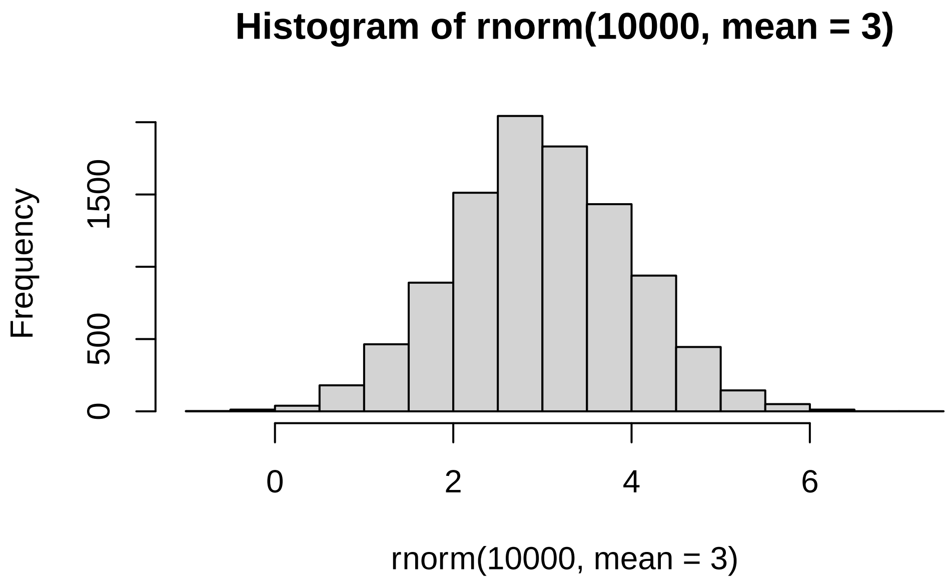
Class07

```r
rnorm(10)
```

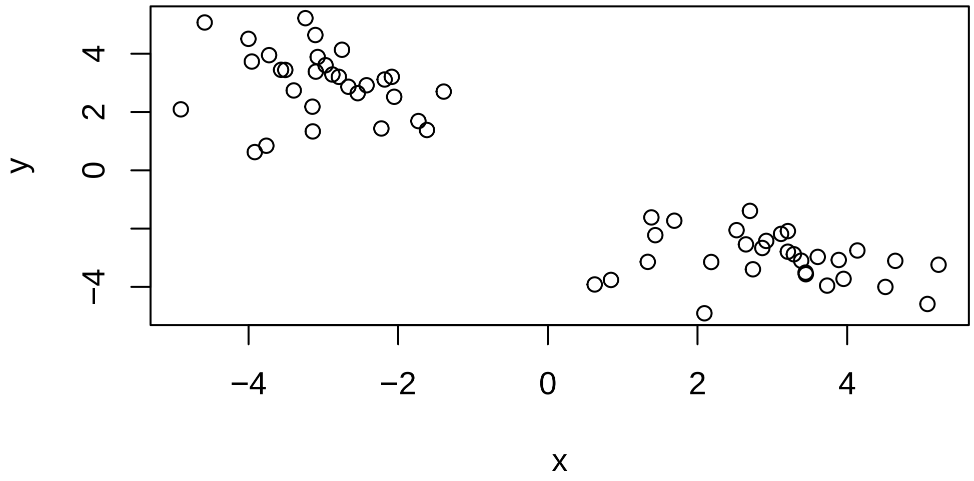
```
 [1] -0.7041508 -0.3406981  1.3403915 -2.0842758  1.7103341  1.0190302
 [7] -1.0318180  0.1484586  1.2454737 -1.3385844
```

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



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

```
plot(x)
```



```
#k<- kmeans(x, centers,iter.max=10L...)
k<-kmeans(x,centers=2,nstart=20)
k
```

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

Cluster means:
          x         y
1  2.994745 -3.014638
2 -3.014638  2.994745

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] 61.44498 61.44498
 (between_SS / total_SS =  89.8 %)
```

