

Lab 7

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Q1

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

```
[1] 17 5
```

```
head(x)
```

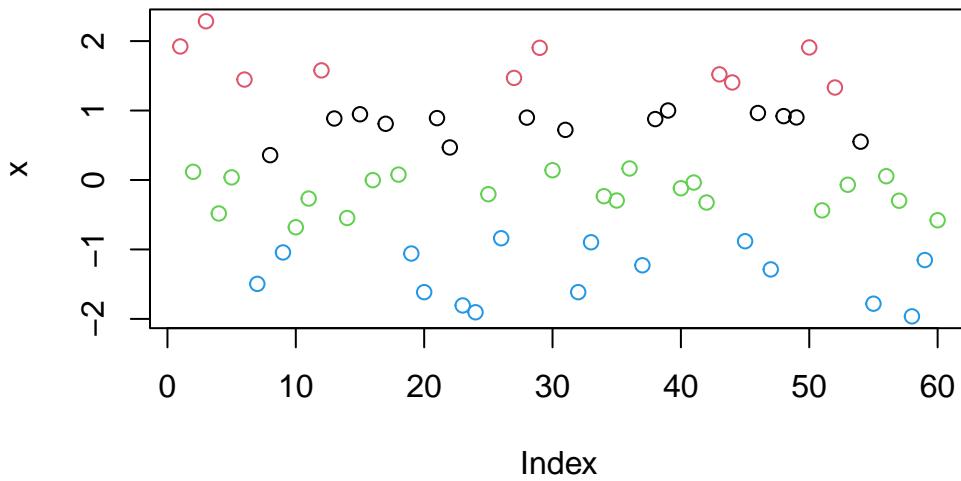
	X	England	Wales	Scotland	N.Ireland
1	Cheese	105	103	103	66
2	Carcass_meat	245	227	242	267
3	Other_meat	685	803	750	586
4	Fish	147	160	122	93
5	Fats_and_oils	193	235	184	209
6	Sugars	156	175	147	139

K means clustering

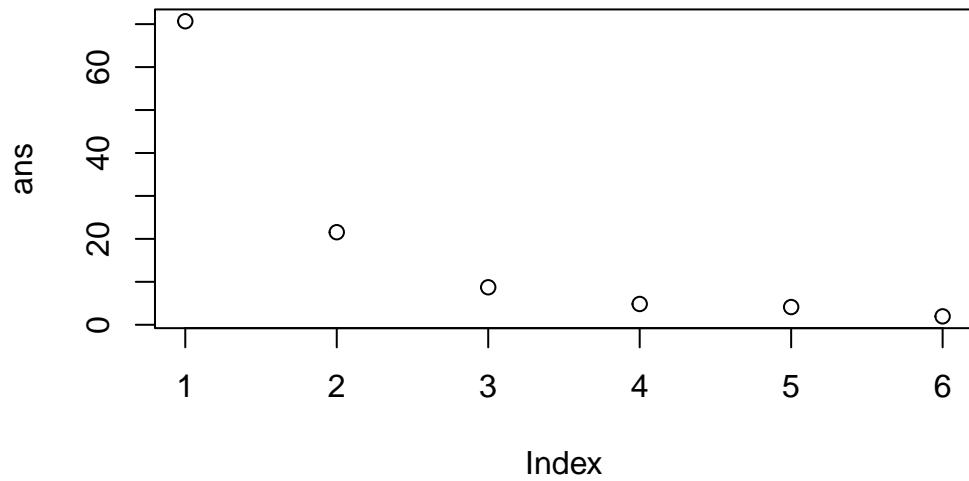
```
x<-(rnorm(60))
```

```
k<- kmeans(x, 4)
```

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



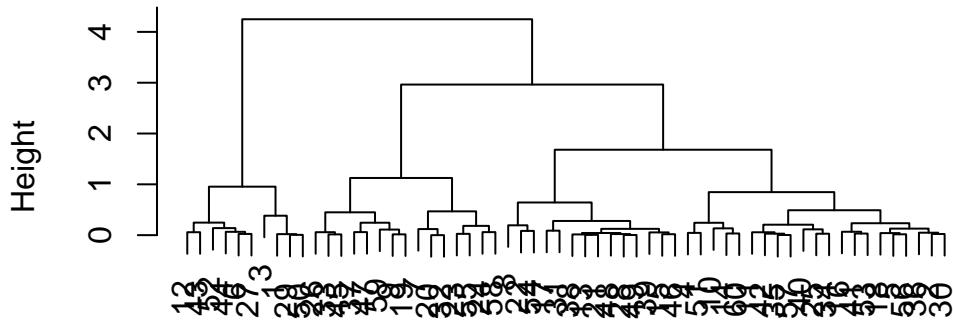
```
ans <- NULL
for (i in 1:6){
  ans <- c(ans, kmeans(x, centers=i)$tot.withinss)
}
plot(ans)
```



