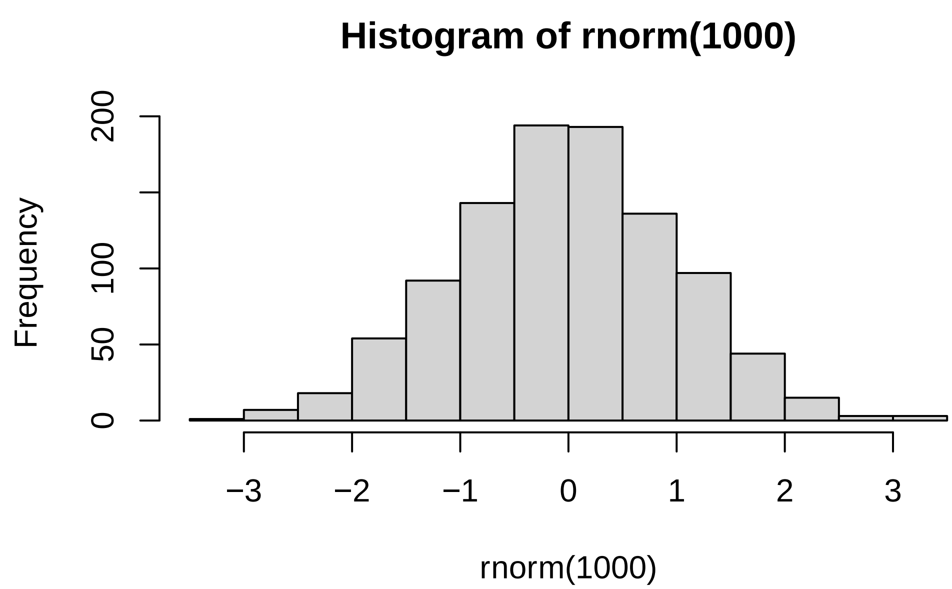
Class 7: Machine Learning 1

Brad Hunter PID:A69038089

Today we will begin our exploration of some "classical" machine learing approaches. We will start with clustering:

First we'll make up some data to cluster with a known answer.

```
hist(rnorm(1000))
```

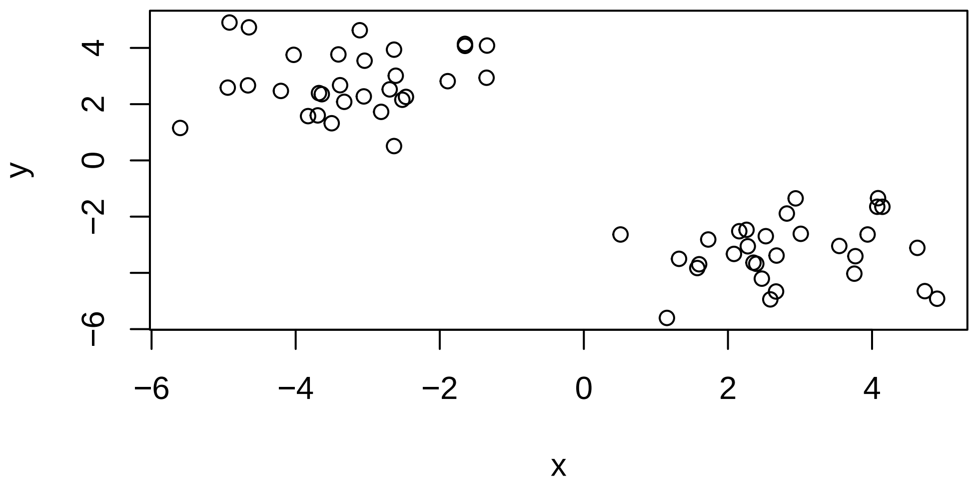



```
x <- c(rnorm(30, mean = -3), rnorm(30, mean = 3))
y <- rev(x)

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

Lets plot our data:

```
plot(z)
```



The main function in “base” R for K-means clustering is called `kmeans()`.

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

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

Cluster means:
          x         y
1 -3.230984  2.822229
2  2.822229 -3.230984

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] 71.42634 71.42634
 (between_SS / total_SS =  88.5 %)
```

```
Available components:

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

Q. How big are the clusters (i.e their size)?