```
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
```

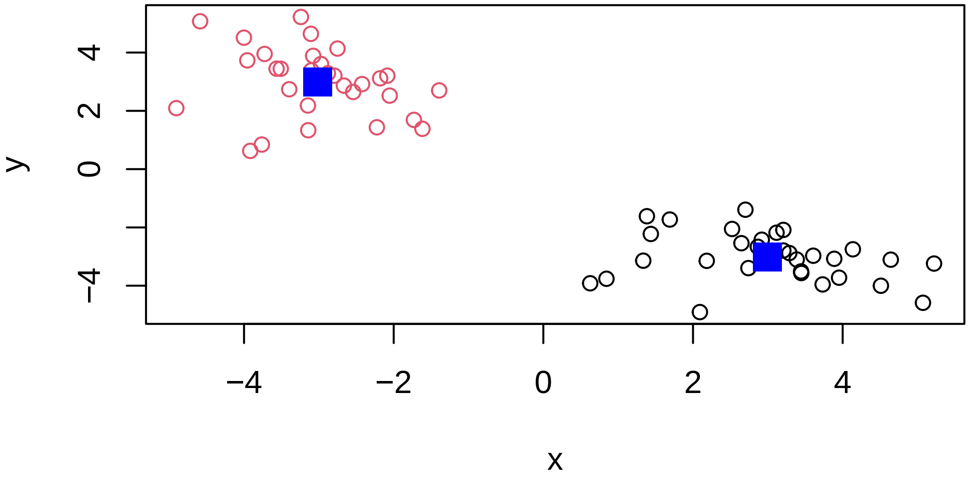
<Q2. The clustering result i.e. membership vector?

```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
```

> Q4. Make a plot of our data colored by clustering results with optionally the cluster centers shown

```r
plot(x,col=k$cluster)
points(k$centers,col="blue",pch=15,cex=2)
```

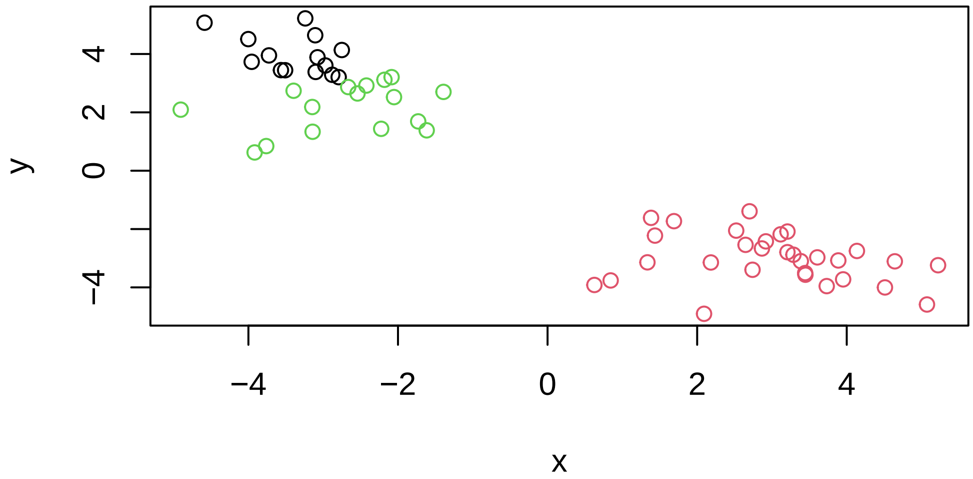


Q5. Run Kmeans again but cluster into 3 groups and plot the results

```
k<-kmeans(x,centers=3,nstart=20)
k$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 3 3 1 3 3 3 3
[39] 3 1 3 1 3 3 1 1 3 3 3 1 1 1 1 3 3 1 3 1 1 1
```

