Class 07: Machine Learning 1

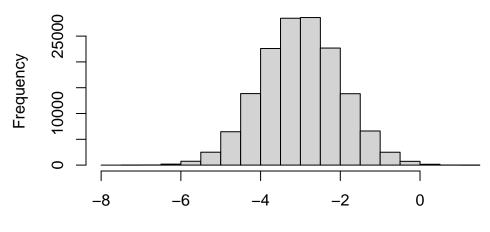
Jessica PID: A15647602

Before we get into the clustering methods let's make some sample data to cluster where we know what the answer should be.

To help with this I will use the 'rnorm()' function.

```
hist( rnorm(150000, mean = c(-3)))
```

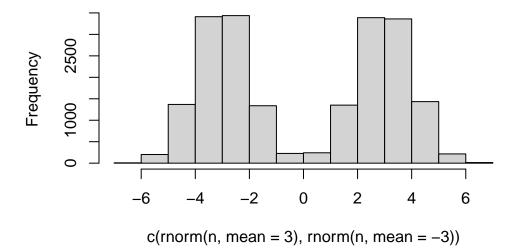
Histogram of rnorm(150000, mean = c(-3))



rnorm(150000, mean = c(-3))

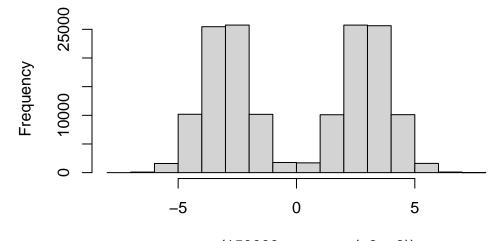
```
n = 10000
hist(c(rnorm(n, mean = 3), rnorm(n, mean = -3)))
```

Histogram of c(rnorm(n, mean = 3), rnorm(n, mean = -3)



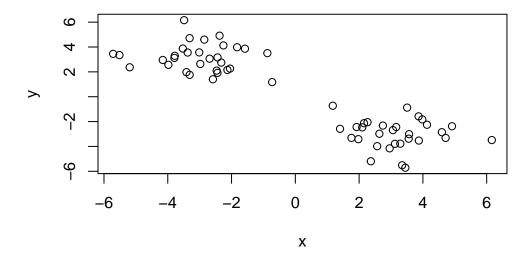
hist(rnorm(150000, mean = c(-3, +3)))

Histogram of rnorm(150000, mean = c(-3, +3))



```
n = 30
x <- c( rnorm(n, mean = 3), rnorm(n, mean = -3))
y <- rev(x)

z <- cbind(x, y)
plot(z)</pre>
```



K-means clustering

The function in base R for k-means clustering is called kmeans()

```
km <- kmeans(z, centers = 2)
km</pre>
```

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

Cluster means:

```
x y
1 -3.005717 3.143865
2 3.143865 -3.005717
```

```
Clustering vector:
```

Within cluster sum of squares by cluster:

[1] 76.47311 76.47311

(between_SS / total_SS = 88.1 %)

Available components:

[1] "cluster" "centers" "totss" "withinss" "tot.withinss"

[6] "betweenss" "size" "iter" "ifault"

km\$centers

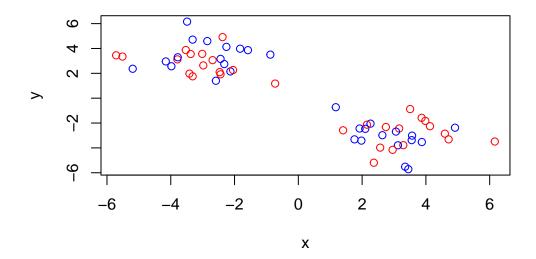
x y 1 -3.005717 3.143865

2 3.143865 -3.005717

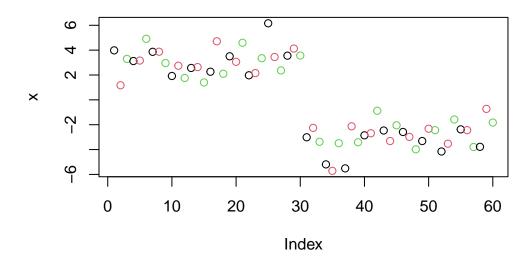
Q. Print out the cluster membership vector (i.e our main answer)

km\$cluster

plot(z, col = c("red", "blue"))



