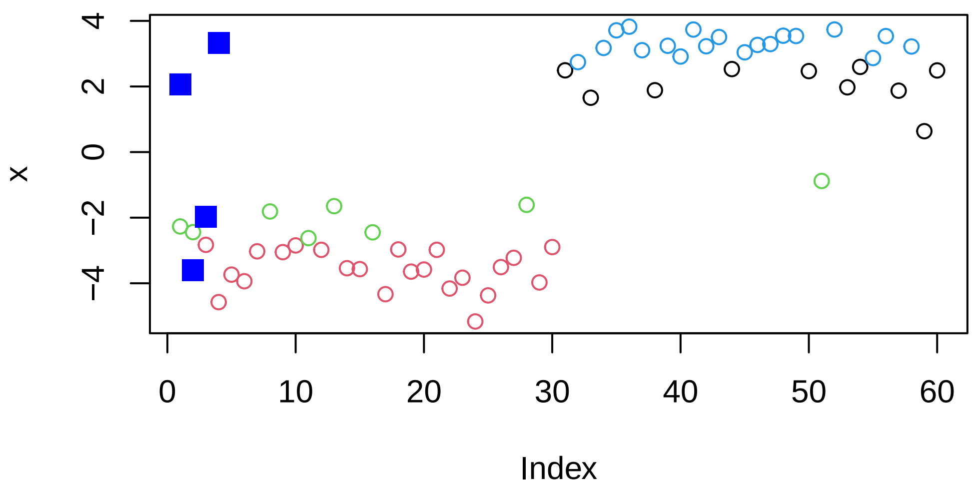



```
plot(x, col=km$cluster)
points(km$centers, col="blue",pch=15,cex=3)
```



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

```
km4 <- kmeans(x, centers = 4)
plot(x, col=km4$cluster)
points(km4$centers, col="blue",pch=15,cex=1.5)
```



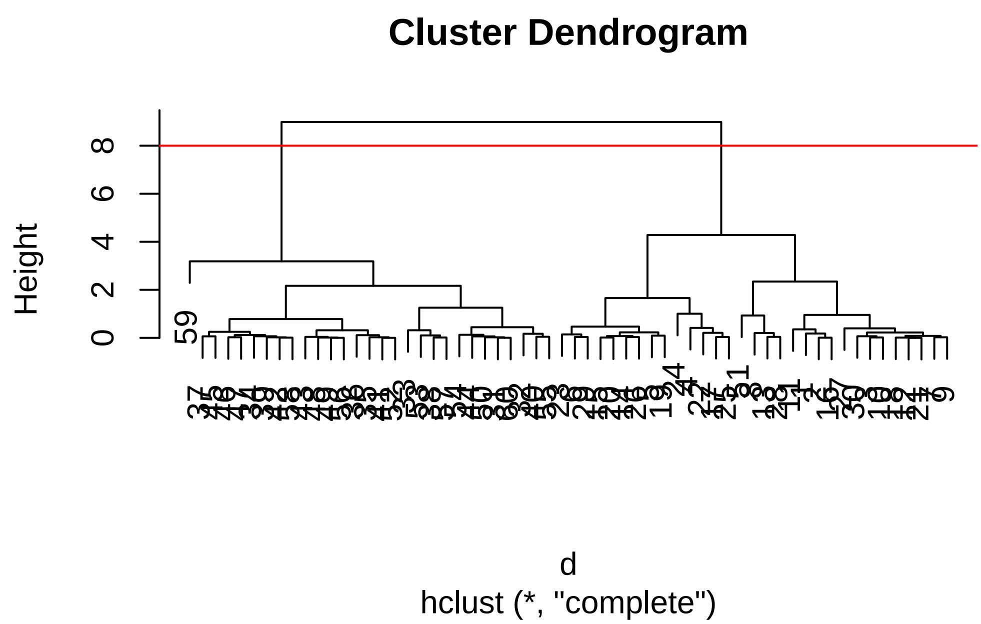
##Hierarchical Cluster Let's take our made up data 'x' and see how hclust works.