```
plot(x,col=k$cluster)
```

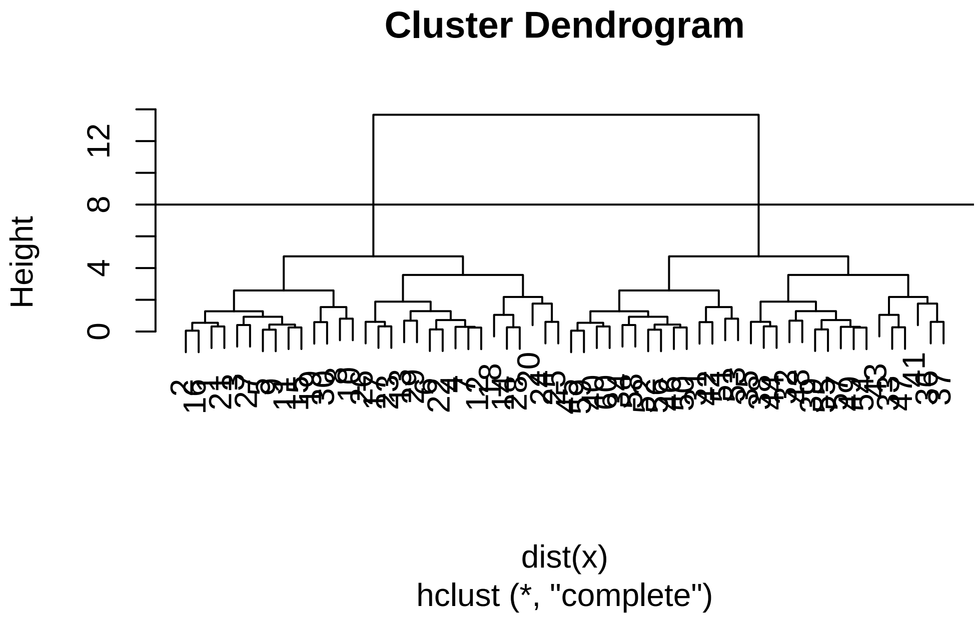


#Hierarchical Clustering

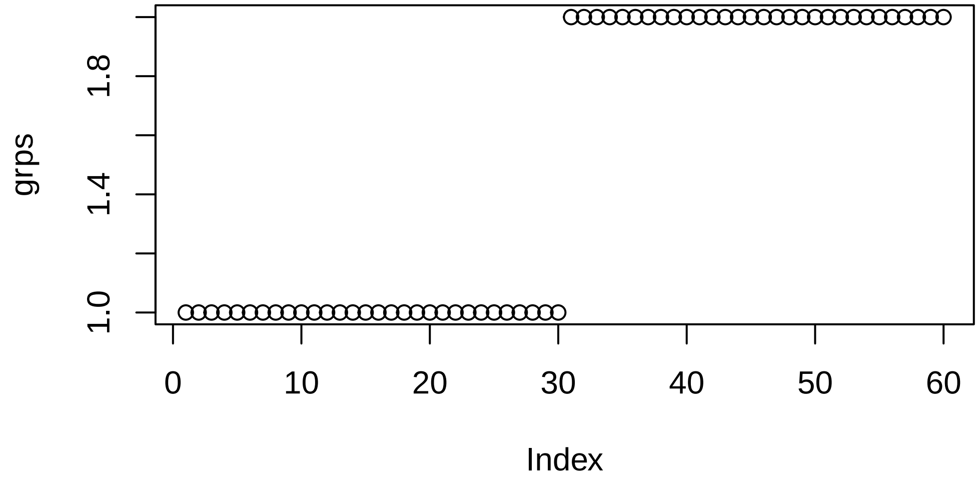
The main function in baseR is 'hclust()'

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

plot(hc)
abline(h=8)
```

