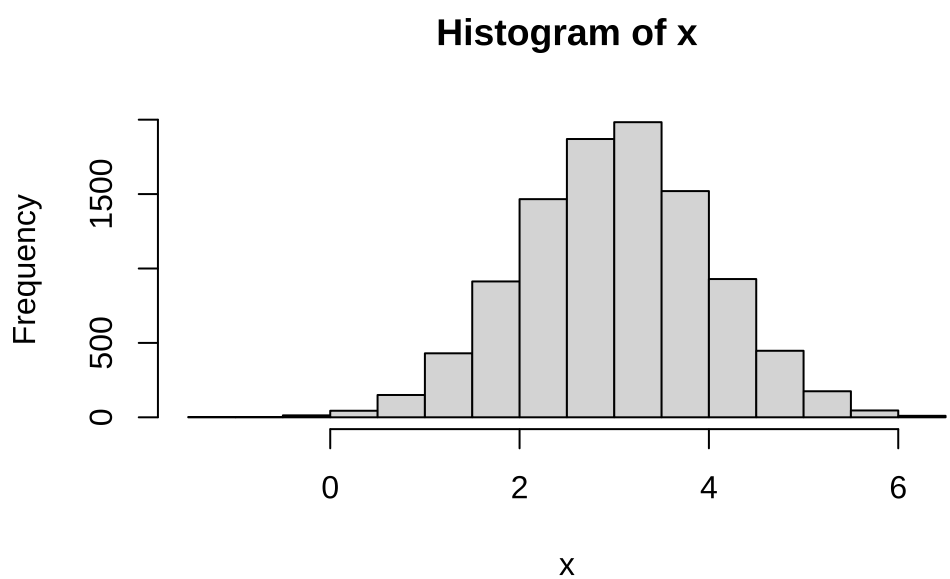
# Class 7

Lauren Waters (A16326738)

#Clustering We will start today's lab with clustering methods, in particular so-called K-means. The main function for this in R is kmeans().

Let's try it on some made up data where we know that the answer should be.

```
x <- rnorm(10000, mean=3)
hist(x)
```

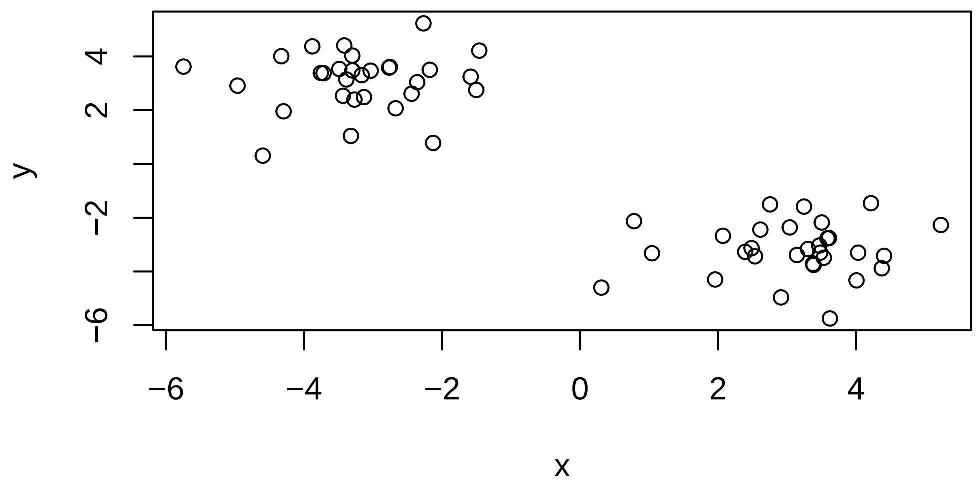



```
tmp <- c(rnorm(30, mean=3), rnorm(30, -3))
x <- cbind(x=tmp, y=rev(tmp))
head(x)
```

```
            x         y
[1,] 2.394197 -3.269939
[2,] 5.230119 -2.269711
[3,] 3.468628 -3.035253
[4,] 1.958489 -4.297168
[5,] 3.303750 -3.165322
[6,] 3.608458 -2.756978
```

