

Class 7

We will import the `UK_foods.csv` dataset

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

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(x)
```

```
[1] 17  5
```

We will want to check that the data has imported correctly

```
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

It seems that the names for the rows was incorrectly counted as a column, let's fix that

```
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

Or alternatively:

```
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
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Fats_and_oils	193	235	184	209
Sugars	156	175	147	139

We see that the problem seems to have been resolved, let's check with `dim()`

```
dim(x)
```

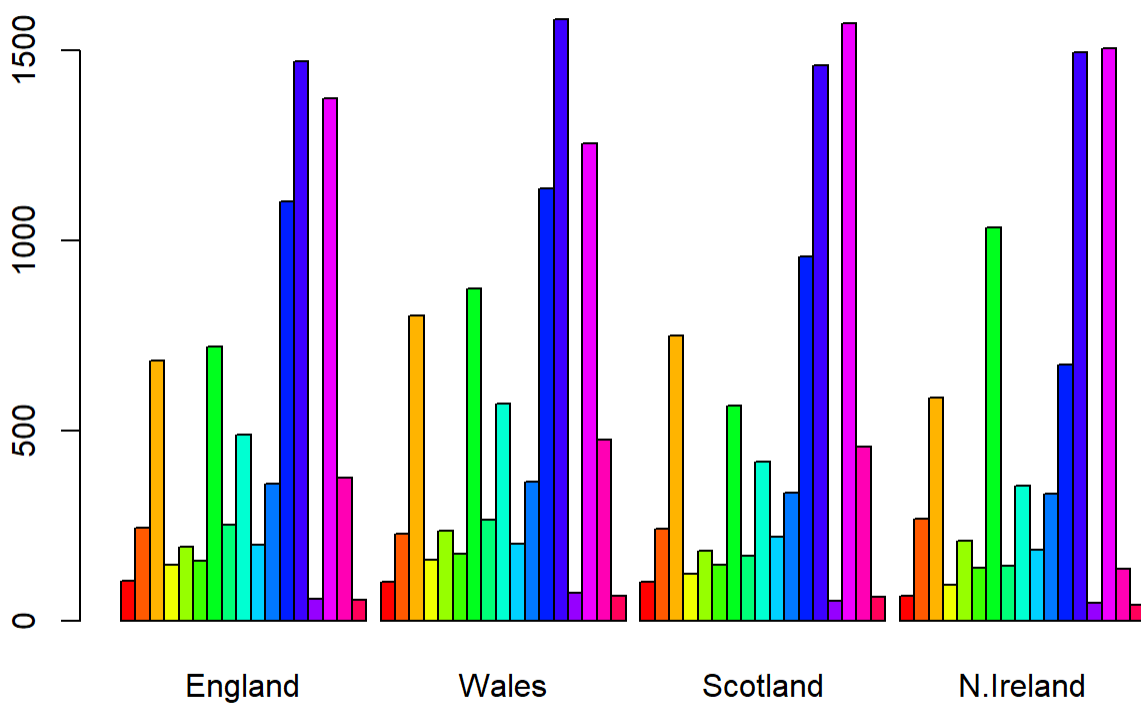
```
[1] 17 4
```

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?

The second approach is better because it applies the change to the entire dataset without having to redefine x, which may become a problem if there are other aspects of the imported dataset that you would like to change

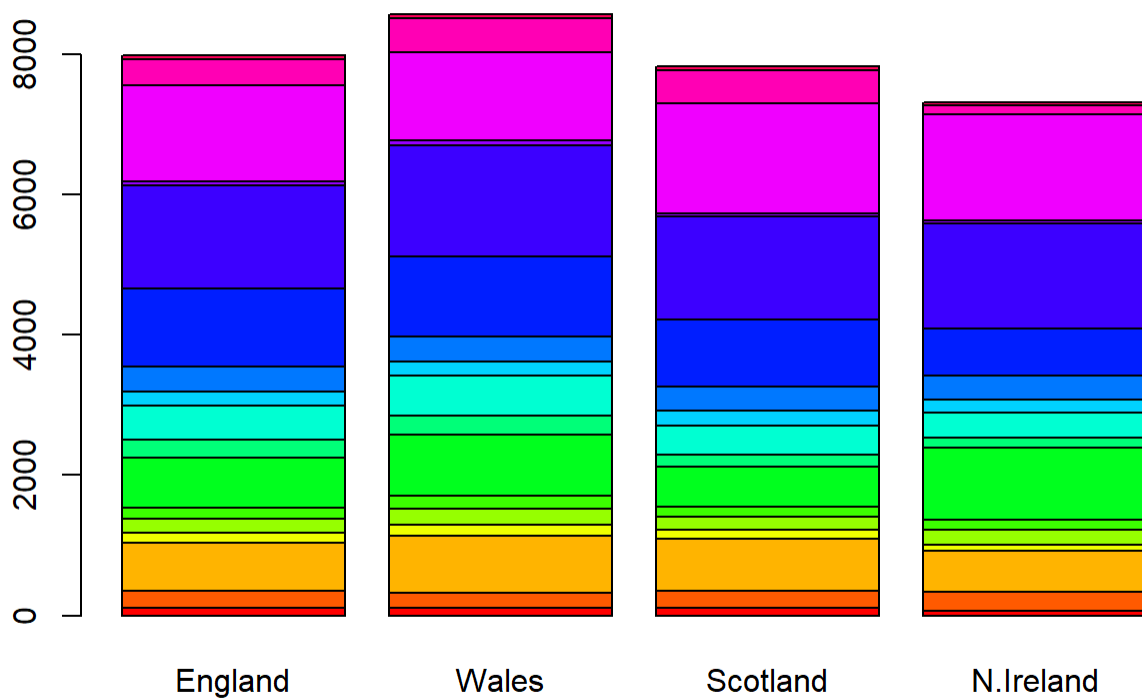
As a table this data does not show us much. Let's graph it:

