Lab7

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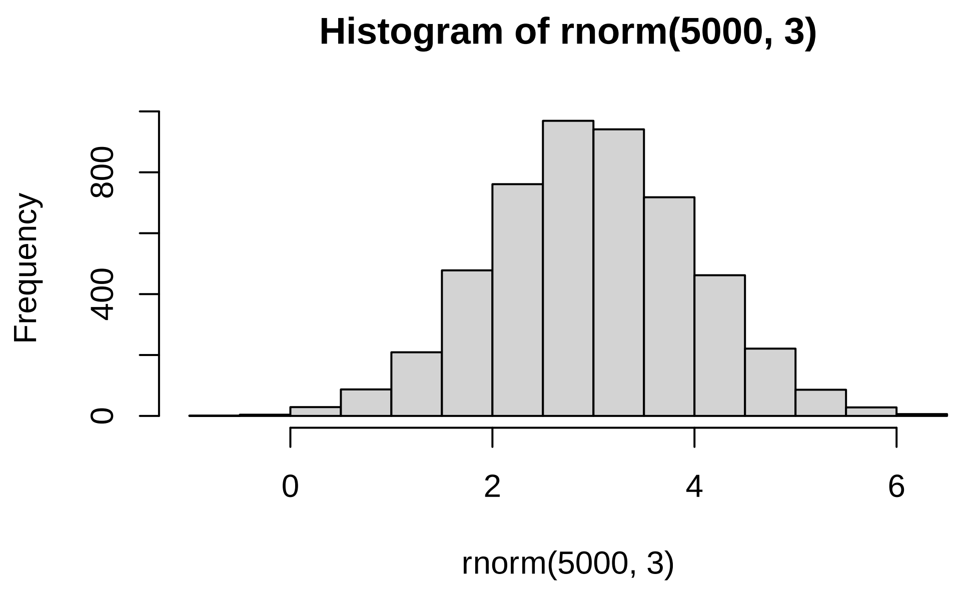
Clustering

First let's make up some data to cluster so we can get a feel for these methods and how to work with them.

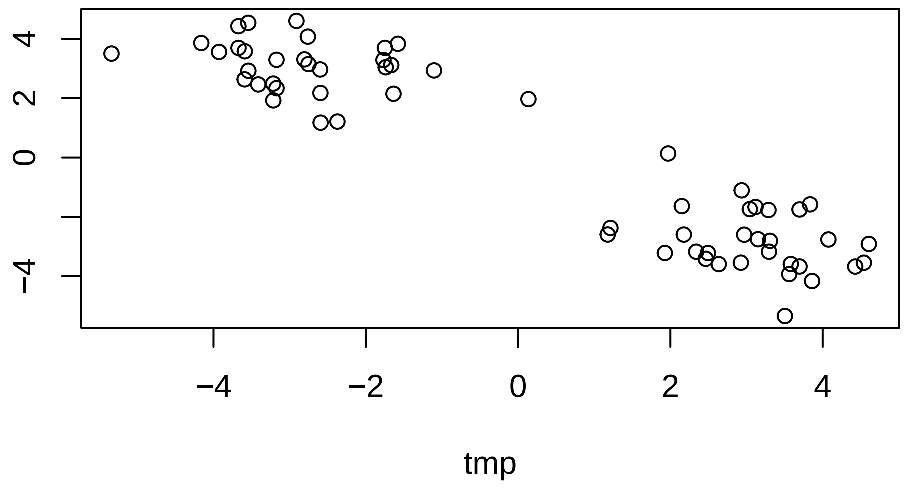
We can use `rnorm()` function to get random numbers from a normal distribution around a given `mean`.

```r
hist(rnorm(5000,3))
```



Let's get 30 points with a mean of 3 and another 30 with a mean of -3. Then make a matrix whose plot has two clusters at two opposite corners in the Euclidean space.

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



K-means clustering

Very popular clustering method, especially for big data set, that we can use with the `kmeans()` function in base R.