We can pass this to the base R `plot()` function for a quick run

```
plot(x)
```




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

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

Cluster means:
          x         y
1  3.081036 -3.189227
2 -3.189227  3.081036
```

```
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] 62.65098 62.65098
 (between_SS / total_SS =  90.4 %)

Available components:

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

Q1. How many point are in each cluter?

```r
k$size
```

```
[1] 30 30
```

Q2. Cluster membership?

```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
```

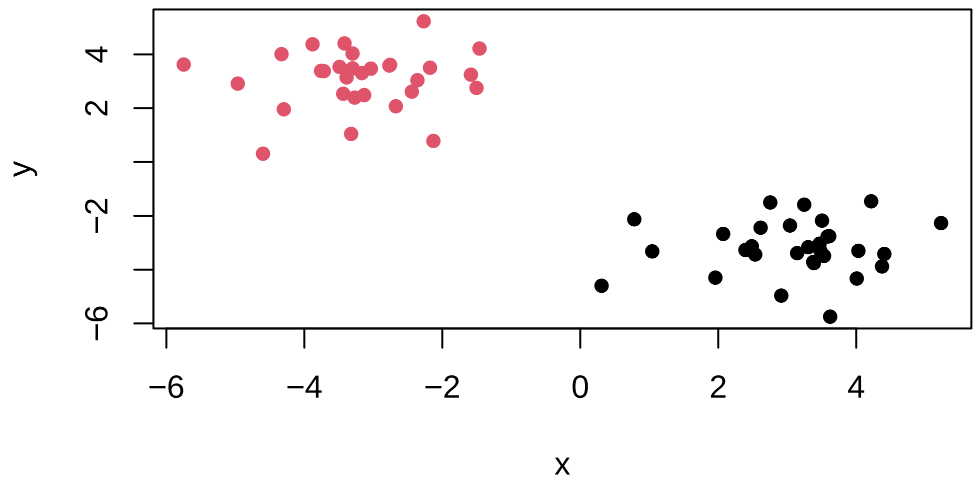
Q3. Cluster centers?

```r
k$centers
```

```
          x         y
1  3.081036 -3.189227
2 -3.189227  3.081036
```

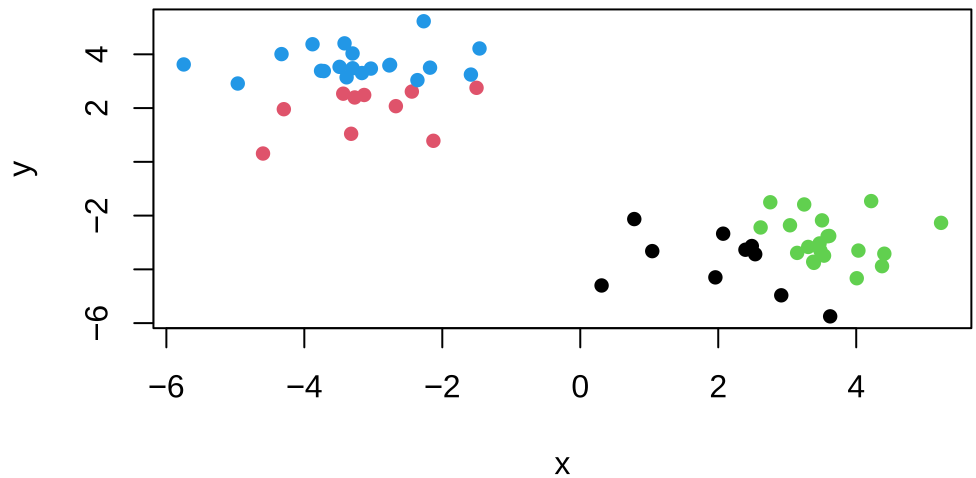
Q4. Plot the cluster results

```r
plot(x, col = k$cluster, pch = 16)
```