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



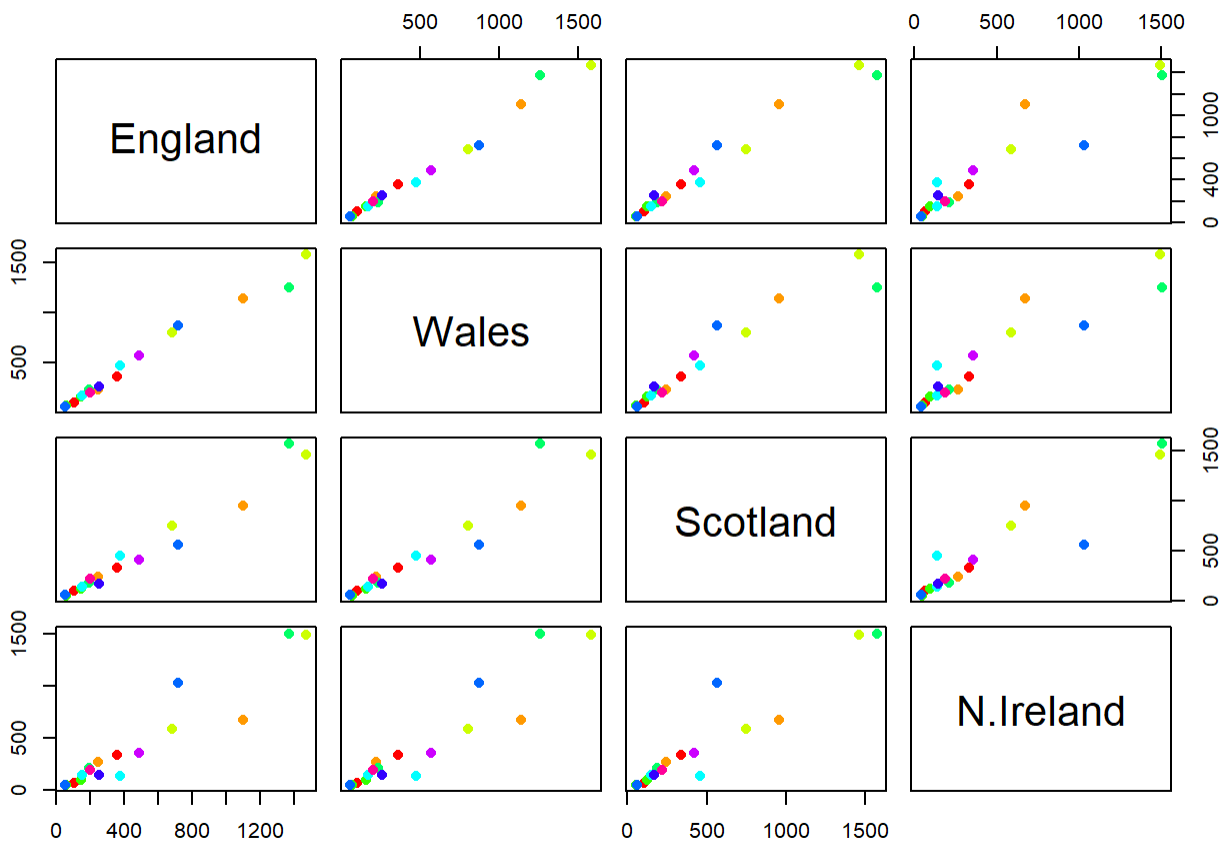
Q3: Changing what optional argument in the above `barplot()` function results in a stacked barplot?

```
#the beside portion is shown as true, needs to be false to stack the bars
barplot(as.matrix(x), beside=F, 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(x, col=rainbow(10), pch=16)
```



The pairs shows graphs of each combination of observations plotted against each other: i.e England against itself, England vs Wales, etc. The closer the dots to the diagonal line the more similarities there are, the further the more differences

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

The first cluster of dots deviate from the diagonal line slightly more than the other plots, it is hard to really say what this means, or even see the differences clearly in the first place b/c we are forced to visually compare with 9 other graphs