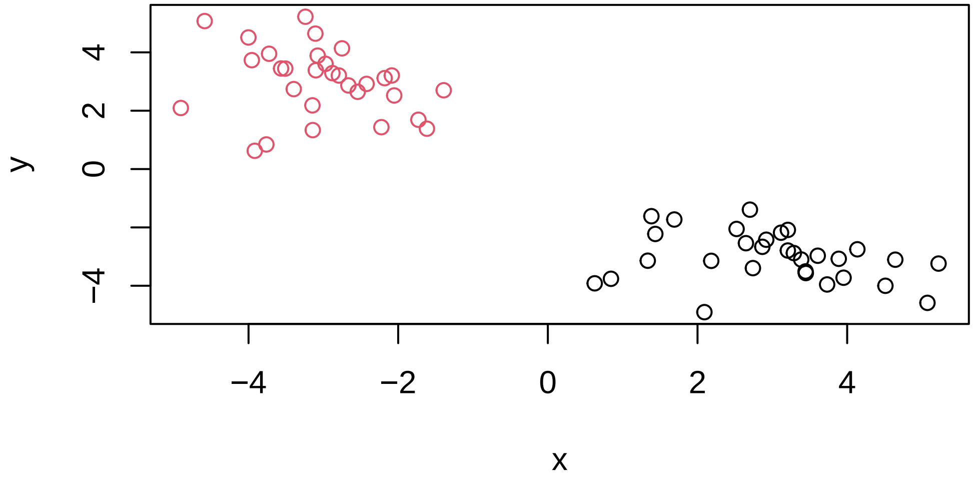


```
grps<-cutree(hc,h=8)
plot(grps)
```



Q. Plot our hclust rsults in terms of our data colored by cluster membership

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



Lab portion

```
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
```

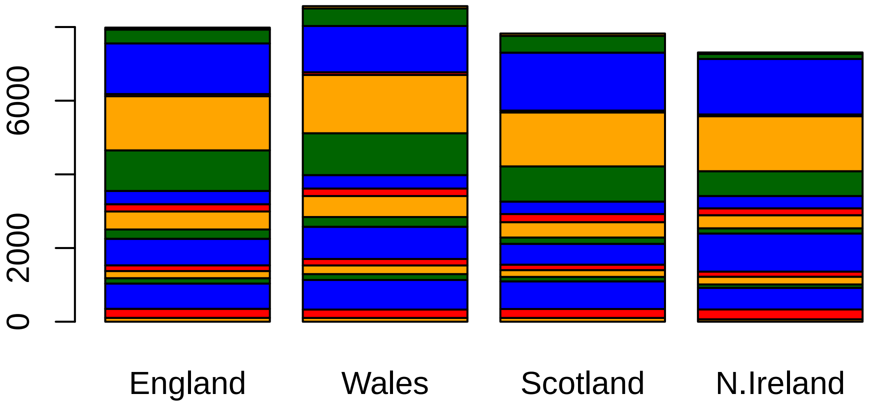
```
dim(x)
```

```
[1] 17  4
```

Q1> 5 columns and 17 rows, but if you do row.names=1, there are 17 rows and 4 columns

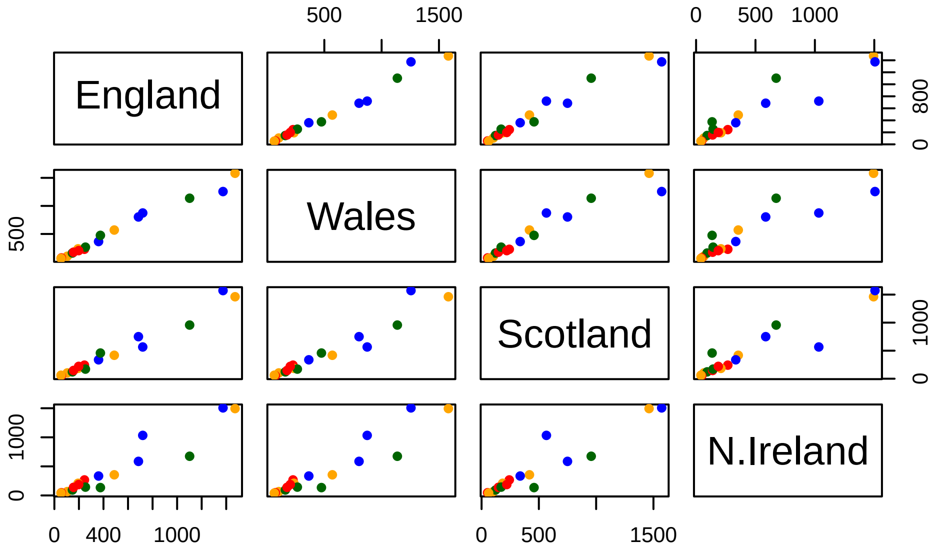
Q2> I prefer to import the df using row.names=1 so I know I am always working with the same df in following lines ‘

```
colors= (c("orange","red","blue","dark green"))
barplot(as.matrix(x), beside=F, col=colors)
```