Q5. Cluster the sata again with `kmeans()` into 4 groups and plot the results.

```
k4 <- kmeans(x, centers = 4, nstart = 20)
plot(x, col = k4$cluster, pch = 16)
```

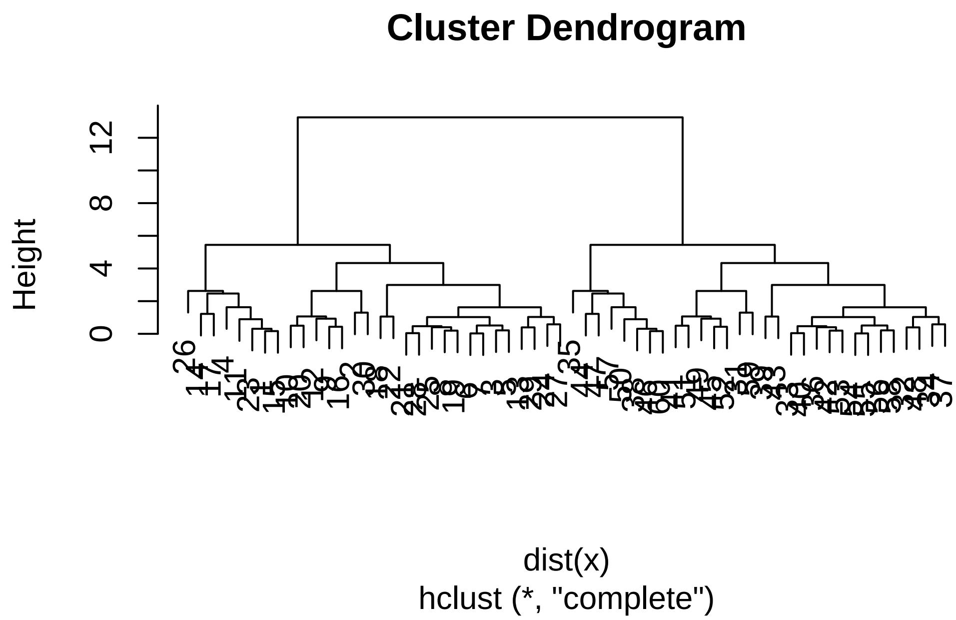



K-means is common becuase it's fast and easy to understand. Limitation: you need to tell it the number of groups (k or centers) you want.

### Hierarchical Clusters

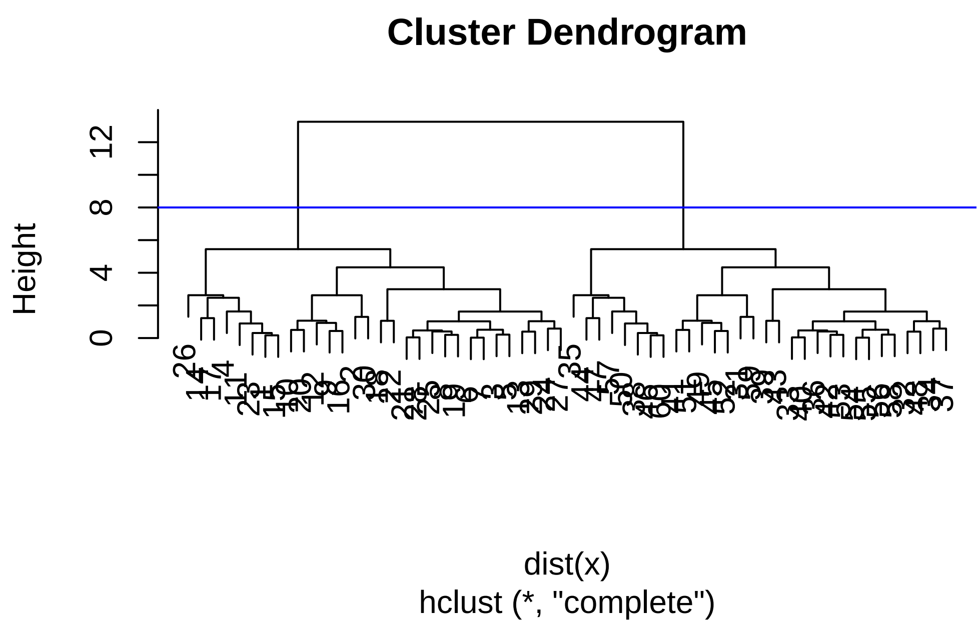
The main function in base R is `hcluster()`. You have to pass it in a "distance matrx" and not just put data in.

