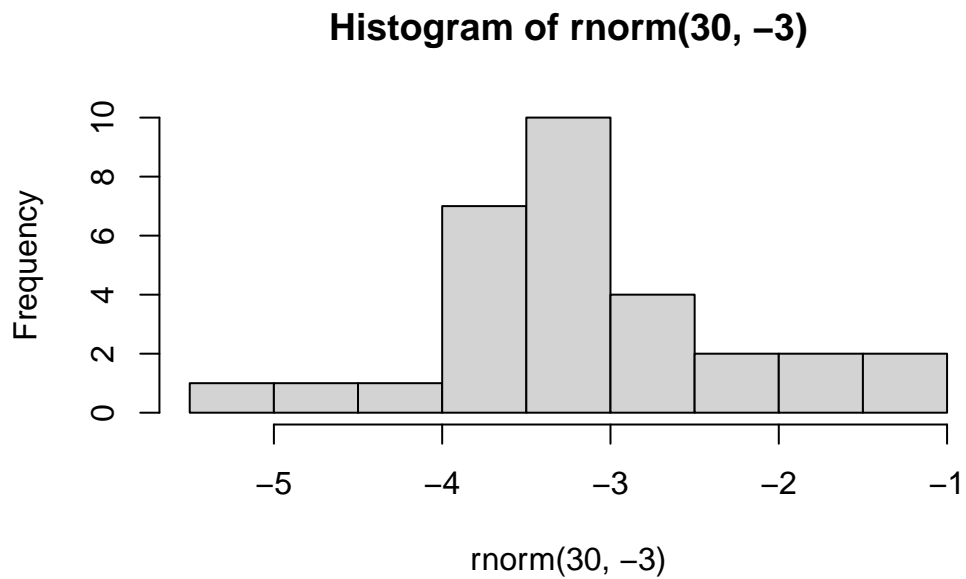


lab07

Xinlong Wan

kmeans

```
hist(rnorm(30, -3))
```

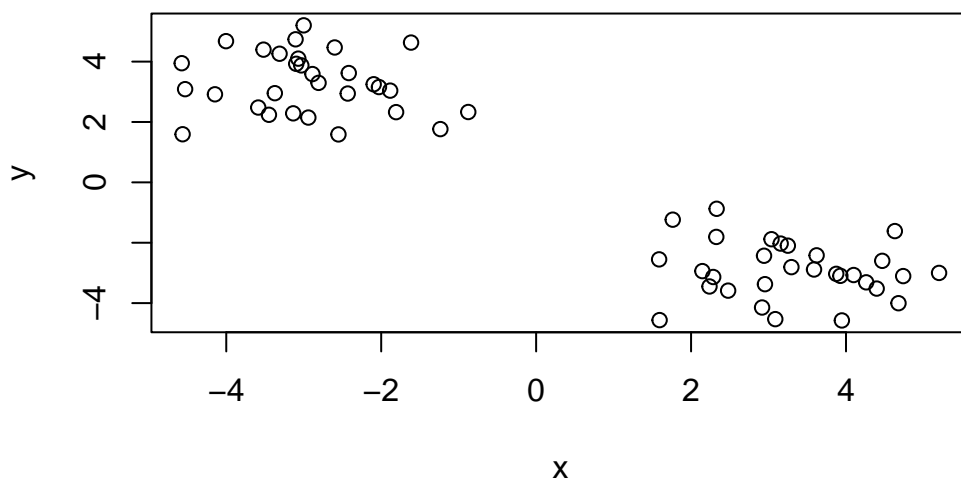


```
tmp <- c(rnorm(30, -3), rnorm(30, +3))  
x <- cbind(x=tmp, y=rev(tmp))  
head(x)
```

```
      x      y  
[1,] -2.028778 3.156471
```

```
[2,] -3.096753 3.927053  
[3,] -4.574697 3.946691  
[4,] -2.940199 2.145891  
[5,] -3.000527 5.201289  
[6,] -3.373100 2.953791
```

```
plot(x)
```



Use the kmeans function

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

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

Cluster means:

	x	y
1	3.293751	-2.922612
2	-2.922612	3.293751

Clustering vector:

```
[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 1 1 1 1 1 1 1
[39] 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 1 1 1 1 1 1 1
```

Within cluster sum of squares by cluster:

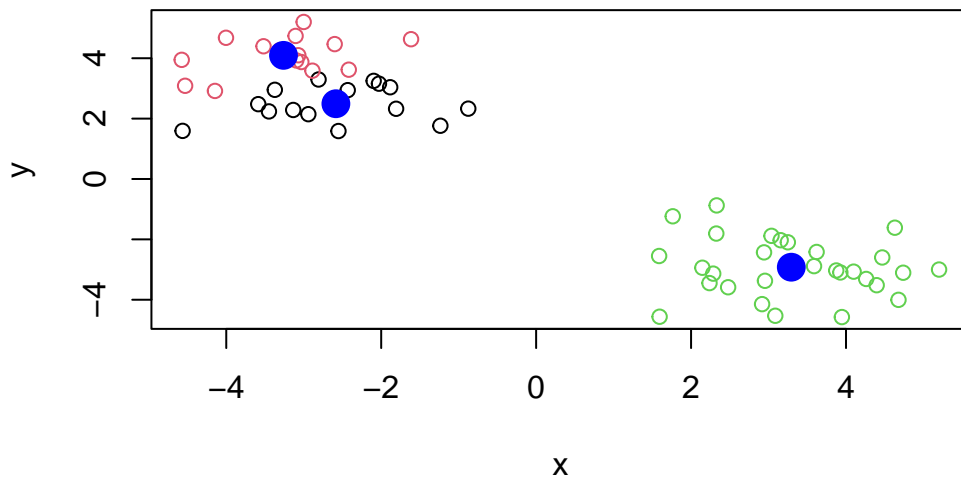
```
[1] 55.13581 55.13581
(between_SS / total_SS = 91.3 %)
```

Available components:

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

```
# play with kmeans and ask for different number of clusters
```

```
km <- kmeans(x, centers=3, nstart=20)
plot(x, col=km$cluster)
points(km$centers, col="blue", pch=16, cex=2)
```



Hierarchical clustering

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

hc
```

Call:

```
hclust(d = d)
```

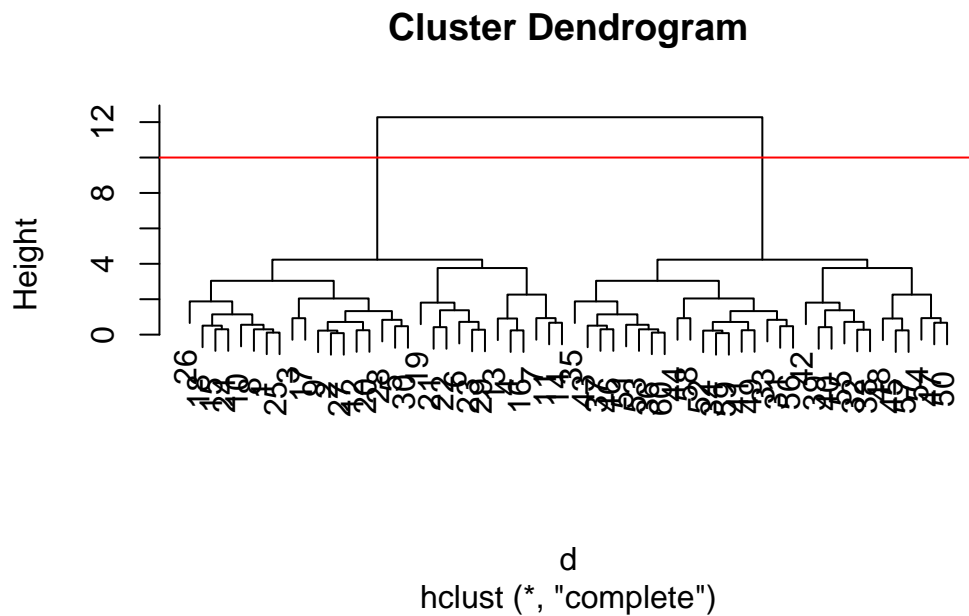
Cluster method : complete

Distance : euclidean

Number of objects: 60

There is a plot method for hclust result.