```r
k$size
```

```
[1] 30 30
```

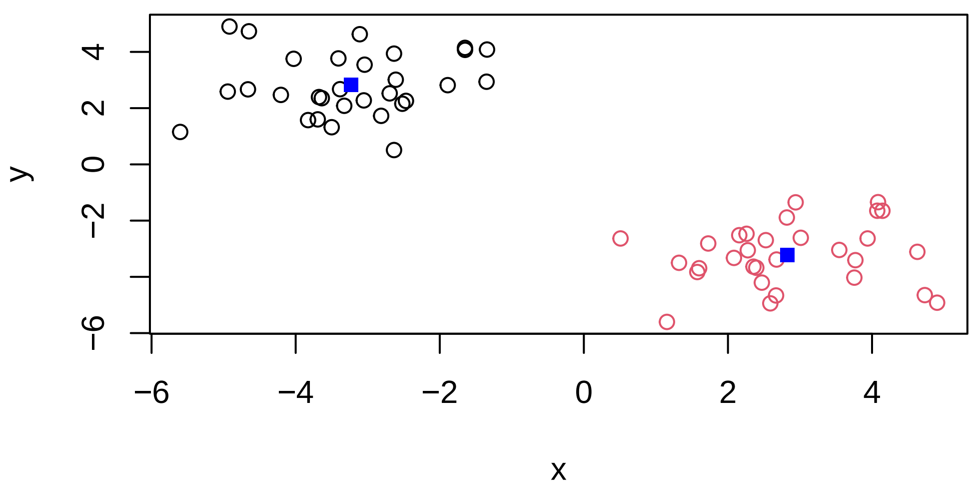
Q. What clusters do my data points reside in?

```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
```

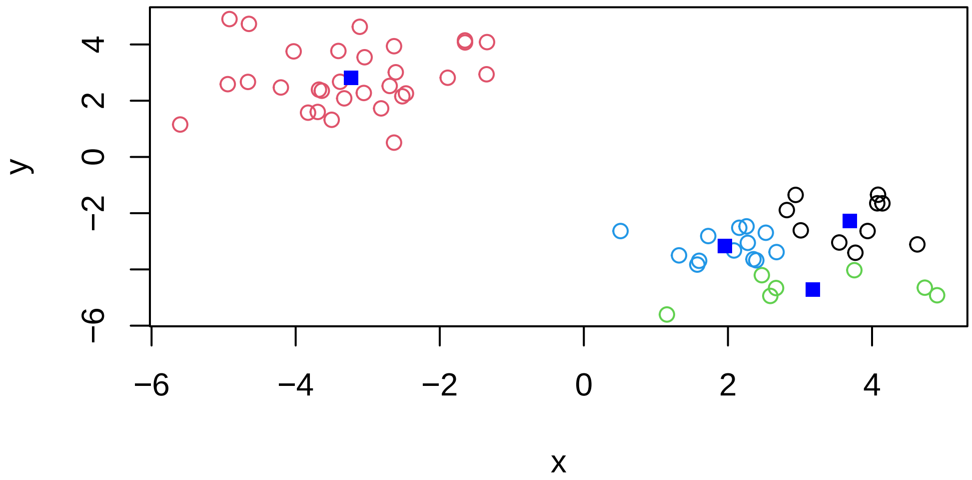
Q. Make a plot of our data colored by cluster assignment - i.e. Make a result figure…

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



Q. Cluster with k-means into 4 clusters and plot your results as above