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

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

Cluster means:
        tmp
1 -2.790689  3.065319
2  3.065319 -2.790689

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

Within cluster sum of squares by cluster:
[1] 56.57847 56.57847
 (between_SS / total_SS =  90.1 %)

Available components:

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

How many points are in each cluster?

```r
km$size
```

```
[1] 30 30
```

What `component` of your result object details

- Cluster size?

  "size"

- Cluster assignment/membership?

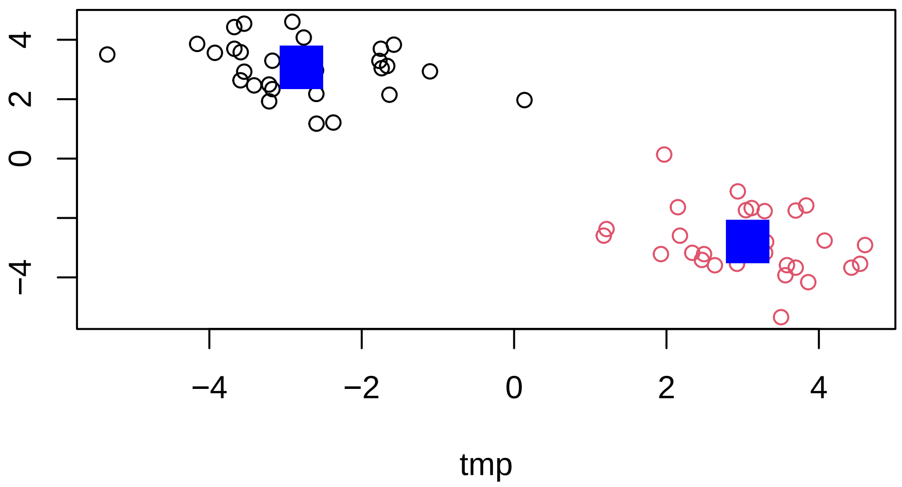
  "cluster"

- Cluster center?

  "centers"

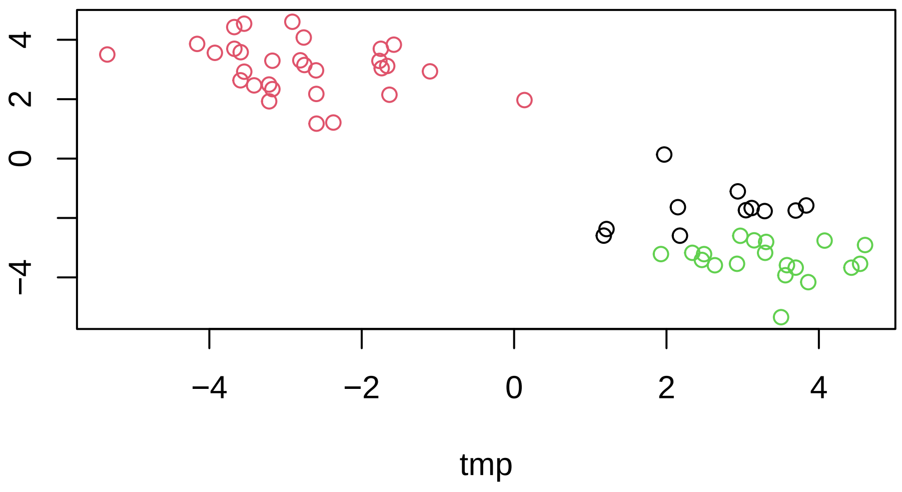
Plot x colored by the kmean cluster assignment and add cluster centers as blue points

```r
mycols <- c(1,5)
# col=km$cluster will split them into two colors
plot(x,col=km$cluster)
points(km$centers,col="blue",pch=15,cex=3)
```



Let’s cluster into 3 groups or same `x` data and make a plot

```
km <- kmeans(x,centers=3)
plot(x,col=km$cluster)
```



Hierarchical Clustering

We can use the `hcluster()` function for Hierarchical Clustering. Unlike `kmeans()`, where we could just pass in our data as input, we need to give `hclust()` a "distance matrix".

We will use the `dist()` function to start with.