First, the data needs to be transposed to work with PCA

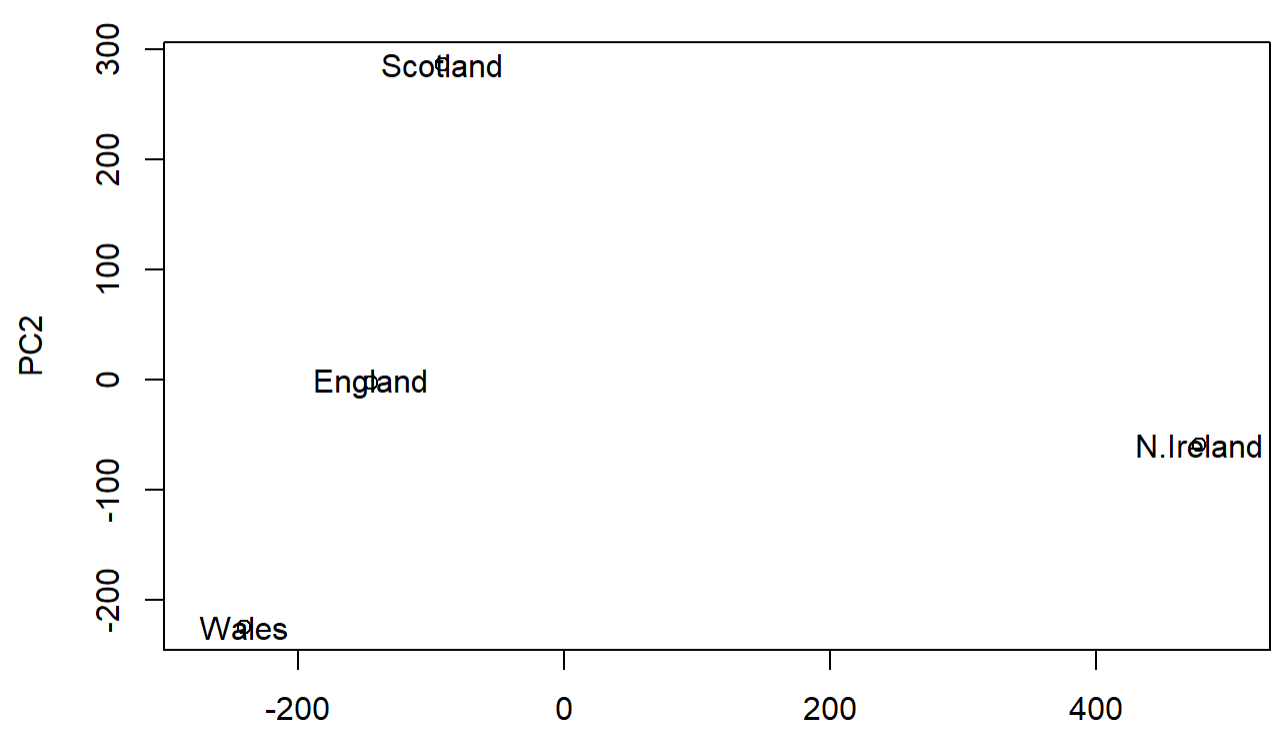
```
pca <- prcomp( t(x) )
summary(pca)
```

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.

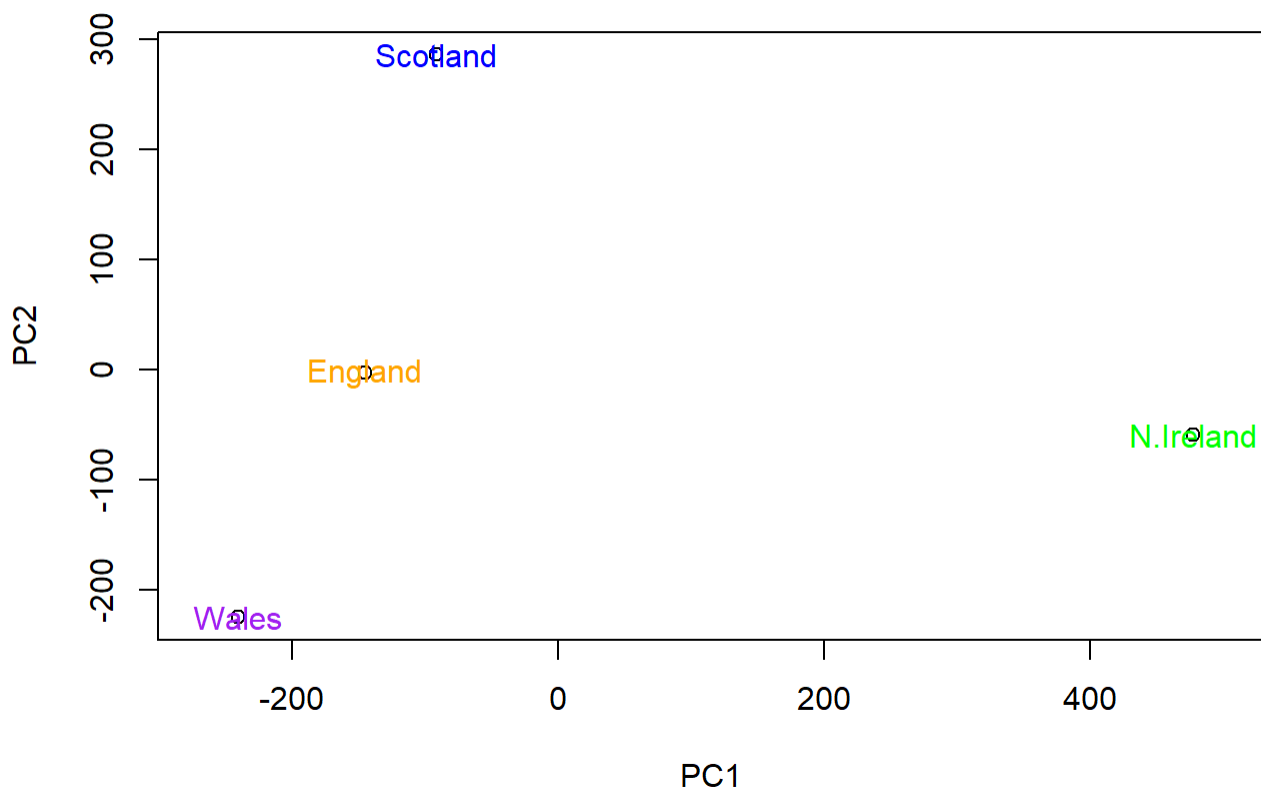
```
plot(pca$x[,1], pca$x[,2], xlab="PC1", ylab="PC2", xlim=c(-270,500))
text(pca$x[,1], pca$x[,2], colnames(x))
```