```
k4 <- kmeans(z, centers=4)
plot(z, col = k4$cluster)
points(k4$centers, col ="blue", pch=15)
```



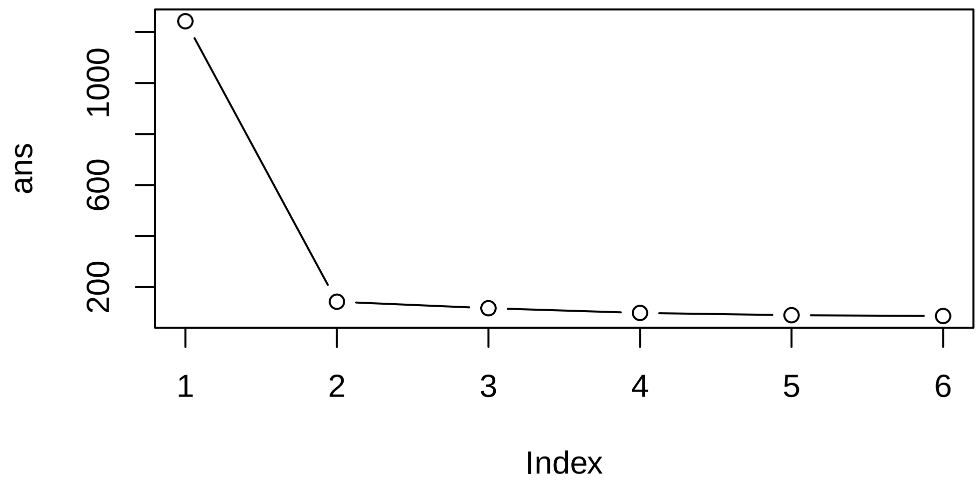
Q. Run kmeans with centers (i.e. values of k) equal 1 to 6, using a for loop

```
ans <- NULL
for(i in 1:6){
  ans <- c(ans, kmeans(z, centers = i)$tot.withinss)
}
ans
```

```
[1] 1242.09413  142.85268  117.46022   98.89684   90.03766   86.73170
```

Plot this "scree-plot"

```
plot(ans, typ="b")
```



Hierarchical Clustering

The main function in "base" R for this is called `hclust()`.

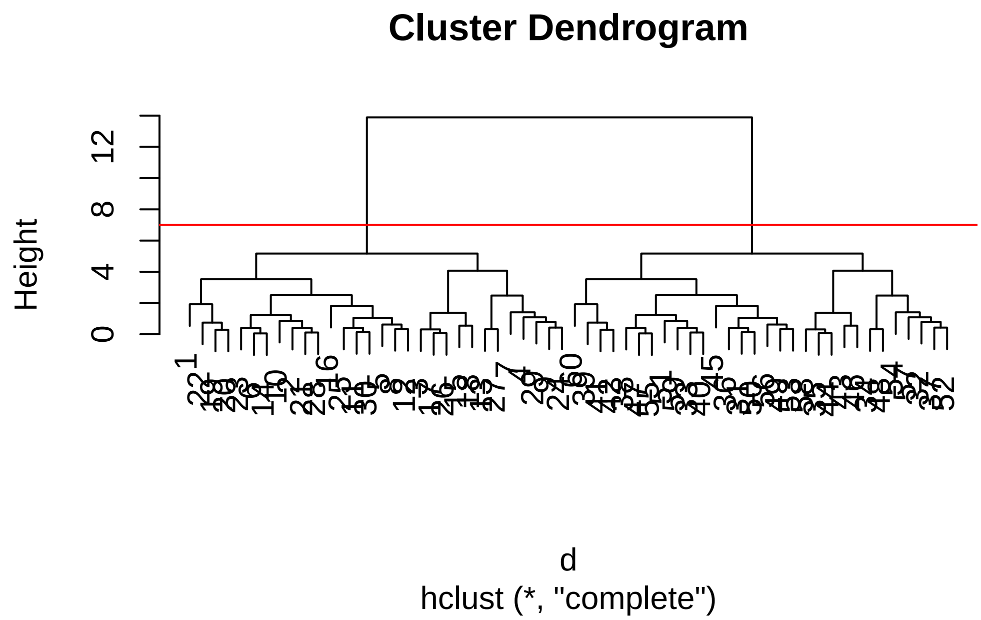
```r
d <- dist(z)
hc <- hclust(d)
hc
```