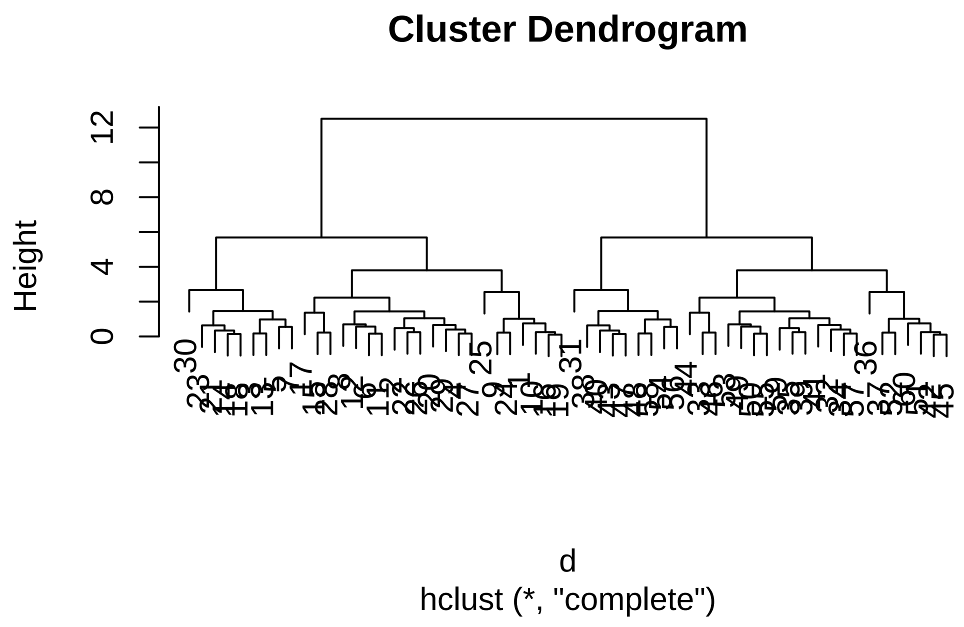
```
d<-dist(x)
hc<-hclust(d)
hc
```

```

Call:
hclust(d = d)

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

```
plot(hc)
```



I can now "cut" my tree with the `cutree()` to yield a cluster membership vector

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

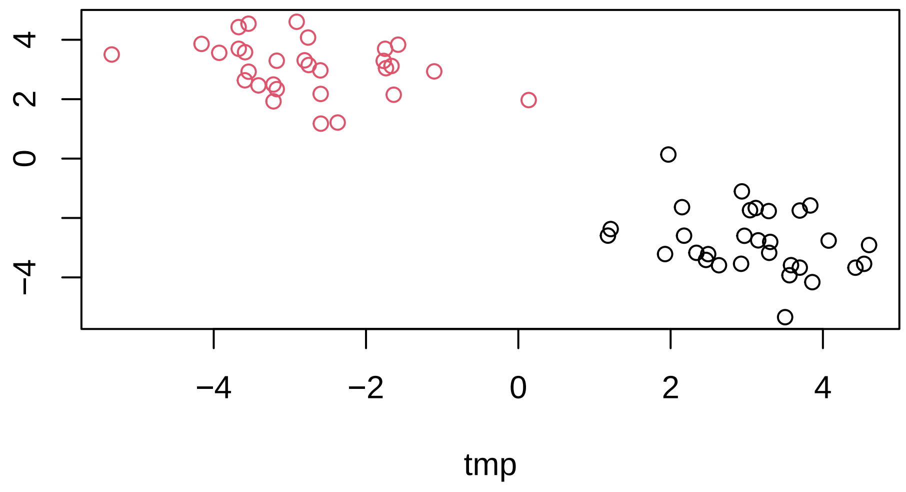
```
 [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2
[39] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
```

You can also tell `cutree()` to cut where it yields "k" groups

```
cutree(hc,k=2)
```

```
 [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
```

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



Principal Component Analysis (PCA)