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

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

```
Call:
hclust(d = d)

Cluster method   : complete
Distance         : euclidean
Number of objects: 60
```

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



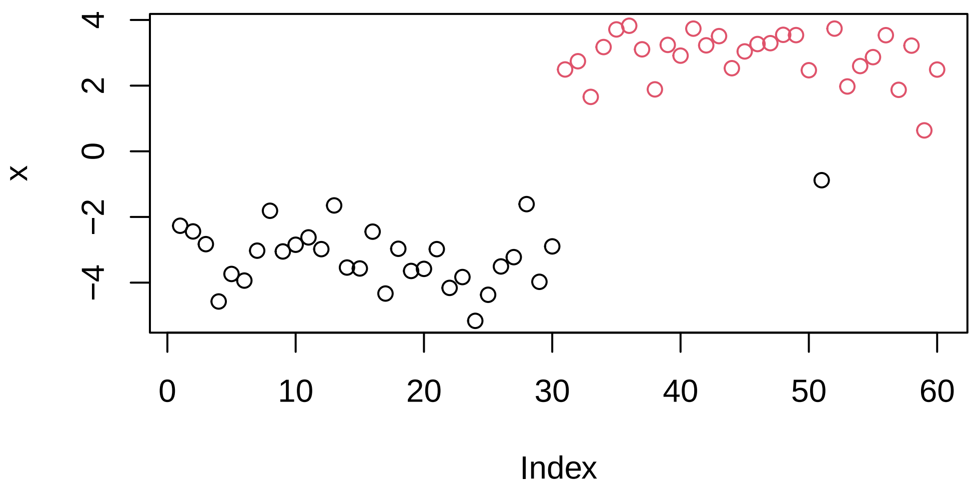
I can get my cluster membershop vector by “cutting the tree” with the ‘cutree()’ fucntion:

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

Can yo upot ‘x’ colored by our hclust results:

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



PCA of UK food data

Read data from the UK on food consumption in dif pats of the UK

> Q1. How many rows and columns are in your new data frame named x? 6 rows | 1-4 of 4 columns What R functions could you use to answer this questions?

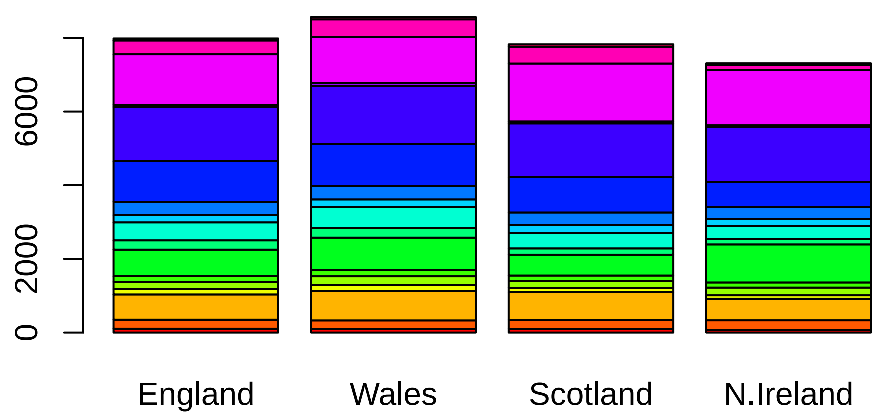
```
url <- "https://tinyurl.com/UK-foods"
x <- read.csv(url, row.names = 1)
head(x, )
```

```
               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
```

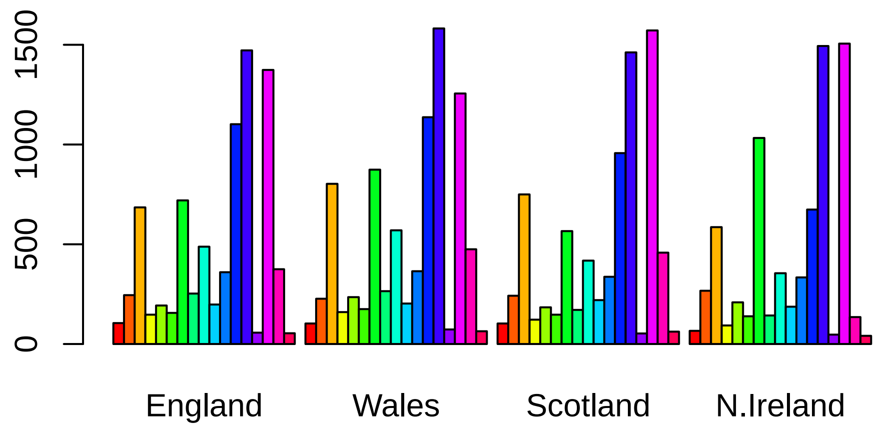
> Q2. Which approach to solving the 'row-names problem' mentioned above do you prefer and why? Is one approach more robust than another under certain circumstances?