```

Call:
hclust(d = d)

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

```r
plot(hc)
abline(h=7, col="red")
```



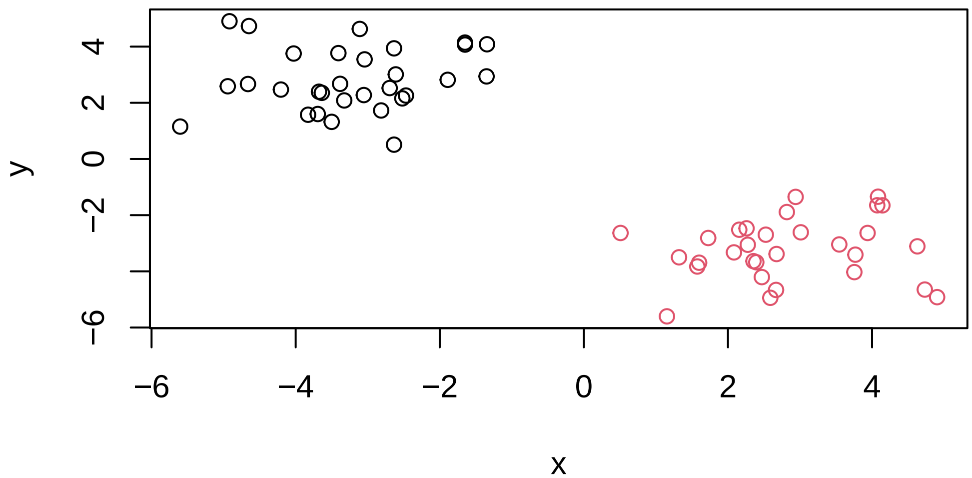
To obtain clusters from our `hclust` object **hc** we "cut" the tree to yield different sub branches. For this we use the `cutree()` function.

```
grps <- cutree(hc, h=7)
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 2 2 2 2 2 2 2 2 2 2
```

Results Figure

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



PCA's!!!!! (Principal Component Analysis)

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

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

```
dim(data)
```

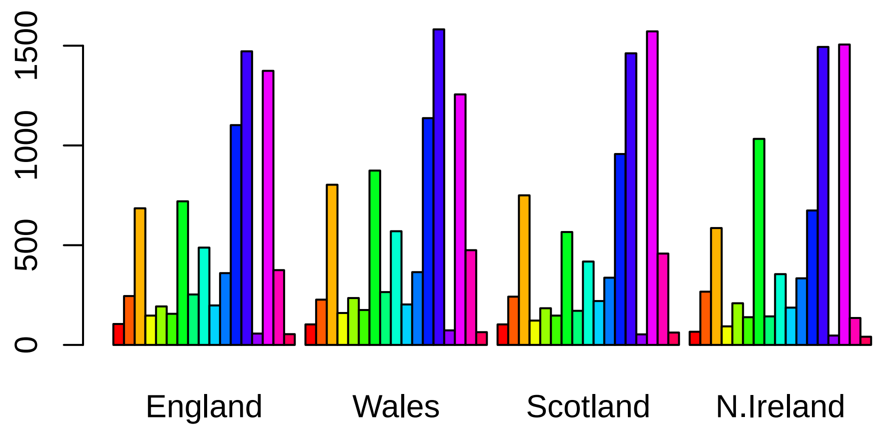
```
[1] 17  4
```

> 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?