```r
url <- "https://tinyurl.com/UK-foods"
x <- read.csv(url, row.names = 1)
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
Fresh_potatoes          720   874      566      1033
Fresh_Veg               253   265      171       143
Other_Veg               488   570      418       355
Processed_potatoes      198   203      220       187
Processed_Veg           360   365      337       334
Fresh_fruit            1102  1137      957       674
Cereals                1472  1582     1462      1494
```

```
Beverages                 57   73     53      47
Soft_drinks             1374 1256   1572    1506
Alcoholic_drinks         375  475    458     135
Confectionery             54   64     62      41
```

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

```r
## Complete the following code to find out how many rows and columns are in x?

dim(x)
```

```
[1] 17  4
```

```r
## Preview the first 6 rows
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
```

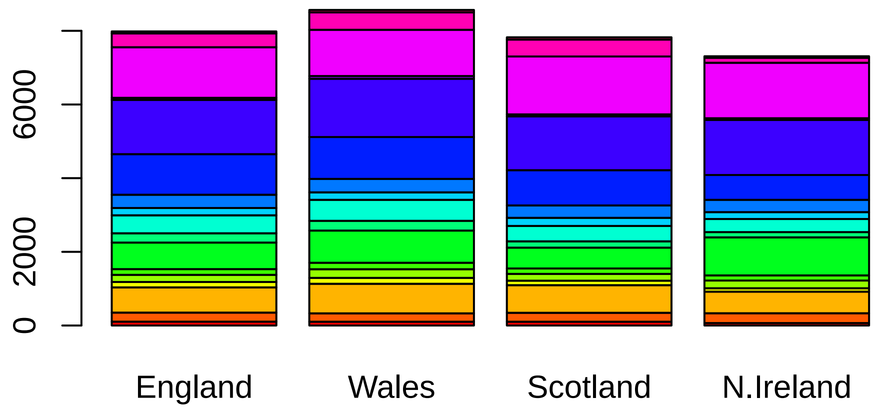
> **Q2.** Which approach to solving the 'row-names problem' mentioned above do you prefer and why? Is one approach more robust than another under certain circumstances?

I prefer the `row.names=1` approach. When you do `x <- x[,-1]` multiple times, it removes the columns one by one until you are left with none.

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

Remove `beside=T` argument.

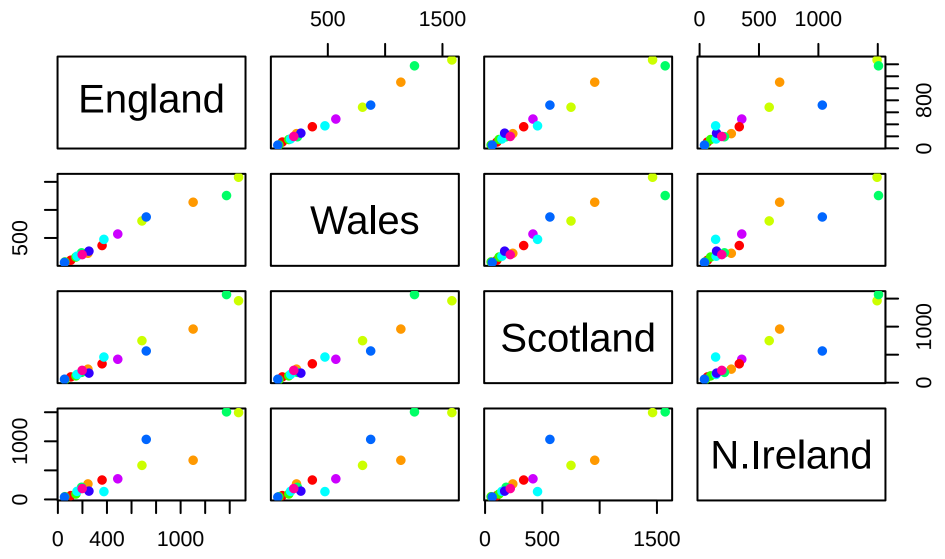
```r
barplot(as.matrix(x), col=rainbow(nrow(x)))
```



> **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?

If a point lies on the diagonal for a given plot, it means the the values are very similar to one another.