Q3: Changing what optional argument in the above barplot() function results in the following plot? barside

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



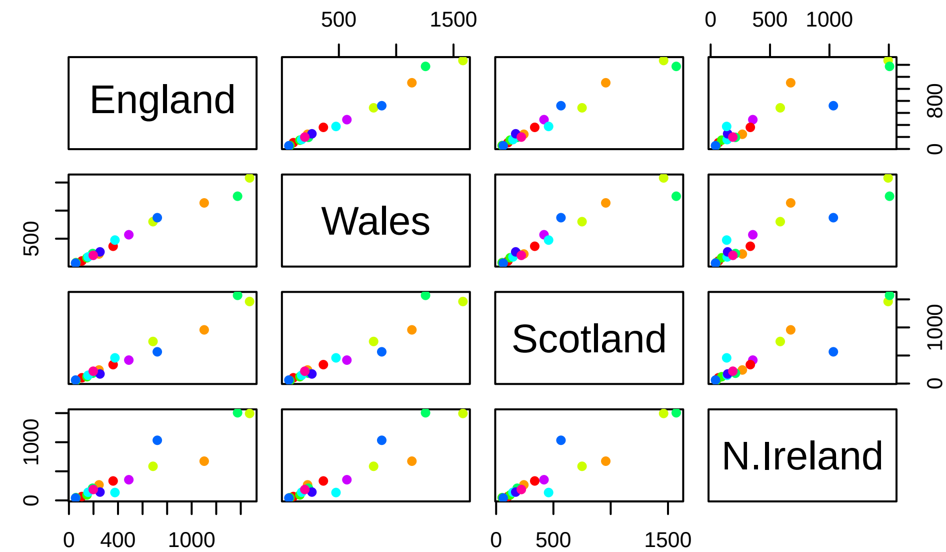

```
#with 'beside=T'
barplot(as.matrix(x), beside=T, col=rainbow(nrow(x)))
```



> Q5: Generating all pairwise plots may help somewhat. Can you make sense of the following code and resulting figure? What does it mean if a given point lies on the diagonal for a given plot?

"Pairs" plot can be useful for small datasets like this one:

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



It is hard to see structure and trends in even this small dta-set. How will we ever do this when we have big datasets with bigger data. >Q6. What is the main differences between N. Ireland and the other countries of the UK in terms of this data-set? the plot is more scattered

###PCA to the rescue (for bigger data)

'prcomp()'this is the main function in base R to do PCA

```
pcs <- prcomp(t(x))
#stats summary from dataset
summary(pcs)
```

```
Importance of components:
                            PC1      PC2      PC3       PC4
Standard deviation     324.1502 212.7478 73.87622 3.176e-14
Proportion of Variance   0.6744   0.2905  0.03503 0.000e+00
Cumulative Proportion    0.6744   0.9650  1.00000 1.000e+00
```

inside 'PCA' object that we created from running 'prcomp()'

```
attributes(pcs)
```