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.

```
my_colors <- c("orange", "purple", "blue", "green")

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 = my_colors)
```



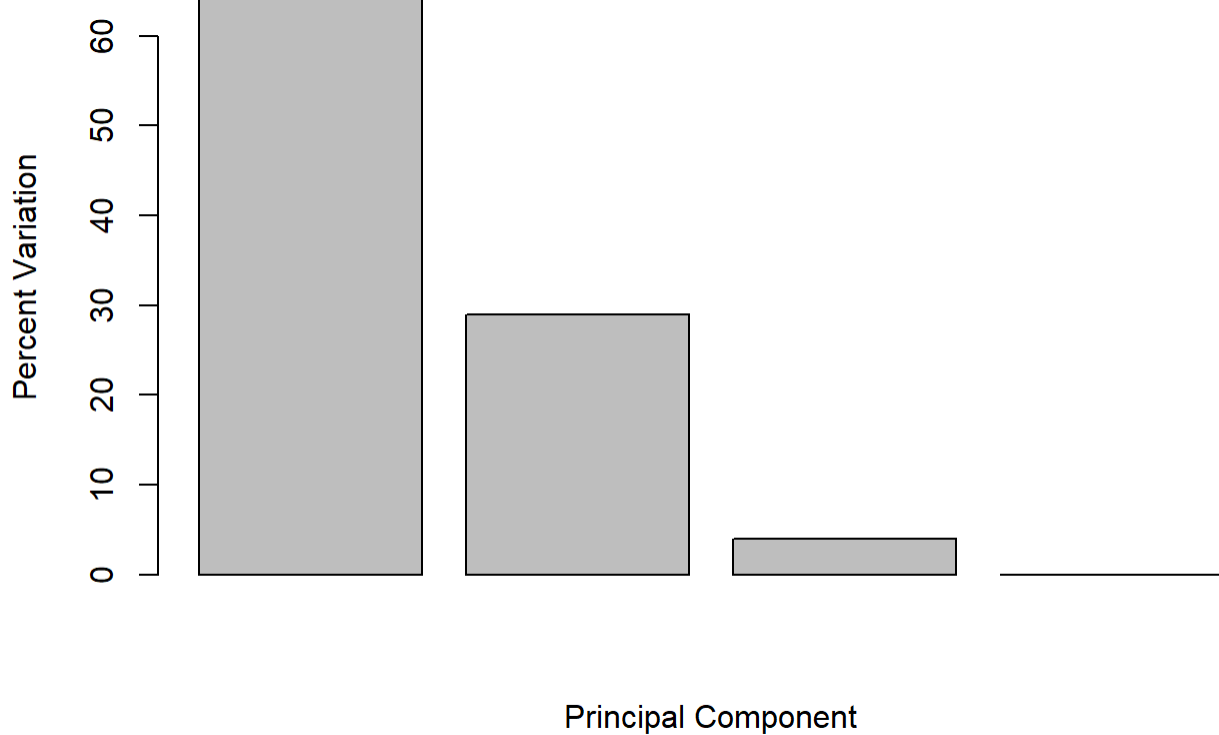
To figure out the variance in the data for each PC we need the standard deviation:

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

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

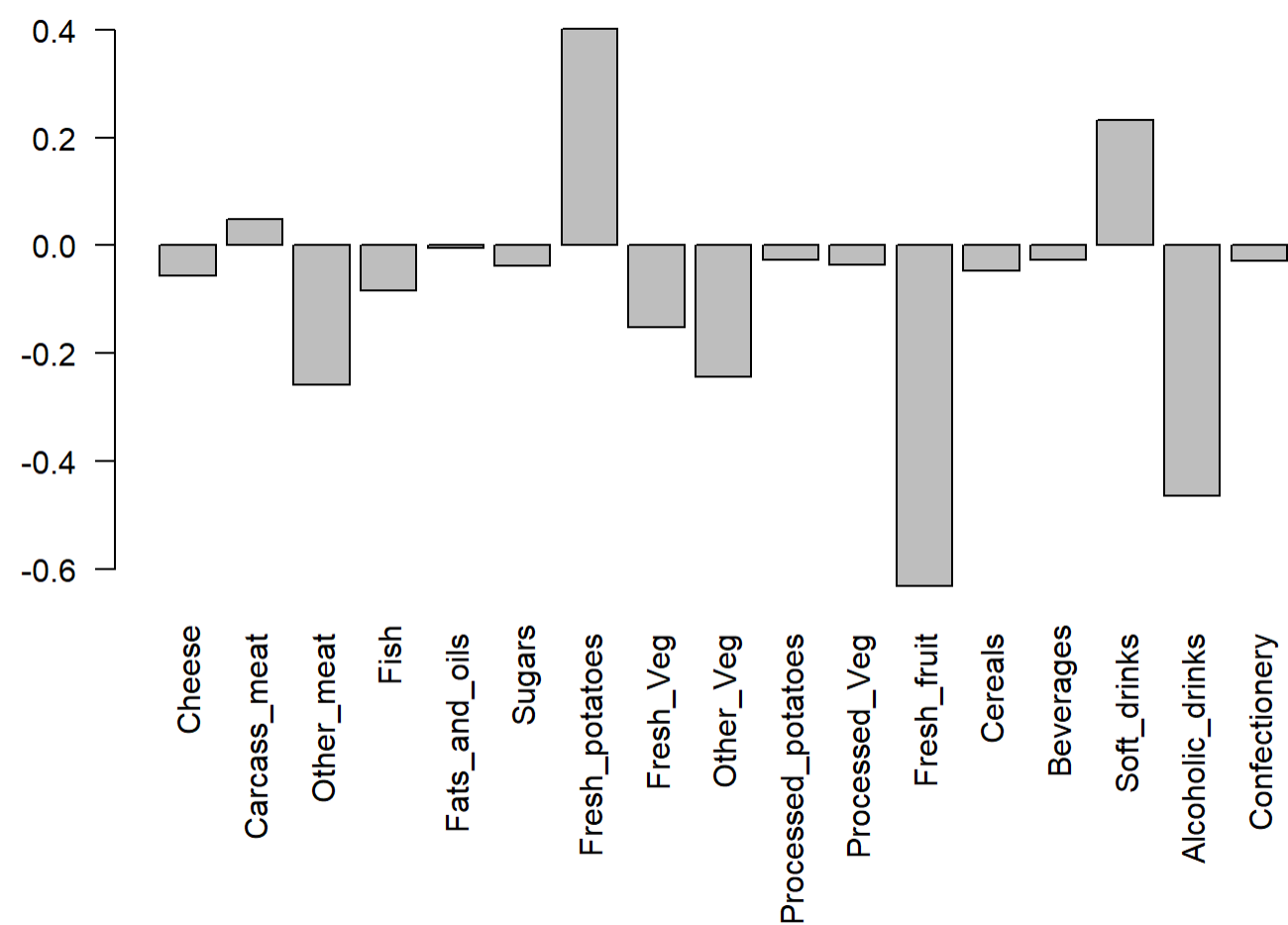
Now to plot the variances

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



To see the influence of each variable on the PCs, aka the loading scores, we use the `$rotation` component:

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

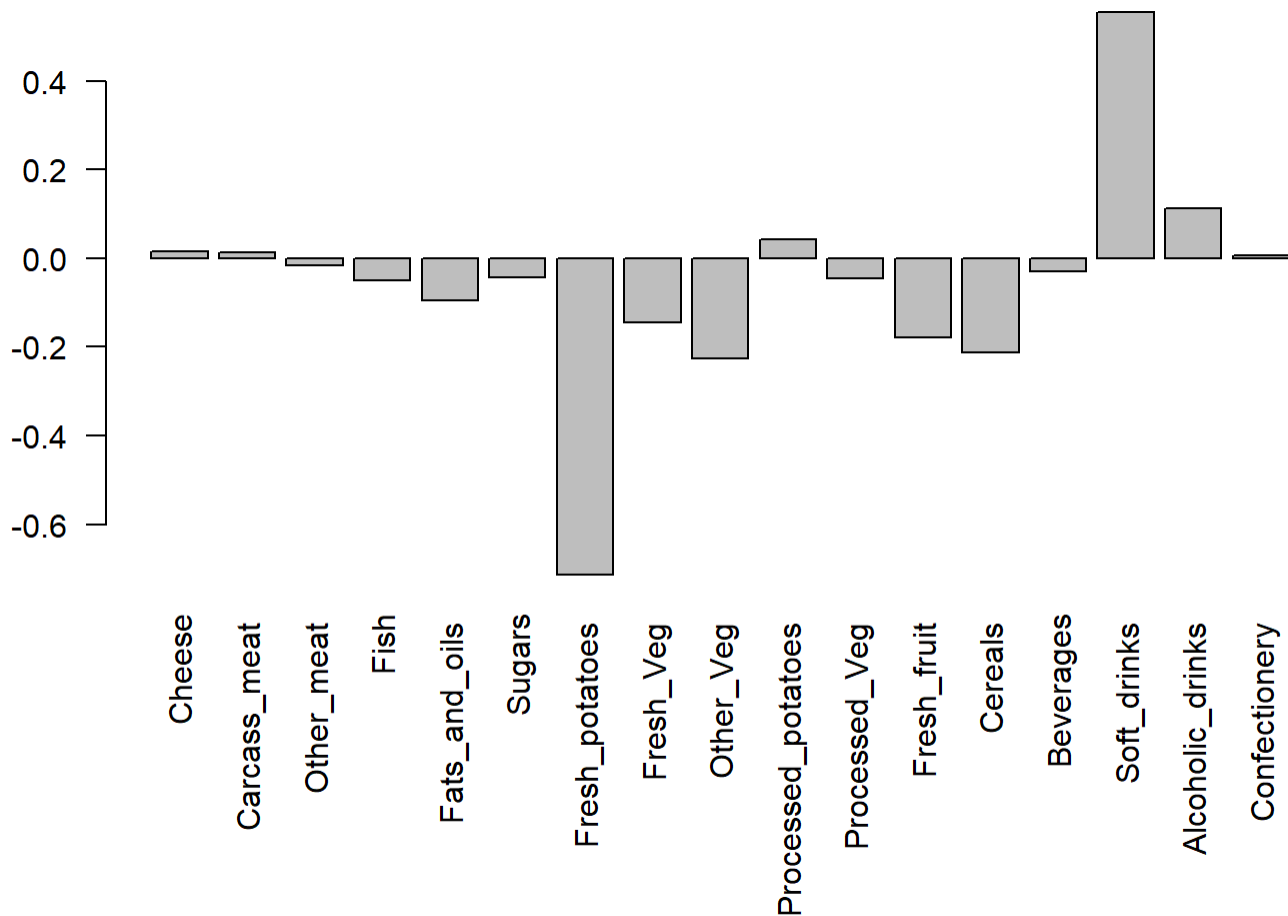


The highest positive values are what cause skewing to the right in the PC1 vs PC2 plot, which is potatoes and soft drinks here. The lowest negative values are what cause skewing to the left in the PC1 vs PC2 plot, which is fresh fruit and alcoholic drinks.

fresh fruit and alcoholic drinks

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

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

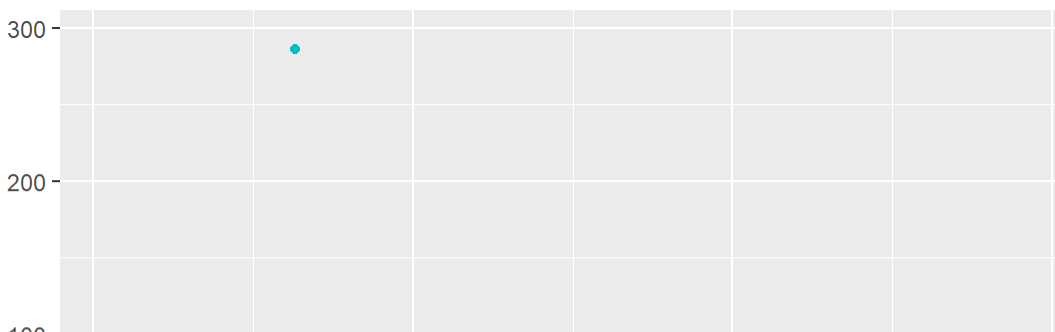


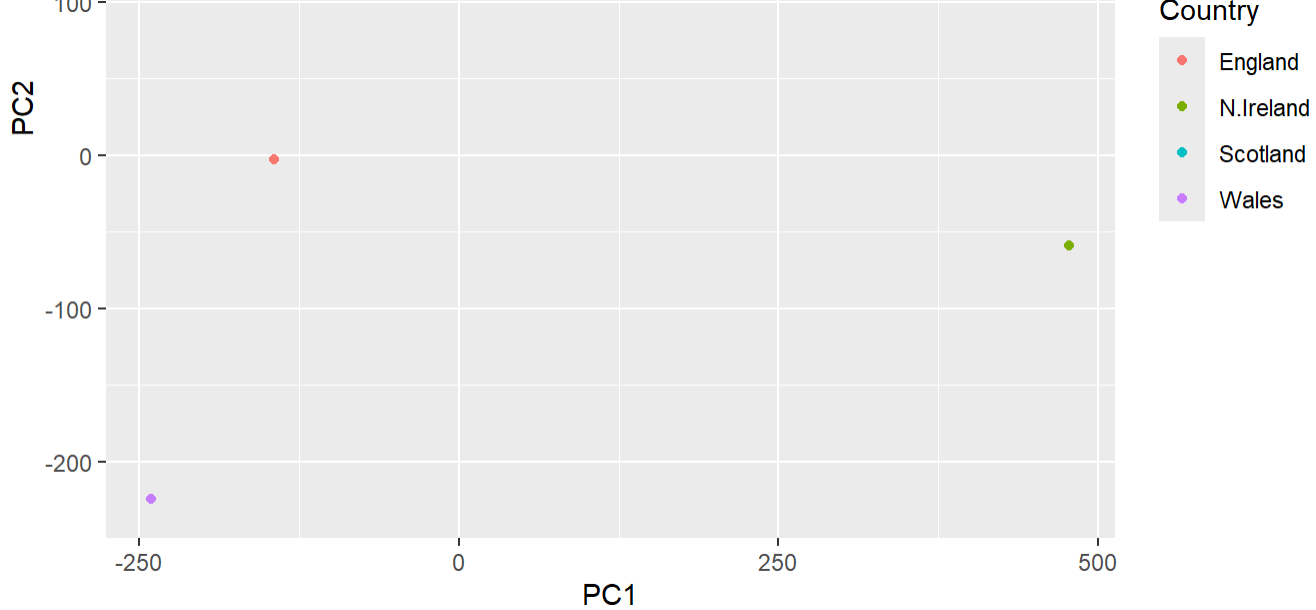
Now we will try to plot the same thing on ggplot2

```
library(ggplot2)

df <- as.data.frame(pca$x)
df_lab <- tibble::rownames_to_column(df, "Country")

ggplot(df_lab) +
  aes(PC1, PC2, col=Country) +
  geom_point()
```