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




To find the clusters (sluter membership vector) from a `hclut()` result we can 'cut' the tree at a certain height we like using `cutree()`

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

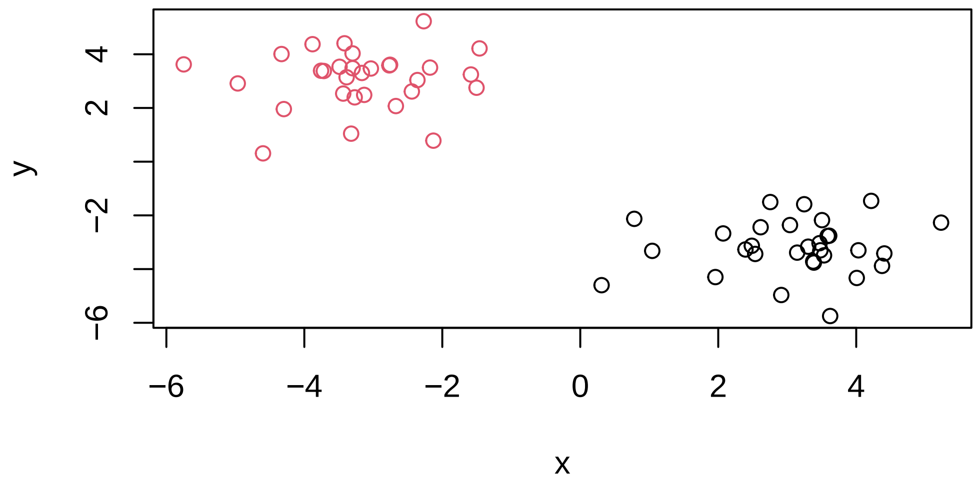



```r
grps <- cutree(hc, h = 8)
table(grps)
```

```
grps
 1  2 
30 30 
```

Q6. Plot the hclust results.

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




### Principle Component Analysis

Read the data showing the consumption in grams of 17 different types of food-stuff measured and averaged in the 4 countries of the UK in 1997.

Let's see how PCA can help us, but first we can try conventional analysis.

```
url <- "https://tinyurl.com/UK-foods"
x <- read.csv(url)
x
```

```
                     X England Wales Scotland N.Ireland
1               Cheese     105   103      103        66
2          Carcass_meat    245   227      242       267
3            Other_meat    685   803      750       586
4                 Fish     147   160      122        93
5          Fats_and_oils   193   235      184       209
6               Sugars     156   175      147       139
7        Fresh_potatoes    720   874      566      1033
8            Fresh_Veg     253   265      171       143
9            Other_Veg     488   570      418       355
10 Processed_potatoes      198   203      220       187
```

```
11      Processed_Veg      360   365       337        334
12        Fresh_fruit     1102  1137       957        674
13            Cereals     1472  1582      1462       1494
14          Beverages       57    73        53         47
15        Soft_drinks     1374  1256      1572       1506
16   Alcoholic_drinks      375   475       458        135
17      Confectionery       54    64        62         41
```

```r
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
```

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

```r
dim(x)
```

```
[1] 17  4
```