Q5> horiz! I”f FALSE, the bars are drawn vertically with the first bar to the left. If TRUE, the bars are drawn horizontally with the first at the bottom.”

```
pairs(x, col=colors, pch=16)
```



Q6> There is a stronger outlier in the N. Ireland dataset that may affect the coorelation value

```
t(x) #transpose x
```

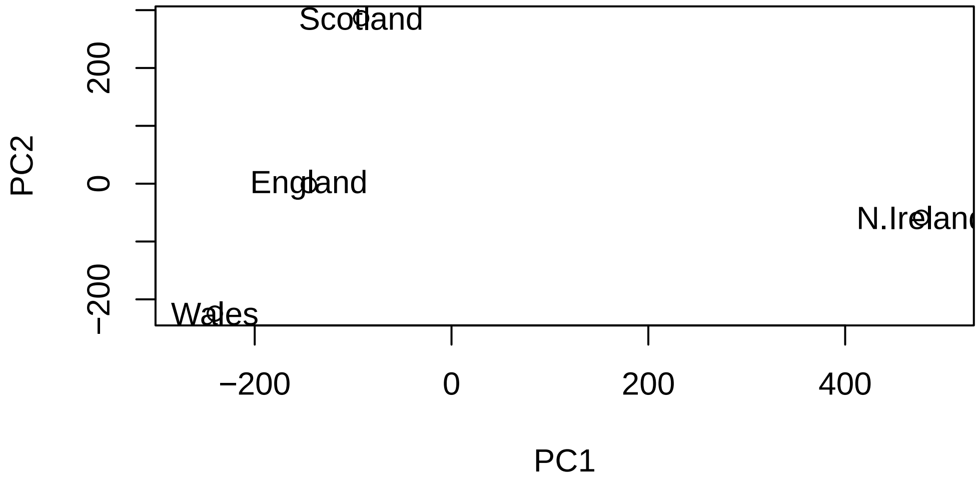
```
          Cheese Carcass_meat  Other_meat  Fish Fats_and_oils  Sugars
England      105         245         685  147         193    156
Wales        103         227         803  160         235    175
Scotland     103         242         750  122         184    147
N.Ireland     66         267   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

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

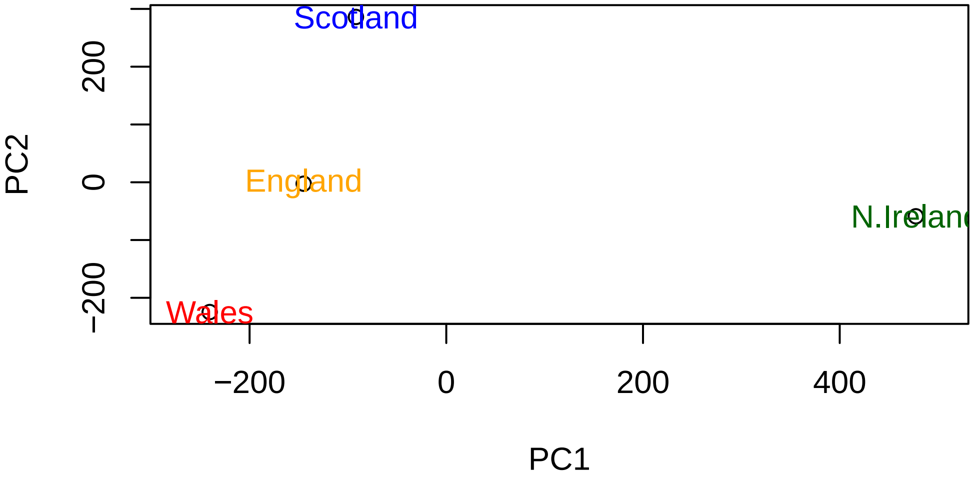
```
Importance of components:
                            PC1      PC2      PC3       PC4
Standard deviation     324.1502 212.7478 73.87622 3.176e-14
Proportion of Variance   0.6744   0.2905  0.03503 0.000e+00
Cumulative Proportion    0.6744   0.9650  1.00000 1.000e+00
```