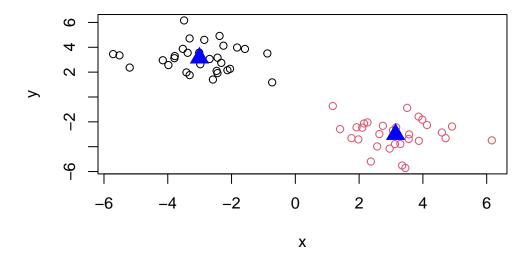
plot(x, col = c(1,2,3))



```
# color by number (1,2,3, etc.)
```

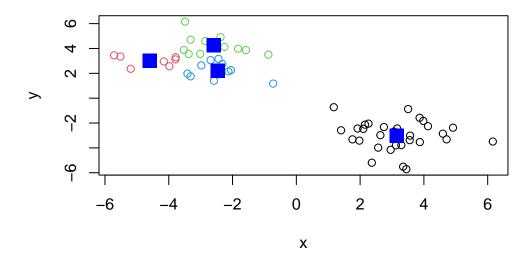
Plot this with clustering result and add cluster centers:

```
plot(z, col = km$cluster)
points(km$centers, col = "blue", pch = 17, cex = 2)
```



Q. Can you cluster our data in z into four clusters please?

```
km4 <- kmeans(z, centers = 4)
plot(z, col = km4$cluster)
points(km4$centers, col = "blue", pch = 15, cex = 2)</pre>
```



Hierarchical Clustering

The main function for hierarchical clustering in base R is called hclust() Unlike kmeans() I can not just pass in my data as input I first need a distance matrix from my data.

```
d <- dist(z)
hc <- hclust(d)
hc</pre>
```

Call:
hclust(d = d)

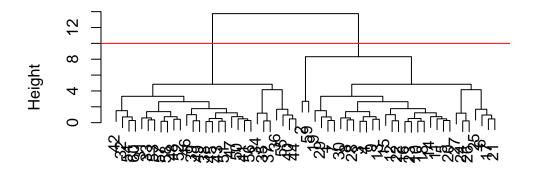
Cluster method : complete
Distance : euclidean

Number of objects: 60

There is a specific hclust plot() method...

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

Cluster Dendrogram

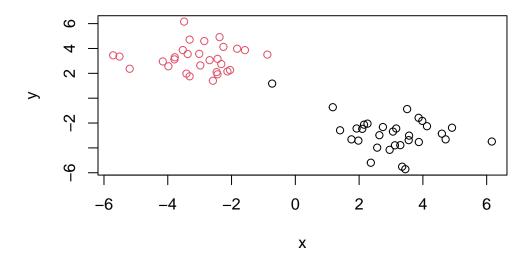


d hclust (*, "complete")

To get my main clustering results (i.e. the membershp vector) I can "cut" my tree at a given height. To do this I will use the ${\tt cutree}()$

```
grps <- cutree(hc, h = 10)
grps</pre>
```

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



Principal Component Analysis (PCA)

#PCA of UK food data

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

Q1. How many rows and columns are in your new data frame named x? What R functions could you use to answer this questions? ## Complete the following code to find out how many rows and columns are in x?

nrow(x)

[1] 17

ncol(x)

[1] 4

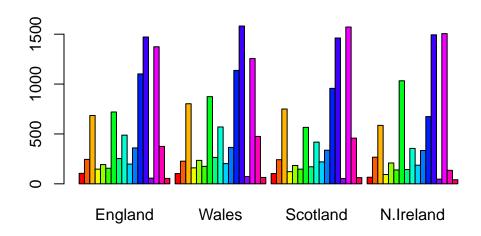
dim(x)

[1] 17 4

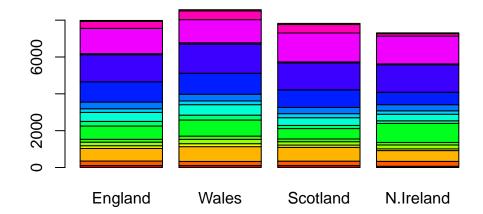
head(x)