I prefer the second method (read.csv(url, row.names=1)) so that my row names are not lost with no danger to losing data (like calling x <- x[,-1] multiple times)

Spotting major differences and trends

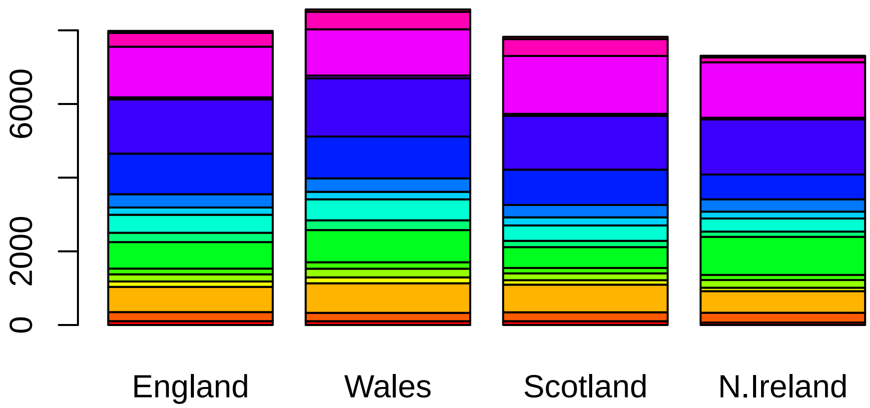
```
barplot(as.matrix(data), beside=T, col=rainbow(nrow(data)))
```



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

Changing the besides arugment to false will result in the following plot

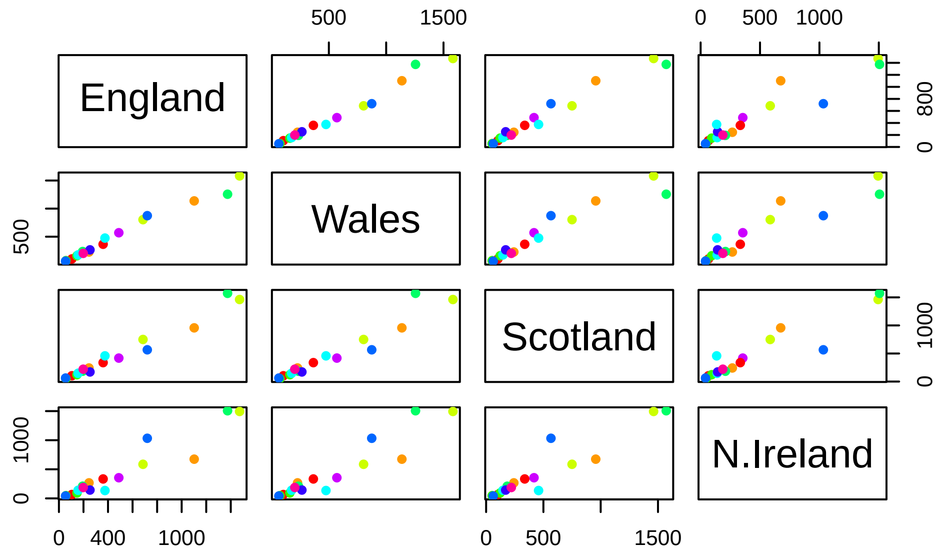
```
barplot(as.matrix(data), beside=F, col=rainbow(nrow(data)))
```



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?

If a given point lies on the diagonal, it is the same (or very similar) for both datasets (countries) being compared.

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



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

It's hard to tell, it seems like N. Ireland consumes more dark blue food group. Wales and England look very similar.

PCA to the rescue

The main function in "base" R for PCA is called `prcomp()`.

But first we must transpose our dataset so the foods (dependent var) are in the columns and the countries (independent var) are in the rows using the `t()` function.