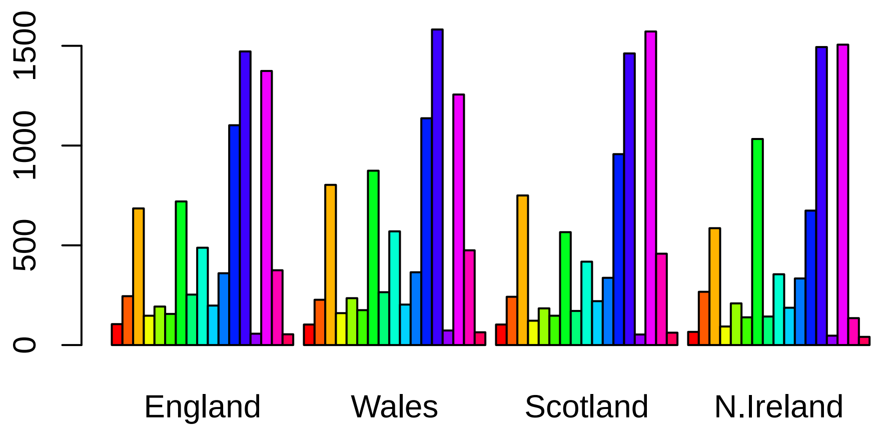
There are 17 rows and 4 columns. Use `dim()` to find rows and columns after using `row.names()` to remove column from being "x"

> 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?

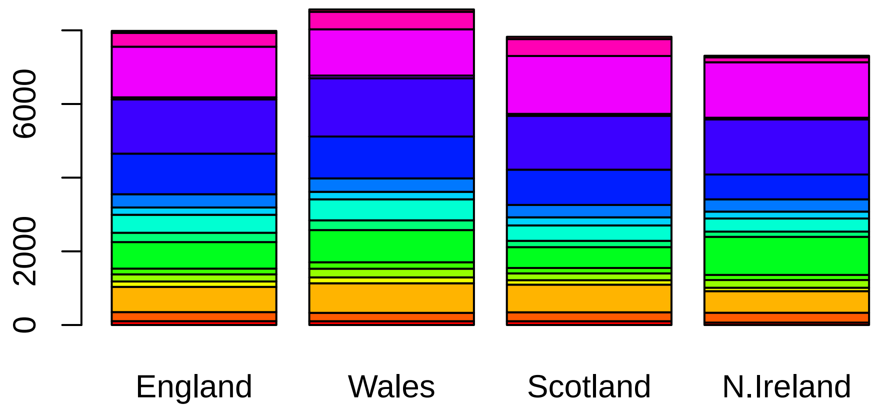
`row.names()` is better because it fixes the designated column, and `x <- x[,-1]` will keep remove a column from the data

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

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



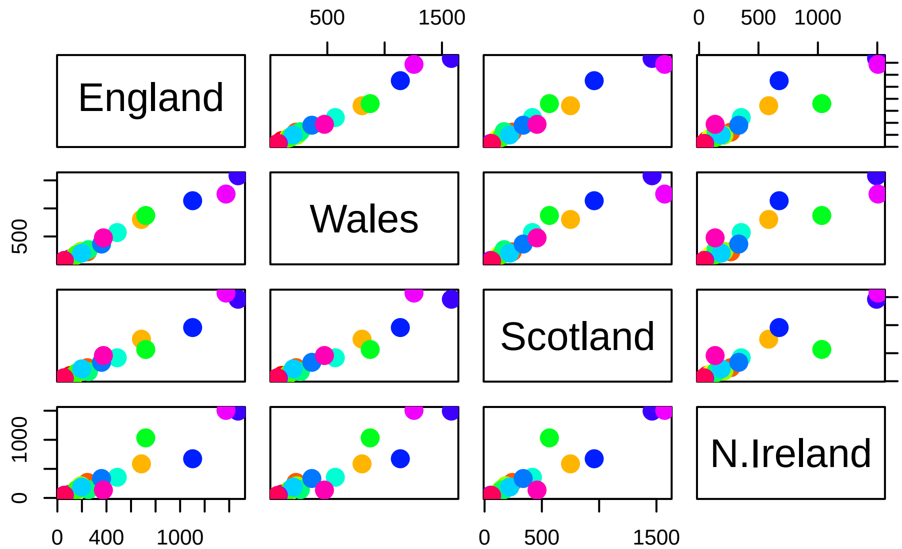

```r
barplot(as.matrix(x), beside = F, col = rainbow(nrow(x)))
```