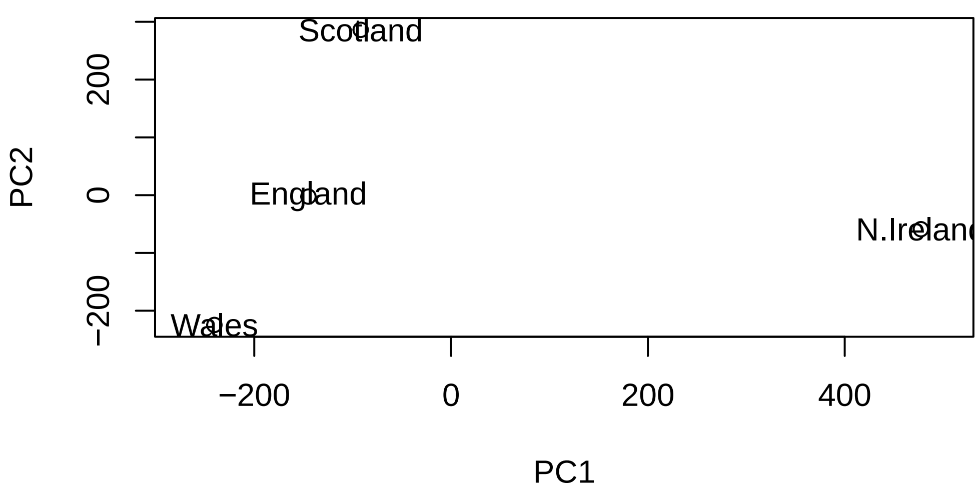
```
$names
[1] "sdev"     "rotation" "center"   "scale"    "x"

$class
[1] "prcomp"
```

```
pcs$x
```

```
                PC1        PC2        PC3           PC4
England   -144.99315   -2.532999 105.768945 -4.894696e-14
Wales     -240.52915 -224.646925 -56.475555  5.700024e-13
Scotland   -91.86934  286.081786 -44.415495 -7.460785e-13
N.Ireland  477.39164  -58.901862  -4.877895  2.321303e-13
```

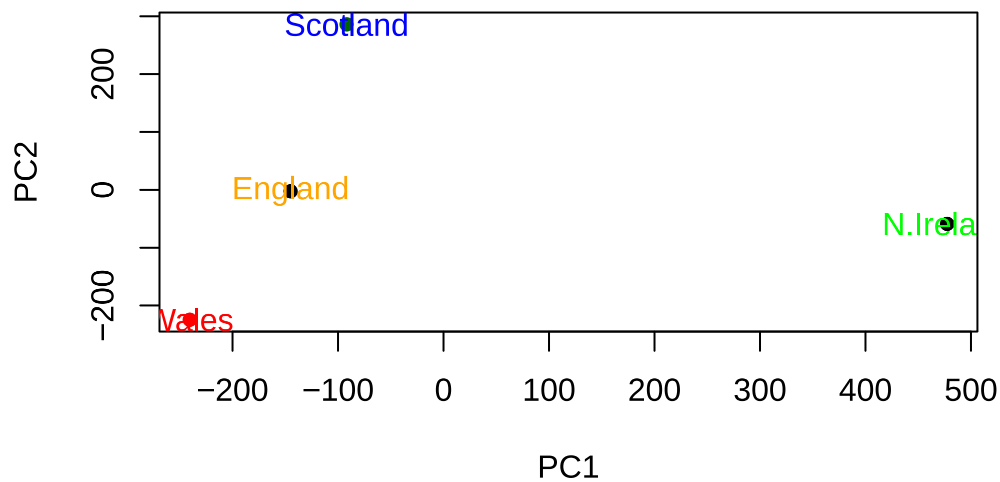
Q7. Complete the code below to generate a plot of PC1 vs PC2. The second line adds text labels over the data points.

```
plot(pcs$x[,1], pcs$x[,2],  xlab="PC1", ylab="PC2", xlim=c(-270,500))
text(pcs$x[,1], pcs$x[,2], colnames(x))
```



8. Customize your plot so that the colors of the country names match the colors in our UK and Ireland map and table at start of this document.

```r
country_cols <-c("orange", "red", "blue", "green")
plot(pcs$x[,1], pcs$x[,2], xlab="PC1", ylab="PC2",
     col=c("black", "red", "darkgreen"), pch=16 )
text(pcs$x[,1], pcs$x[,2], colnames(x), col=country_cols)
```