```
plot(hc)
abline(h=10, col='red')
```

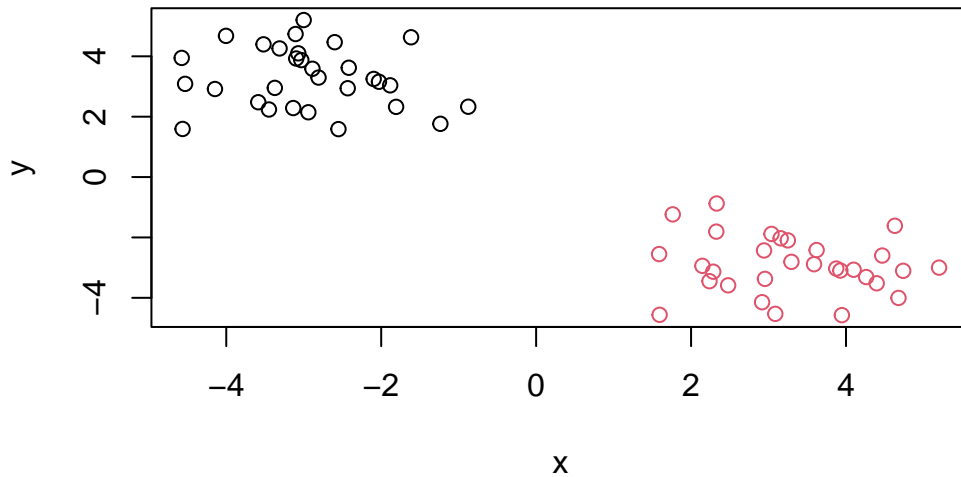


To get all the members of a given cluster residing in the same cut branch.

```
cut_hc <- cutree(hc, h=10)
cut_hc
```

```
[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
```

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



It is often helpful to use “k” instead of “h=” in cutree.

```
cutree(hc, k=4)
```

[1] 1 1 1 2 1 2 2 1 1 1 2 1 2 2 1 2 1 1 2 1 2 2 2 1 1 1 1 1 2 1 3 4 3 3 3 3 3 4
[39] 4 4 3 4 3 3 4 3 4 4 3 4 3 3 3 4 4 3 4 3 3 3

PCA

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

```
ncol(x)
```

```
[1] 5
```

```
nrow(x)
```

```
[1] 17
```

Q1. 5 columns 17 rows.

```
#View(head(x, 6))
head(x,6)
```

	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

```
# change the index to first column
```

```
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

```
dim(x)
```

```
[1] 17  4
```

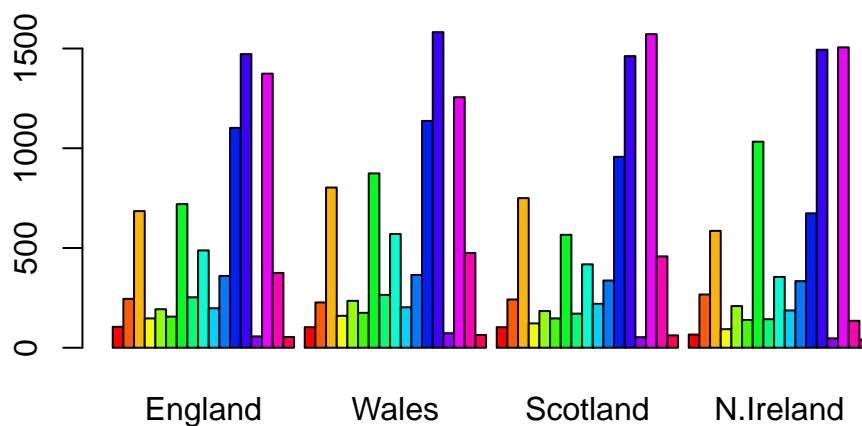
```
x <- read.csv(url, row.names=1)  
head(x)
```

	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

Q2. the second approach is more robust. Since we don't need to reassign x. And we can have two dataset from the same url but with different columns as rownames.