`beside=()` turns a bar graph into a stacked bar graph

> 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(x, col = rainbow(17), pch = 16, cex = 2)
```




It made the biaganal lines show the standard and any data that skew are values that differ from the OG.

> Q6. What is the main differences between N. Ireland and the other countries of the UK in terms of this data-set?

N. Ireland has the biggest deviation from the other countries becuase there are more data points skewed from the line.

### Principal Compenent Analysis (PCA)

PCA can help make sense of these kinds of datasets.

The main function in "base" R is `prcomp()`. In this case we want to first take the transpose of our input x so the columns are the food types and the countries are the rows.

```
head (t(x))
```

```
         Cheese Carcass_meat  Other_meat  Fish Fats_and_oils  Sugars
England     105          245         685   147           193     156
Wales       103          227         803   160           235     175
Scotland    103          242         750   122           184     147
```

```
N.Ireland     66           267          586   93             209    139
          Fresh_potatoes  Fresh_Veg  Other_Veg  Processed_potatoes
England              720        253        488                198
Wales                874        265        570                203
Scotland             566        171        418                220
N.Ireland           1033        143        355                187
          Processed_Veg  Fresh_fruit  Cereals  Beverages Soft_drinks
England             360         1102     1472         57        1374
Wales               365         1137     1582         73        1256
Scotland            337          957     1462         53        1572
N.Ireland           334          674     1494         47        1506
          Alcoholic_drinks  Confectionery
England                375             54
Wales                  475             64
Scotland               458             62
N.Ireland              135             41
```

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

```
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
```

PC1 captures 67.44% of all data, PC2 captures 96.50% of all data, …

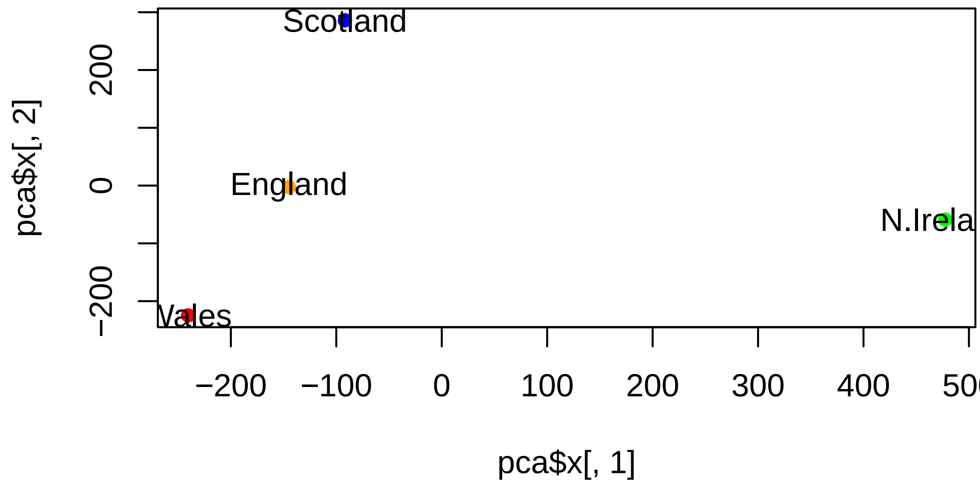
> Q7. Complete the code below to generate a plot of PC1 vs PC2. The second line adds text labels over the data points.