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

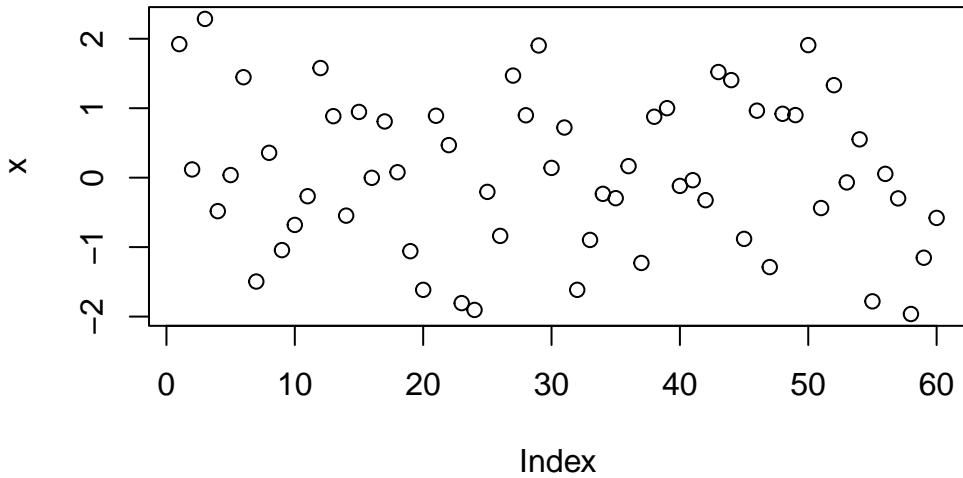
plot(hc)
```

Cluster Dendrogram



d
hclust (*, "complete")

```
grps <- cutree(hc, h=7)  
plot(x, col= grps)
```



PCA

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

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

```
[1] 17 5
```

```
head(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

```
rownames(x) <- x[,1]
x <- x[,-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

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

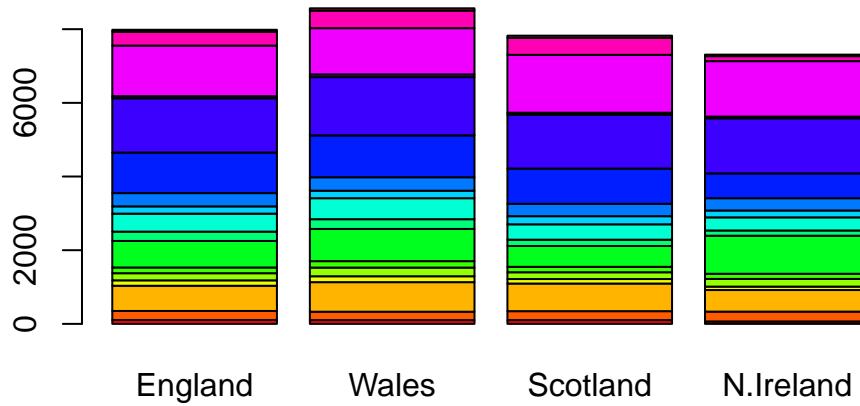
	England	Wales	Scotland	N.Ireland
Cheese	105	103	103	66
Carcass_meat	245	227	242	267
Other_meat	685	803	750	586
Fish	147	160	122	93
Fats_and_oils	193	235	184	209
Sugars	156	175	147	139

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? I like to read the names as it comes in via the url, since we don’t have to deal with dropping a column after.

```
rainbow(nrow(x))
```

```
[1] "#FF0000" "#FF5A00" "#FFB400" "#FOFF00" "#96FF00" "#3CFF00" "#00FF1E"  
[8] "#00FF78" "#00FFD2" "#00D2FF" "#0078FF" "#001EFF" "#3C00FF" "#9600FF"  
[15] "#F00OFF" "#FF00B4" "#FF005A"
```

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



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

```
library(tidyr)
```

```
Warning: package 'tidyr' was built under R version 4.3.3
```

```
# Convert data to long format for ggplot with `pivot_longer()`  

x_long <- x |>  

  tibble::rownames_to_column("Food") |>  

  pivot_longer(cols = -Food,  

                names_to = "Country",  

                values_to = "Consumption")  
  

dim(x_long)
```

[1] 68 3

Q4: Changing what optional argument in the above ggplot() code results in a stacked barplot figure? Change position = “dodge” to “stack”