##Digging deeper

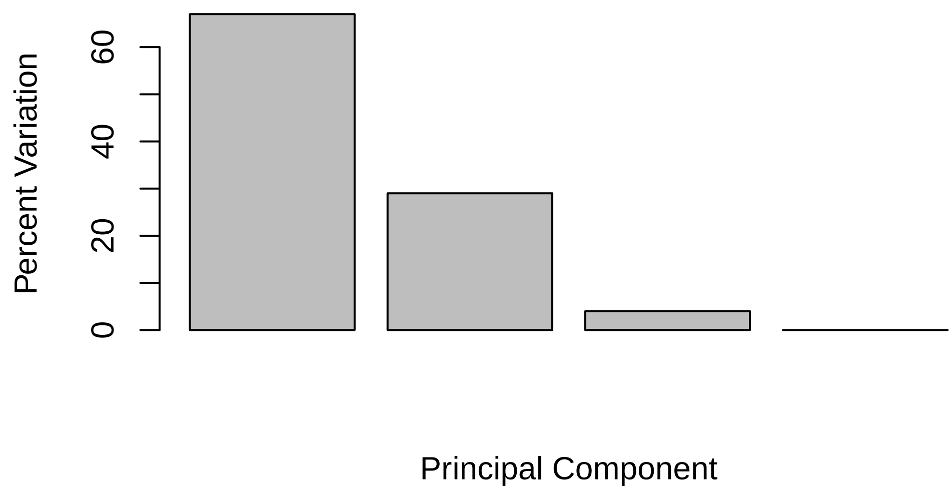
```r
v <- round( pcs$sdev^2/sum(pcs$sdev^2) * 100 )
v
```

```
[1] 67 29  4  0
```

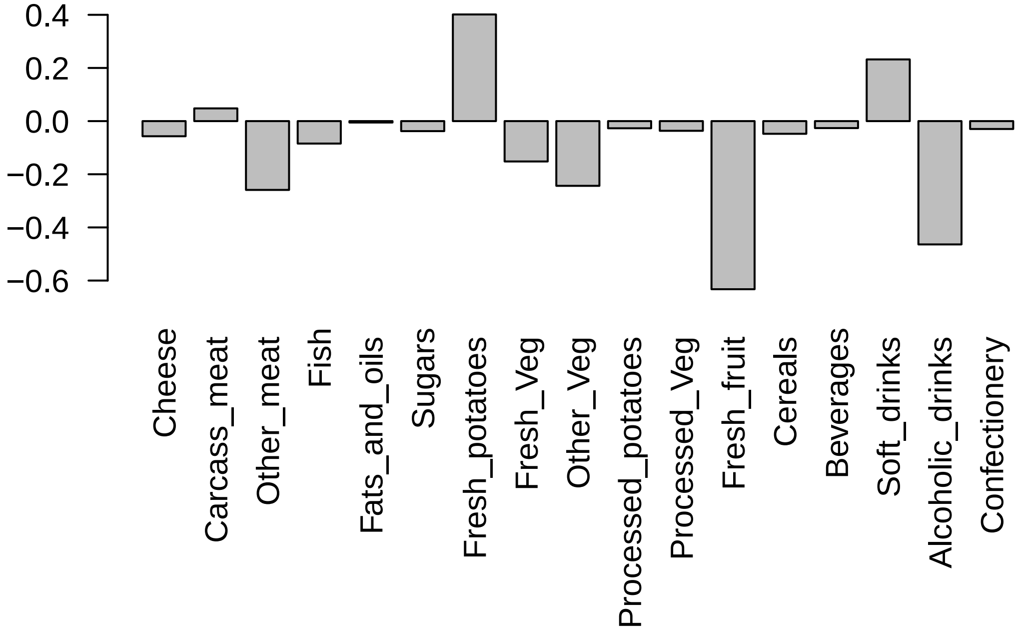
```r
x <- summary(pcs)
x$importance
```

```
                            PC1       PC2      PC3          PC4
Standard deviation     324.15019 212.74780 73.87622 3.175833e-14
Proportion of Variance   0.67444   0.29052  0.03503 0.000000e+00
Cumulative Proportion    0.67444   0.96497  1.00000 1.000000e+00
```

```r
barplot(v, xlab="Principal Component", ylab="Percent Variation")
```




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


0.4
0.2
0.0
−0.2
−0.4
−0.6
Cheese
Carcass_meat
Other_meat
Fish
Fats_and_oils
Sugars
Fresh_potatoes
Fresh_Veg
Other_Veg
Processed_potatoes
Processed_Veg
Fresh_fruit
Cereals
Beverages
Soft_drinks
Alcoholic_drinks
Confectionery