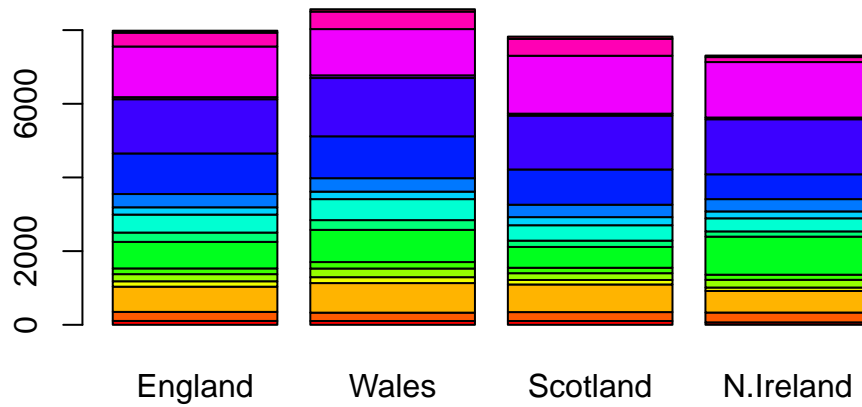
Visualize the data

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



Q3. # change the beside to False to get a stacked barplot

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

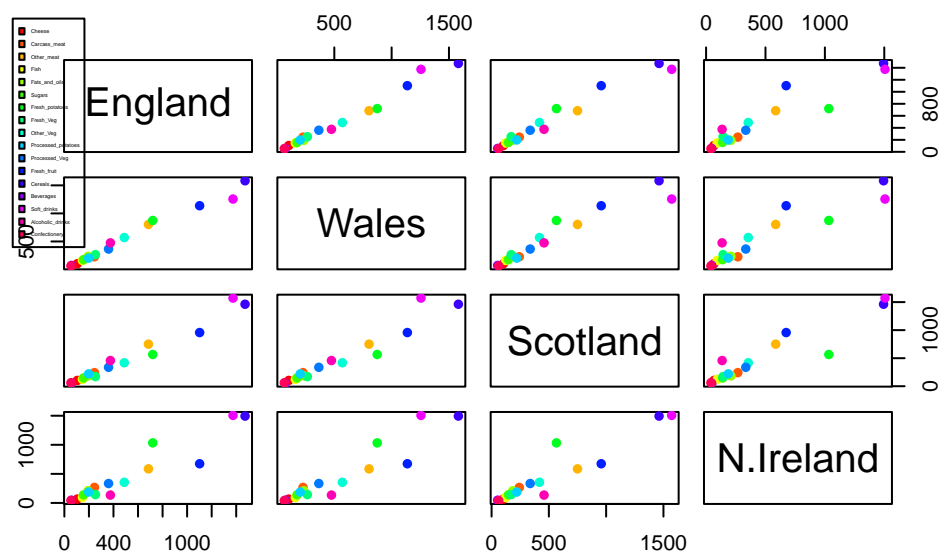


```
x$color <- rainbow(nrow(x))
```

```
pairs(x[, 1:4], col=x$color, pch=16)
```

```
par(xpd=TRUE)
```

```
legend("topleft", fill = unique(x$color), legend = c( rownames(x) ), cex=0.2)
```

Q5. It makes pairwise comparison of each combination. `plot(2,3)` is comparing Wales and Scotland for the prize of each different food type. Points on diagonal mean the prize of that specific food cost the same in the two countries in comparison.

Q6. Certain food is higher in N. Ireland. But it's generally hard to compare.

Use the PCA on the dataset

```
x <- x[, 1:4]

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

Importance of components:

	PC1	PC2	PC3	PC4
Standard deviation	324.1502	212.7478	73.87622	5.552e-14
Proportion of Variance	0.6744	0.2905	0.03503	0.000e+00
Cumulative Proportion	0.6744	0.9650	1.00000	1.000e+00