```
library(ggplot2)
```

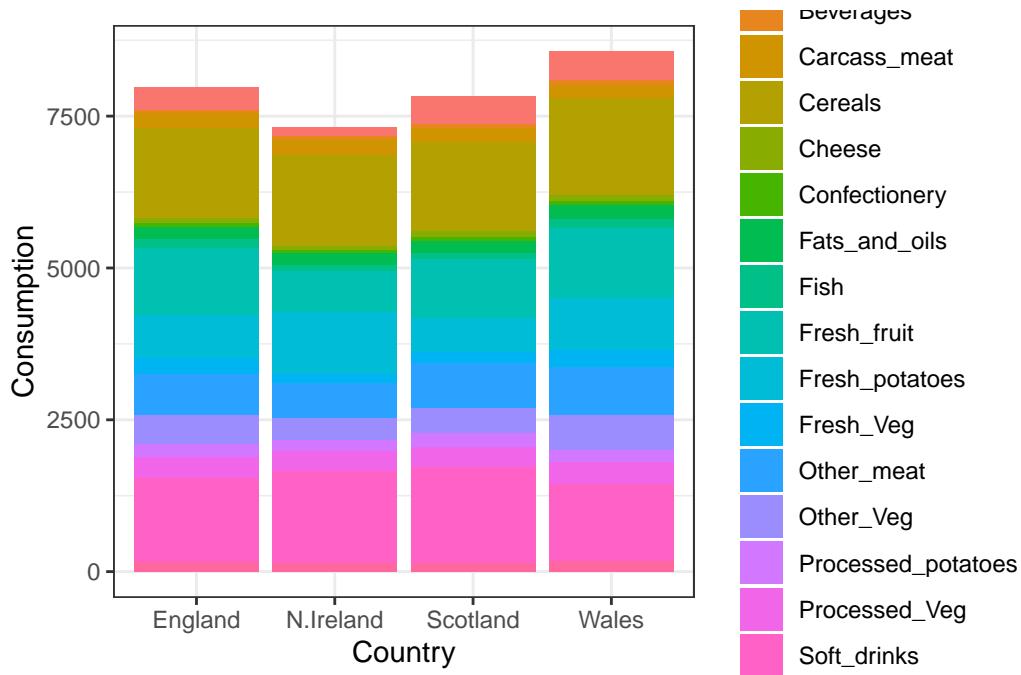
Warning: package 'ggplot2' was built under R version 4.3.3