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

Our result object is called `pca` and it has a `$x` componenent that we will look at first

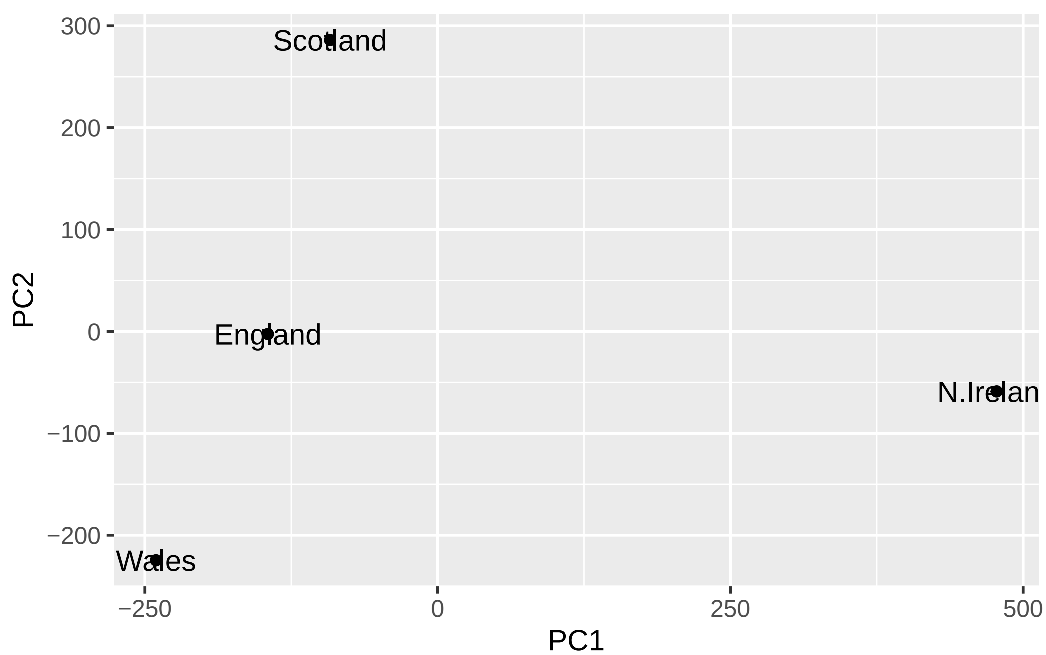
```
pca$x
```

```
               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
```

Making a ordination plot

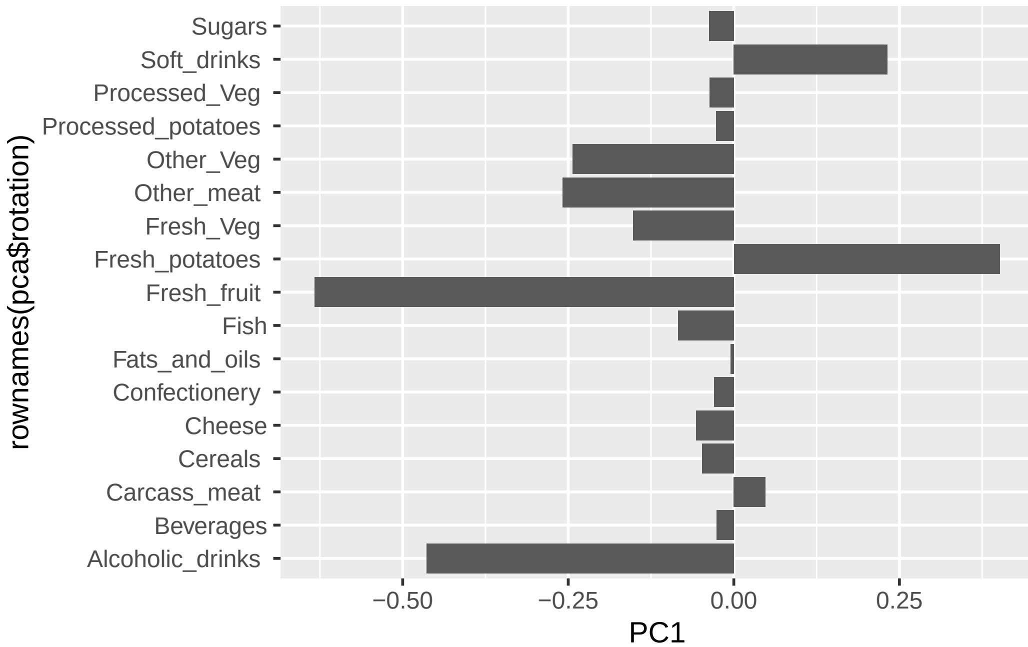
```
library(ggplot2)

ggplot(pca$x,aes(PC1,PC2, label=rownames(pca$x))) +
  geom_point() +
  geom_text()
```