```
head(pca)
```

\$sdev

[1] 3.241502e+02 2.127478e+02 7.387622e+01 5.551558e-14

\$rotation

	PC1	PC2	PC3	PC4
Cheese	-0.056955380	-0.016012850	-0.02394295	-0.537717586
Carcass_meat	0.047927628	-0.013915823	-0.06367111	0.827327785
Other_meat	-0.258916658	0.015331138	0.55384854	-0.054885657
Fish	-0.084414983	0.050754947	-0.03906481	-0.017195729
Fats_and_oils	-0.005193623	0.095388656	0.12522257	0.039441462
Sugars	-0.037620983	0.043021699	0.03605745	0.002788534
Fresh_potatoes	0.401402060	0.715017078	0.20668248	-0.030319813
Fresh_Veg	-0.151849942	0.144900268	-0.21382237	-0.051070911
Other_Veg	-0.243593729	0.225450923	0.05332841	0.060355222
Processed_potatoes	-0.026886233	-0.042850761	0.07364902	0.003645959
Processed_Veg	-0.036488269	0.045451802	-0.05289191	-0.003672450
Fresh_fruit	-0.632640898	0.177740743	-0.40012865	0.031359988
Cereals	-0.047702858	0.212599678	0.35884921	0.073618516
Beverages	-0.026187756	0.030560542	0.04135860	-0.005163295
Soft_drinks	0.232244140	-0.555124311	0.16942648	-0.009904437
Alcoholic_drinks	-0.463968168	-0.113536523	0.49858320	0.088180533
Confectionery	-0.029650201	-0.005949921	0.05232164	0.004029923

\$center

	Cheese	Carcass_meat	Other_meat	Fish
	94.25	245.25	706.00	130.50
Fats_and_oils		Sugars	Fresh_potatoes	Fresh_Veg
	205.25	154.25	798.25	208.00
Other_Veg	Processed_potatoes		Processed_Veg	Fresh_fruit
	457.75	202.00	349.00	967.50
Cereals	Beverages		Soft_drinks	Alcoholic_drinks
	1502.50	57.50	1427.00	360.75
Confectionery				
	55.25			

\$scale

[1] FALSE

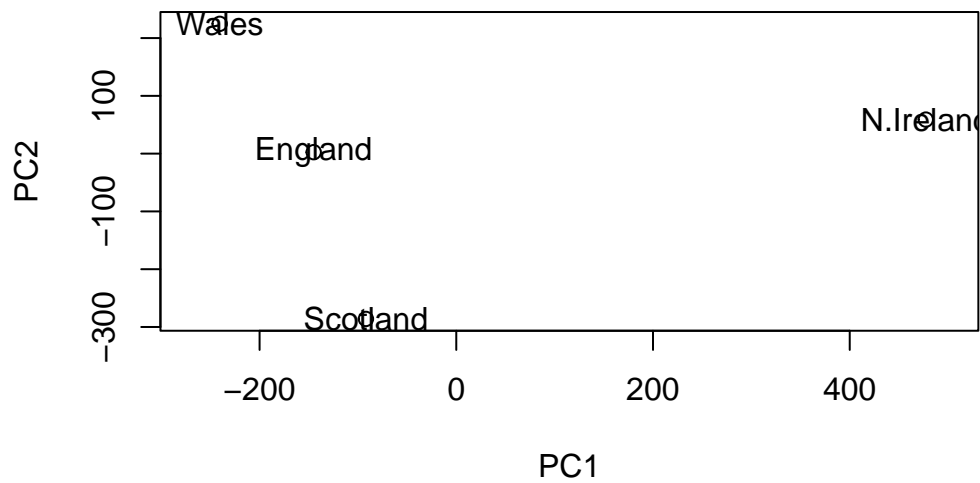
\$x

	PC1	PC2	PC3	PC4
England	-144.99315	2.532999	-105.768945	1.042460e-14
Wales	-240.52915	224.646925	56.475555	9.556806e-13
Scotland	-91.86934	-286.081786	44.415495	-1.257152e-12

N.Ireland 477.39164 58.901862 4.877895 2.872787e-13

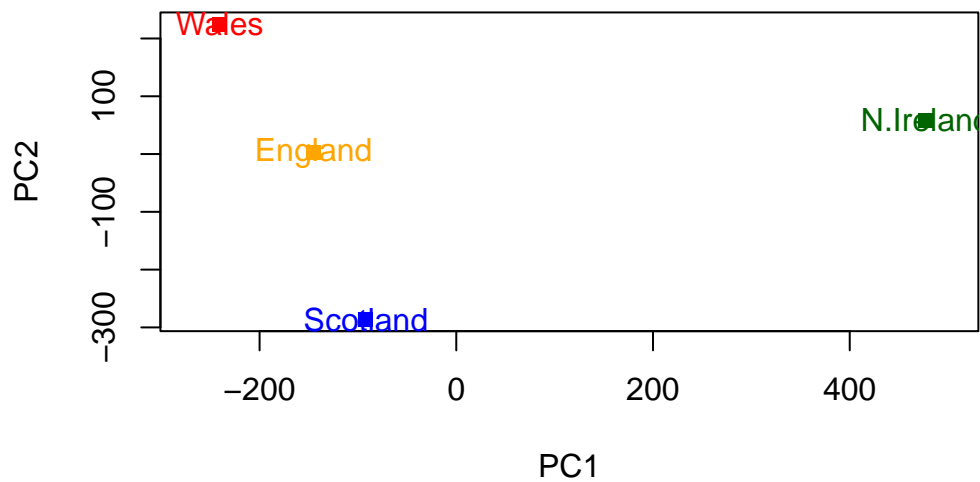
Q7

```
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.

```
plot(pca$x[,1], pca$x[,2], xlab="PC1", ylab="PC2", xlim=c(-270,500), pch=15,  
     col=c('orange', 'red', 'blue', 'darkgreen'))  
text(pca$x[,1], pca$x[,2], colnames(x), col=c('orange', 'red', 'blue', 'darkgreen'))
```