```r
pairs(x, 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?

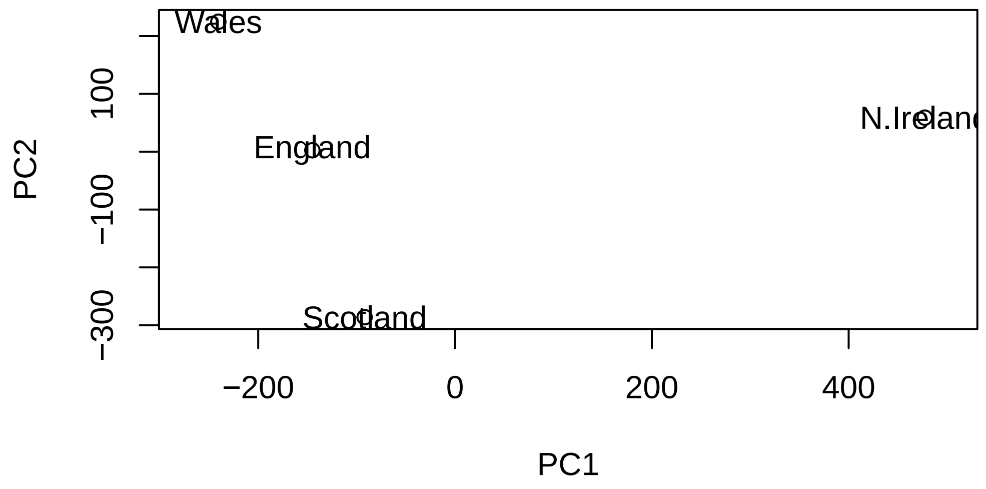
There are more wiggles in plots for country vs N. Ireland (less aligned diagonal line). The blue point is of higher value in N. Ireland compared to other countries.

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

```r
# Use the prcomp() PCA function
pca <- prcomp( t(x) )
summary(pca)
```

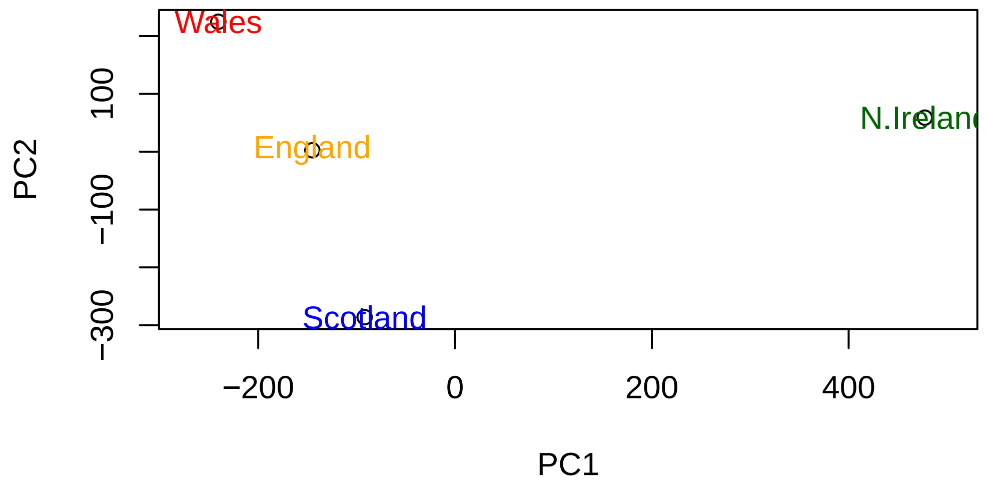
```
Importance of components:
                            PC1      PC2      PC3       PC4
Standard deviation     324.1502 212.7478 73.87622 4.189e-14
Proportion of Variance   0.6744   0.2905  0.03503 0.000e+00
Cumulative Proportion    0.6744   0.9650  1.00000 1.000e+00
```

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


Wales
England
N.Irelanc
Scotland
PC2
100
−100
−300
−200
0
200
400
PC1