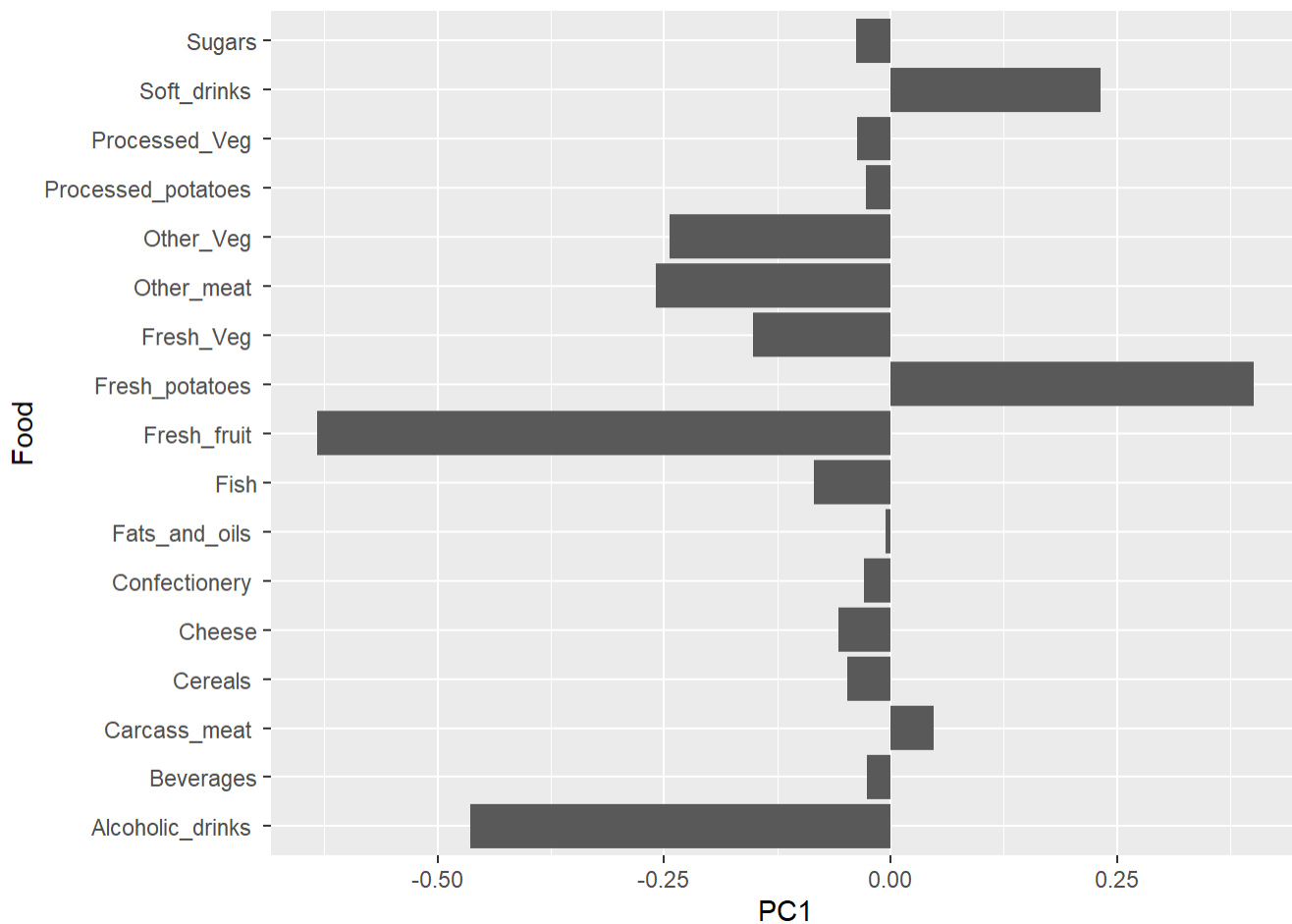




Now to plot the loading plot:

```
ld <- as.data.frame(pca$rotation)
ld_lab <- tibble::rownames_to_column(ld, "Food")

ggplot(ld_lab) +
  aes(PC1, Food) +
  geom_col()
```



Another way to see this information together with the main PCA plot is in a so-called biplot:

```
biplot(pca)
```


	PC8	PC9	PC10
Cumulative Proportion	0.9202	0.9455	0.96045
Standard deviation	0.62065	0.60342	3.457e-15
Proportion of Variance	0.00385	0.00364	0.000e+00
Cumulative Proportion	0.99636	1.00000	1.000e+00

Q How many genes in this dataset?

```
nrow(rna.data)
```

```
[1] 100
```

```
head(pca$x)
```