```r
pca$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
```

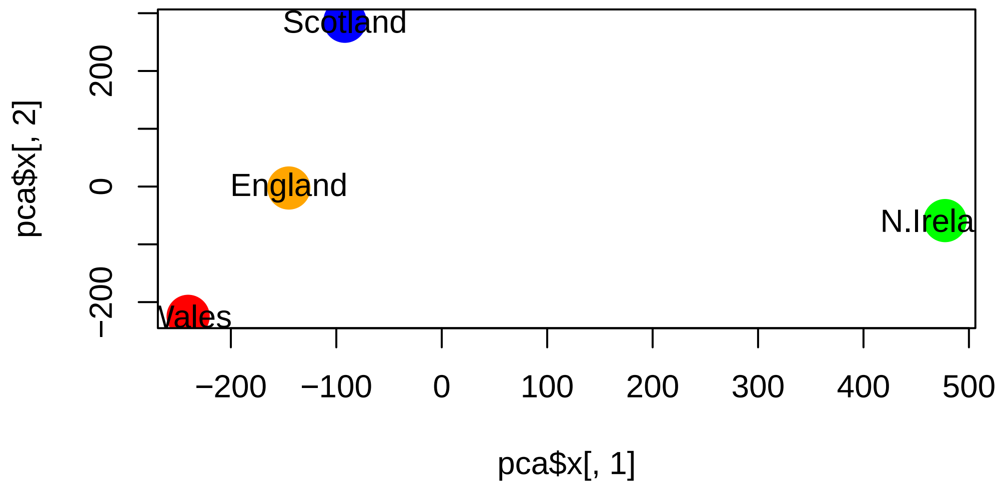
### Plot PC1 vs PC2

```
plot(pca$x[,1], pca$x[,2], col=c("orange", "red", "blue", "green"), pch = 16)
text(pca$x[,1], pca$x[,2], colnames(x))
```




Q8. 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.

```
plot(pca$x[,1], pca$x[,2], col=c("orange", "red", "blue", "green"), pch = 16, cex = 3)
text(pca$x[,1], pca$x[,2], colnames(x))
```




The “loadings” tells us how much the original variables (in this case the foods) contribute to the new variables (i.e. the PCs).

```
pca$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
```

```
pca$rotation
```

```
                            PC1          PC2         PC3          PC4
Cheese             -0.056955380  0.016012850  0.02394295 -0.694538519
Carcass_meat        0.047927628  0.013915823  0.06367111  0.489884628
Other_meat         -0.258916658 -0.015331138 -0.55384854  0.279023718
Fish               -0.084414983 -0.050754947  0.03906481 -0.008483145
Fats_and_oils      -0.005193623 -0.095388656 -0.12522257  0.076097502
Sugars             -0.037620983 -0.043021699 -0.03605745  0.034101334
```

```
Fresh_potatoes       0.401402060 -0.715017078 -0.20668248 -0.090972715
Fresh_Veg           -0.151849942 -0.144900268  0.21382237 -0.039901917
Other_Veg           -0.243593729 -0.225450923 -0.05332841  0.016719075
Processed_potatoes  -0.026886233  0.042850761 -0.07364902  0.030125166
Processed_Veg       -0.036488269 -0.045451802  0.05289191 -0.013969507
Fresh_fruit         -0.632640898 -0.177740743  0.40012865  0.184072217
Cereals             -0.047702858 -0.212599678 -0.35884921  0.191926714
Beverages           -0.026187756 -0.030560542 -0.04135860  0.004831876
Soft_drinks          0.232244140  0.555124311 -0.16942648  0.103508492
Alcoholic_drinks    -0.463968168  0.113536523 -0.49858320 -0.316290619
Confectionery       -0.029650201  0.005949921 -0.05232164  0.001847469
```

Lets focus on PC1 as it accounts for > 90% of variance

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