```
# Plot PC1 vs PC2
plot(pca$x[,1], pca$x[,2], xlab="PC1", ylab="PC2", xlim=c(-270,500))
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 PC1 vs PC2
plot(pca$x[,1], pca$x[,2], xlab="PC1", ylab="PC2", xlim=c(-270,500))
text(pca$x[,1], pca$x[,2], colnames(x),col=colors)
```



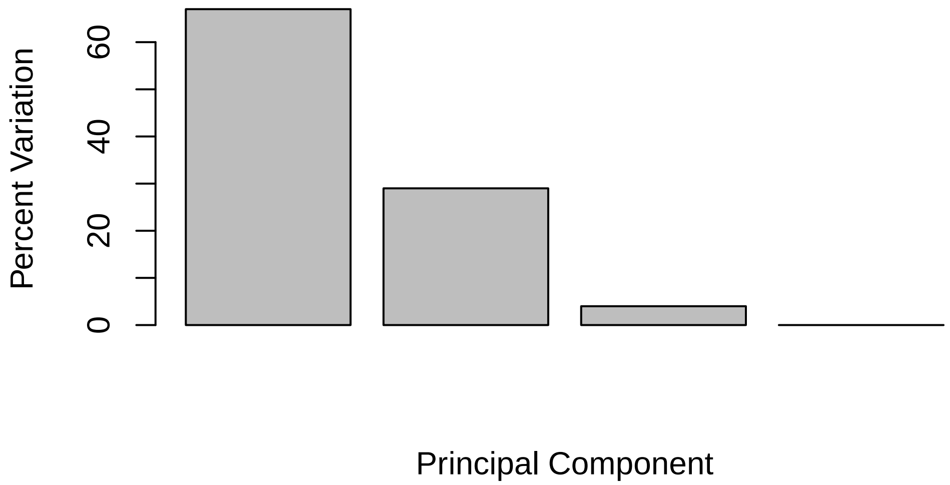
```
#variance from diff PC
v <- round( pca$sdev^2/sum(pca$sdev^2) * 100 )
v
```

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

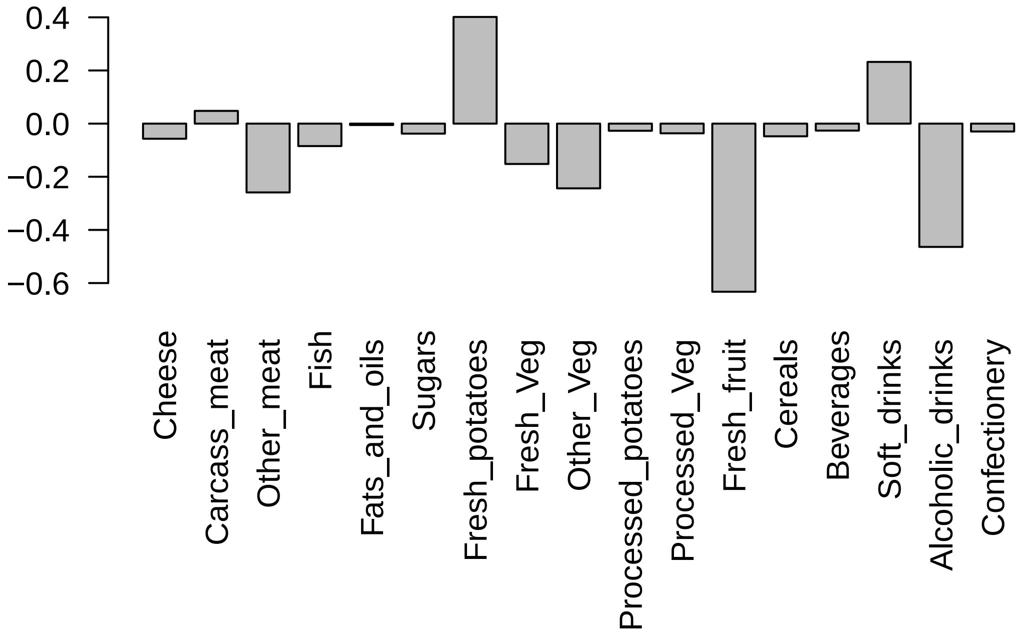
```
## or the second row here...
z <- summary(pca)
z$importance
```