Another major result out of PCA is the so-called "variable loadings" or `$rotation` that tells us how the origional variables (foods) contribute to PCs (i.e. our new axis).

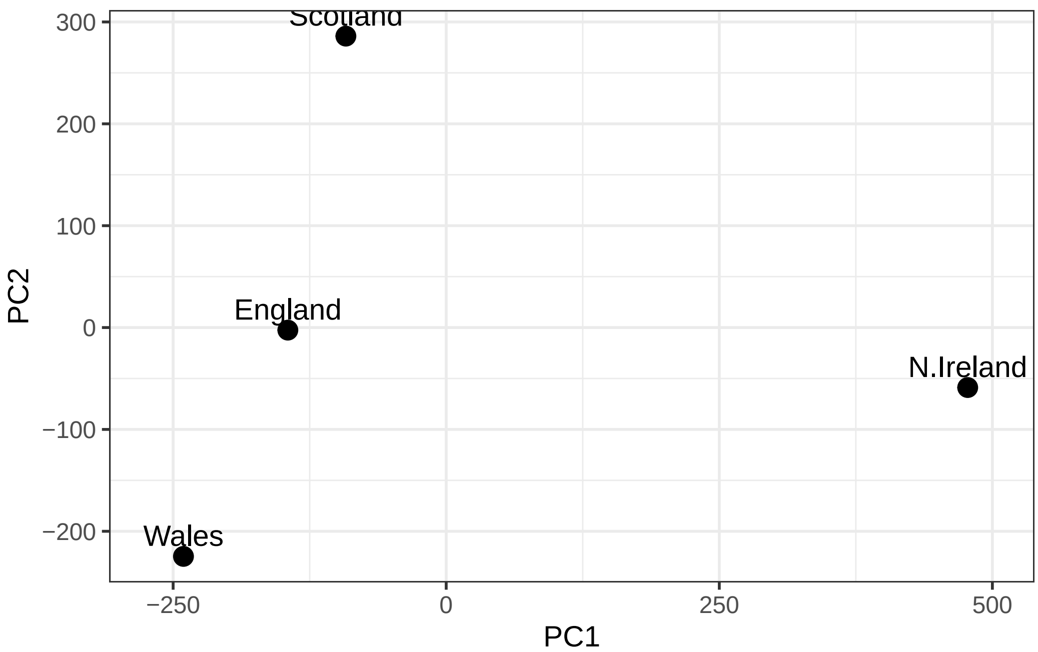
```r
ggplot(pca$rotation) +
  aes(PC1, rownames(pca$rotation)) +
  geom_col()
```



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

```r
# Create a data frame for plotting
df <- as.data.frame(pca$x)
df$Country <- rownames(df)

# Plot PC1 vs PC2 with ggplot
ggplot(pca$x) +
  aes(x = PC1, y = PC2, label = rownames(pca$x)) +
  geom_point(size = 3) +
  geom_text(vjust = -0.5) +
  xlim(-270, 500) +
  xlab("PC1") +
  ylab("PC2") +
  theme_bw()
```



Scotland
England
N.Ireland
Wales
300
200
100
0
−100
−200
PC2
−250
0
250
500
PC1