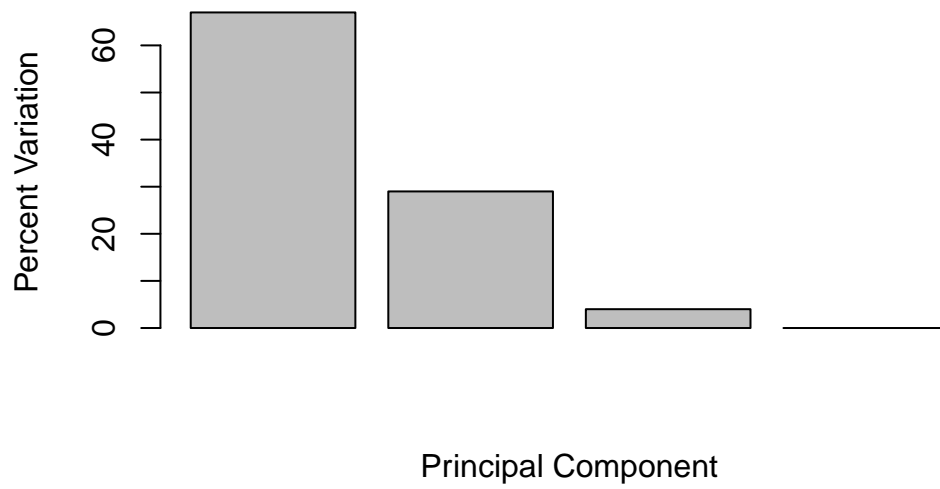
```
v <- round( pca$sdev^2/sum(pca$sdev^2) * 100 )
v
```

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

```
z <- summary(pca)
z$importance
```

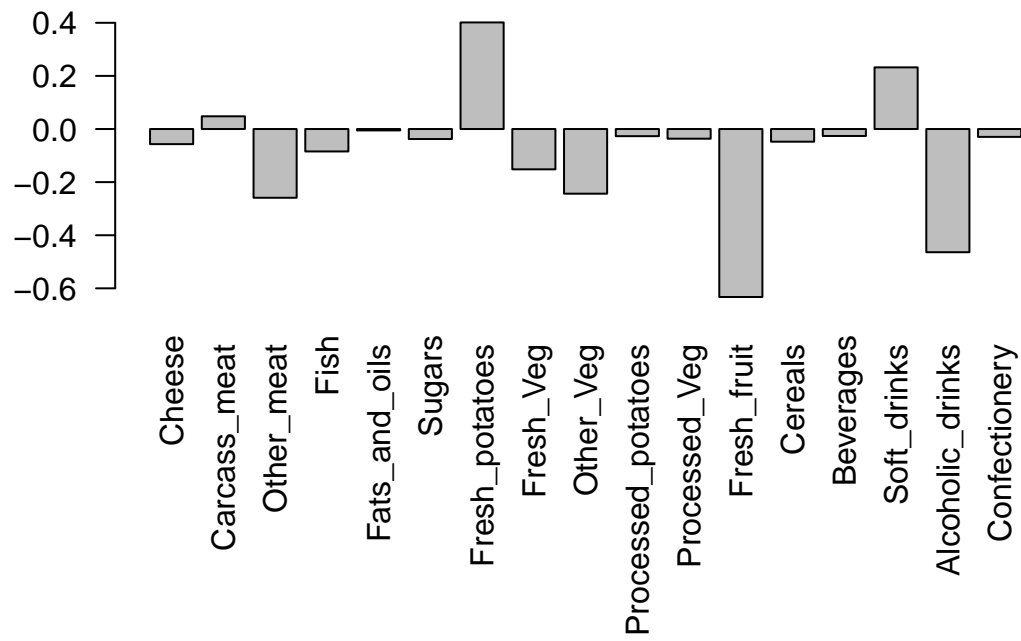
	PC1	PC2	PC3	PC4
Standard deviation	324.15019	212.74780	73.87622	5.551558e-14
Proportion of Variance	0.67444	0.29052	0.03503	0.000000e+00
Cumulative Proportion	0.67444	0.96497	1.00000	1.000000e+00

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



The first two PCs capture most of the variance.

```
# visualize the loading for each variables in PC1.  
par(mar=c(10, 3, 0.35, 0))  
barplot( pca$rotation[,1], las=2 )
```



Q9

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