	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

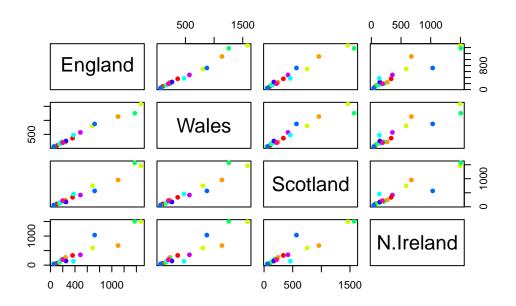
barplot(as.matrix(x), beside=T, col=rainbow(nrow(x)))



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



pairs(x, col=rainbow(10), pch=16)



PCA to the rescue

The main function to do PCA in base R is called prcomp()

Note that I need to take the transpose of this particular data as that is what theprcomp() help page was asking for.

```
pca <- prcomp(t(x))
summary(pca)</pre>
```

Importance of components:

```
PC1 PC2 PC3 PC4
Standard deviation 324.1502 212.7478 73.87622 2.921e-14
Proportion of Variance 0.6744 0.2905 0.03503 0.000e+00
Cumulative Proportion 0.6744 0.9650 1.00000 1.000e+00
```

Let's see what is inside our result object pca that we just calculated:

```
attributes(pca)
```

\$names

```
[1] "sdev" "rotation" "center" "scale" "x"
```

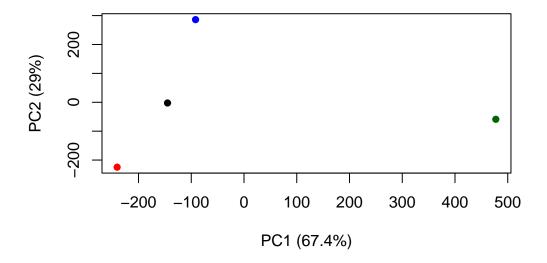
\$class

[1] "prcomp"

pca\$x

```
PC1 PC2 PC3 PC4
England -144.99315 -2.532999 105.768945 -9.152022e-15
Wales -240.52915 -224.646925 -56.475555 5.560040e-13
Scotland -91.86934 286.081786 -44.415495 -6.638419e-13
N.Ireland 477.39164 -58.901862 -4.877895 1.329771e-13
```

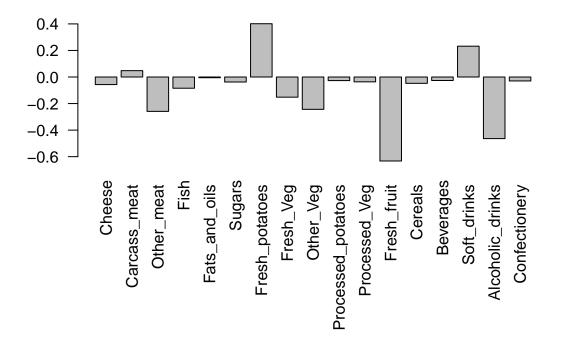
To make our main result figure, called a "PC plot" (or "score plot", "ordination plot", or "PC1 vs PC2 plot").



Variable loadings plot

Can give us insight on how the original variables vary.

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



pca\$rotation

	PC1	PC2	PC3	PC4
Cheese	-0.056955380	0.016012850	0.02394295	-0.409382587
Carcass_meat	0.047927628	0.013915823	0.06367111	0.729481922
Other_meat	-0.258916658	-0.015331138	-0.55384854	0.331001134
Fish	-0.084414983	-0.050754947	0.03906481	0.022375878
Fats_and_oils	-0.005193623	-0.095388656	-0.12522257	0.034512161
Sugars	-0.037620983	-0.043021699	-0.03605745	0.024943337
Fresh_potatoes	0.401402060	-0.715017078	-0.20668248	0.021396007
Fresh_Veg	-0.151849942	-0.144900268	0.21382237	0.001606882
Other_Veg	-0.243593729	-0.225450923	-0.05332841	0.031153231
Processed_potatoes	-0.026886233	0.042850761	-0.07364902	-0.017379680
Processed_Veg	-0.036488269	-0.045451802	0.05289191	0.021250980
Fresh_fruit	-0.632640898	-0.177740743	0.40012865	0.227657348
Cereals	-0.047702858	-0.212599678	-0.35884921	0.100043319
Beverages	-0.026187756	-0.030560542	-0.04135860	-0.018382072
Soft_drinks	0.232244140	0.555124311	-0.16942648	0.222319484
Alcoholic_drinks	-0.463968168	0.113536523	-0.49858320	-0.273126013
Confectionery	-0.029650201	0.005949921	-0.05232164	0.001890737

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