```
                             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
```

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

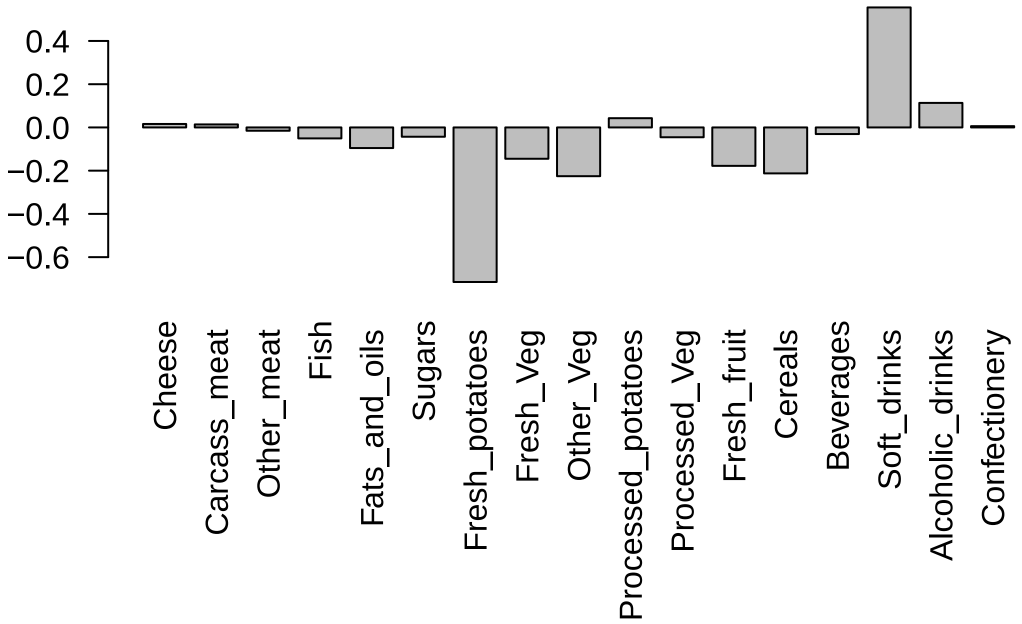


```
## Lets focus on PC1 as it accounts for > 90% of variance
par(mar=c(10, 3, 0.35, 0))
barplot( pca$rotation[,1], las=2 )
```



Q9: Generate a similar 'loadings plot' for PC2. What two food groups feature prominantely and what does PC2 maninly tell us about?

```r
##PC2
par(mar=c(10, 3, 0.35, 0))
barplot( pca$rotation[,2], las=2 )
```



It tells us about Fresh_potatoes and soft_drinks. wales eats more fresh potatoes than the rest and drinks fewer soft drinks.

Q10> How many genes and samples are in this data set?

```r
url2 <- "https://tinyurl.com/expression-CSV"
rna.data <- read.csv(url2, row.names=1)
head(rna.data)
```

```
       wt1 wt2  wt3  wt4 wt5 ko1 ko2 ko3 ko4 ko5
gene1  439 458  408  429 420  90  88  86  90  93
gene2  219 200  204  210 187 427 423 434 433 426
gene3 1006 989 1030 1017 973 252 237 238 226 210
gene4  783 792  829  856 760 849 856 835 885 894
gene5  181 249  204  244 225 277 305 272 270 279
gene6  460 502  491  491 493 612 594 577 618 638
```

```r
dim(rna.data)
```

```
[1] 100  10
```