```
ggplot(x_long) +  

  aes(x = Country, y = Consumption, fill = Food) +  

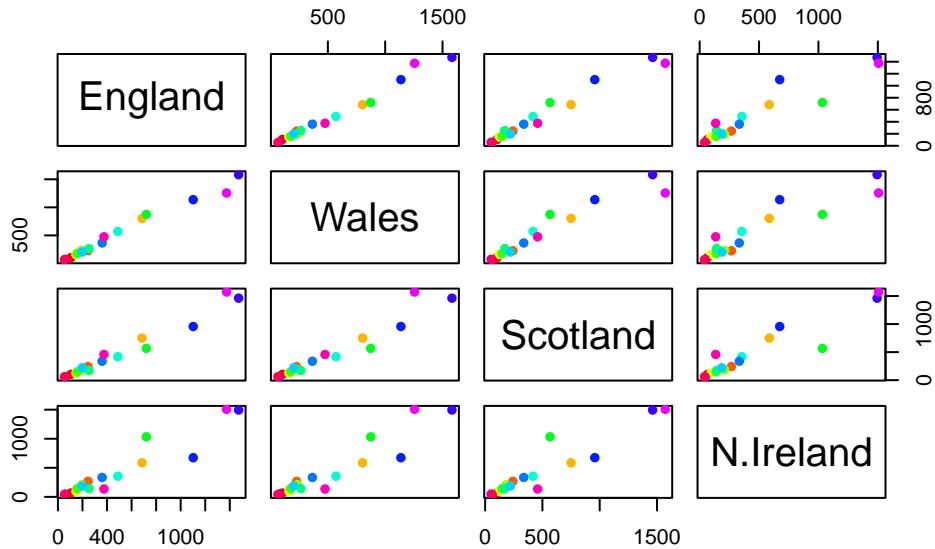
  geom_col(position = "stack") +  

  theme_bw()
```



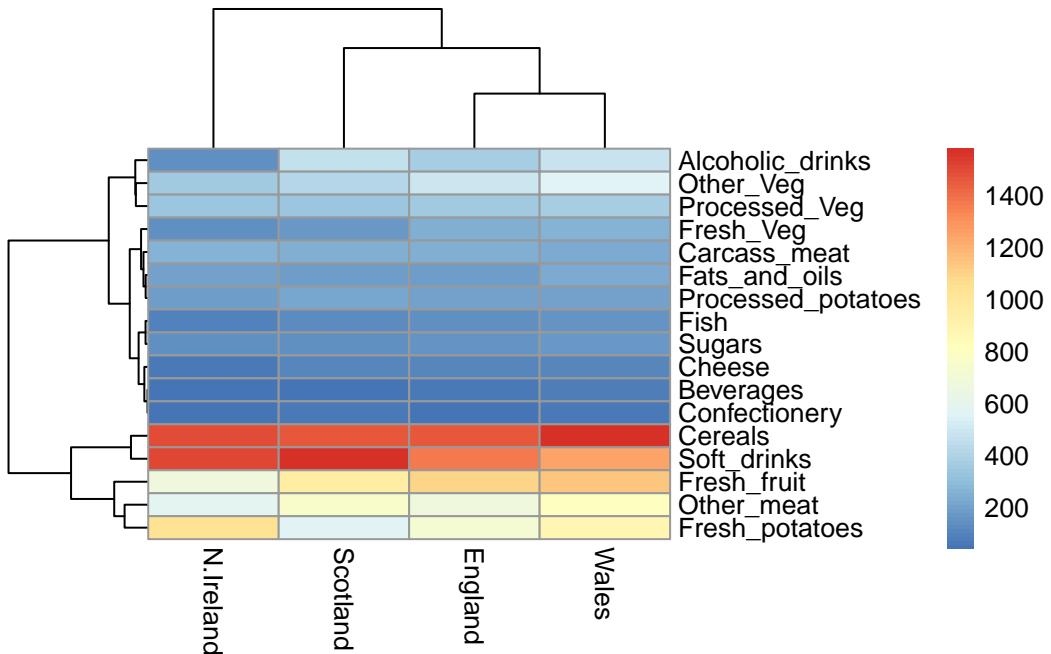
Q5: We can use the pairs() function to generate all pairwise plots for our countries. Can you make sense of the following code and resulting figure? What does it mean if a given point lies on the diagonal for a given plot? It is the correlation of the two countries together. Dots on the diagonal are the same for both countries on the axis.

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



Q6. Based on the pairs and heatmap figures, which countries cluster together and what does this suggest about their food consumption patterns? Can you easily tell what the main differences between N. Ireland and the other countries of the UK in terms of this data-set? No, it's hard to tell

```
library(pheatmap)
pheatmap( as.matrix(x) )
```



PCA Time

$t(x)$

	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

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

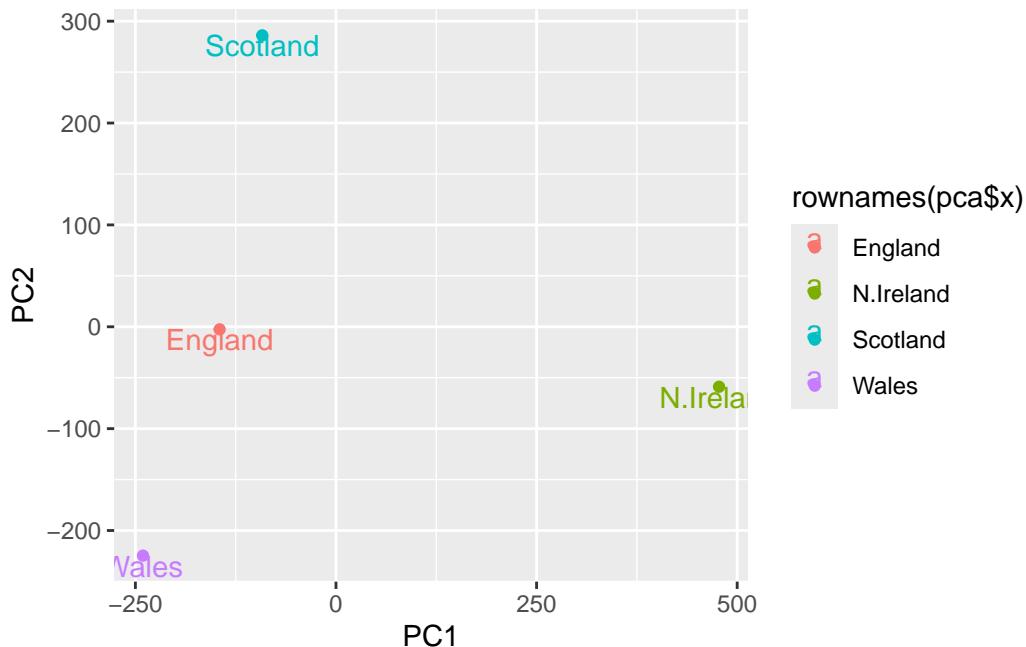
summary(pca)
```

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

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

```
library(ggplot2)
ggplot(pca$x) + aes(PC1, PC2, label=rownames(pca$x), colour = rownames(pca$x)) + geom_point()
  ylab("PC2")
```



```
ggplot(pca$x) + aes(PC1, PC2, label=rownames(pca$x)) + geom_point() + geom_text(vjust=1) + xlab("PC1") + ylab("PC2")
```