	PC1	PC2	PC3	PC4	PC5	PC6
wt1	-9.697374	1.5233313	-0.2753567	0.7322391	-0.6749398	1.1823860
wt2	-9.138950	0.3748504	1.0867958	-1.9461655	0.7571209	-0.4369228
wt3	-9.054263	-0.9855163	0.4152966	1.4166028	0.5835918	0.6937236
wt4	-8.731483	-0.7468371	0.5875748	0.2268129	-1.5404775	-1.2723618
wt5	-9.006312	-0.2945307	-1.8498101	-0.4303812	0.8666124	-0.2496025
ko1	8.846999	2.2345475	-0.1462750	-1.1544333	-0.6947862	0.7128021

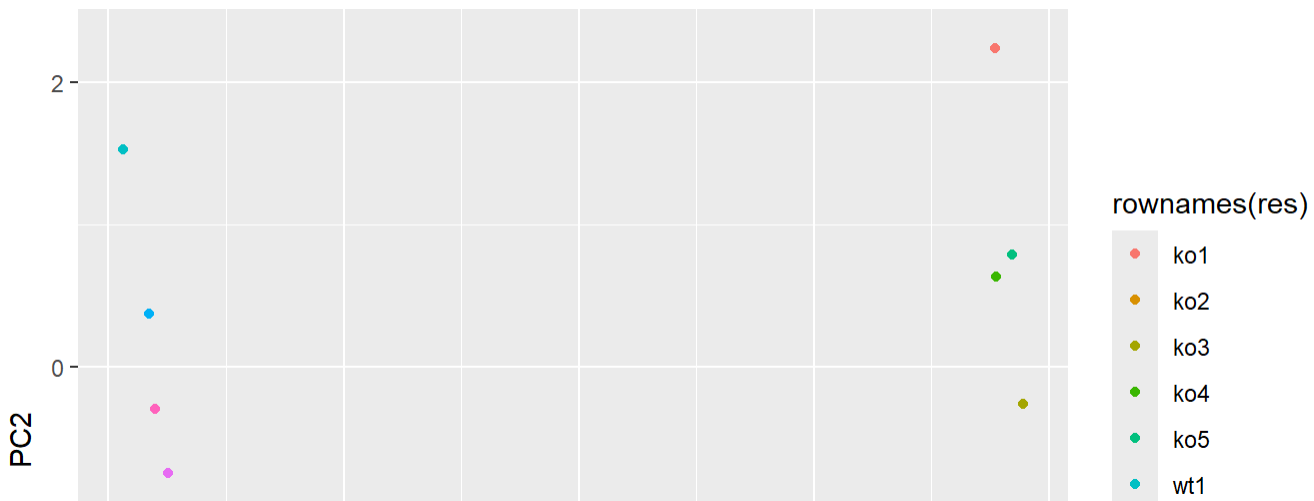
	PC7	PC8	PC9	PC10
wt1	-0.24446614	1.03519396	0.07010231	3.073930e-15
wt2	-0.03275370	0.26622249	0.72780448	1.963707e-15
wt3	-0.03578383	-1.05851494	0.52979799	2.893519e-15
wt4	-0.52795595	-0.20995085	-0.50325679	2.872702e-15
wt5	0.83227047	-0.05891489	-0.81258430	1.693090e-15
ko1	-0.07864392	-0.94652648	-0.24613776	4.052314e-15

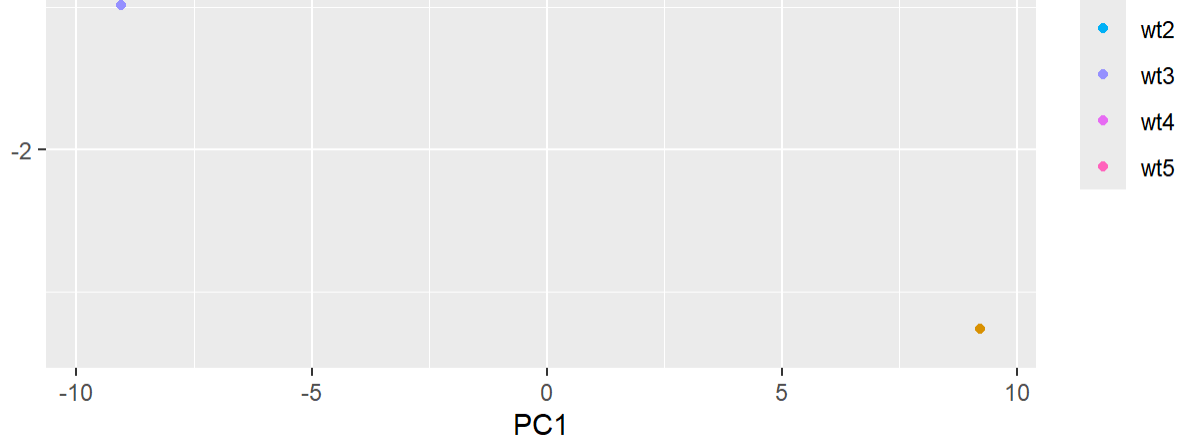
i will make a main result figure use ggplot:

```
library(ggplot2)
```

```
res <- as.data.frame(pca$x)
```

```
ggplot(res) +
  aes(x=PC1, y=PC2, col=rownames(res))+
  geom_point()
```





```
colnames(rna.data)
```

```
[1] "wt1" "wt2" "wt3" "wt4" "wt5" "ko1" "ko2" "ko3" "ko4" "ko5"
```