# Class 07

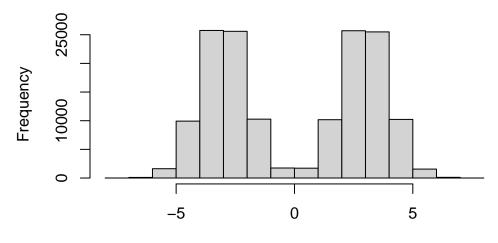
### Tim

Before we get into 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(-3,3)))
```

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



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

```
n = 30

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

[1] 4.46798260 1.70986137 3.11466763 1.84850216 3.61366384 4.55704813 [7] 2.75938463 4.00389788 4.11800034 4.76220242 2.83079482 3.29563264

```
[13] 2.42820720 2.76138019 2.63215105 3.05591783 2.46939160 1.54592873
[19] 2.74807696 2.84649996 2.69952664 2.29459172 3.98195685 3.81474001
[25] 2.55975609 2.66517484 4.78479526 4.31640984 2.83285575 2.38094406
[31] -3.74718670 -3.44746008 -3.85879755 -3.50152870 -2.42079140 -3.69978722
[37] -3.91135027 -2.71269649 -0.01924523 -2.92619162 -2.38492765 -3.05953810
[43] -2.62313602 -2.06880033 -2.97530611 -2.39972763 -4.04424115 -2.51361118
[49] -3.48955271 -2.20588842 -2.71849569 -4.37886667 -3.06276331 -3.02540176
[55] -2.74616314 -1.50486908 -3.36118161 -2.12471253 -3.53789646 -3.36443972

n = 30

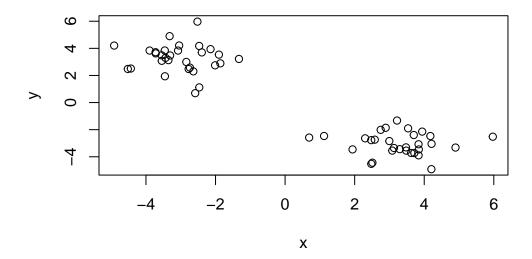
x <- c(rnorm(n, mean = 3), rnorm(n, mean = -3))

y <- rev(x)
```

```
X
 [1,] 3.8437796 -3.4589188
 [2,] 4.1762924 -2.4695557
 [3,] 3.2963815 -3.4372782
 [4,] 2.8921501 -1.8610734
 [5,] 2.4766729 -2.7723950
 [6,] 4.2054365 -4.9145777
 [7,] 3.9413800 -2.1432397
 [8,] 0.6922059 -2.5838340
 [9,] 3.4835335 -3.5453459
[10,] 3.6258424 -3.7191912
[11,] 4.8991739 -3.3194950
[12,] 3.8358012 -3.0769935
[13,] 3.5365574 -1.9025199
[14,] 3.2178716 -1.3263781
[15,] 2.4781840 -4.5206557
[16,] 3.1302859 -3.3534977
[17,] 2.5787255 -2.7368924
[18,] 1.9393225 -3.4550168
[19,] 3.4752526 -3.3056928
[20,] 2.7482718 -2.0124376
[21,] 3.7149897 -3.7240890
[22,] 2.9965440 -2.8402164
[23,] 1.1201352 -2.4668303
[24,] 5.9717116 -2.5200286
[25,] 3.0811756 -3.5451109
```

```
[26,] 2.5106591 -4.4347691
[27,] 2.3014675 -2.6381747
[28,] 3.6999026 -2.3938830
[29,] 4.2105840 -3.0455282
[30,] 3.8379190 -3.8951172
[31,] -3.8951172 3.8379190
[32,] -3.0455282 4.2105840
[33,] -2.3938830 3.6999026
[34,] -2.6381747 2.3014675
[35,] -4.4347691 2.5106591
[36,] -3.5451109 3.0811756
[37,] -2.5200286 5.9717116
[38,] -2.4668303 1.1201352
[39,] -2.8402164 2.9965440
[40,] -3.7240890 3.7149897
[41,] -2.0124376 2.7482718
[42,] -3.3056928 3.4752526
[43,] -3.4550168 1.9393225
[44,] -2.7368924 2.5787255
[45,] -3.3534977
                 3.1302859
[46,] -4.5206557 2.4781840
[47,] -1.3263781 3.2178716
[48,] -1.9025199 3.5365574
[49,] -3.0769935
                 3.8358012
[50,] -3.3194950 4.8991739
[51,] -3.7191912 3.6258424
[52,] -3.5453459 3.4835335
[53,] -2.5838340 0.6922059
[54,] -2.1432397
                 3.9413800
[55,] -4.9145777 4.2054365
[56,] -2.7723950 2.4766729
[57,] -1.8610734 2.8921501
[58,] -3.4372782 3.2963815
[59,] -2.4695557 4.1762924
[60,] -3.4589188 3.8437796
```

#### plot(z)



### K-means clustering

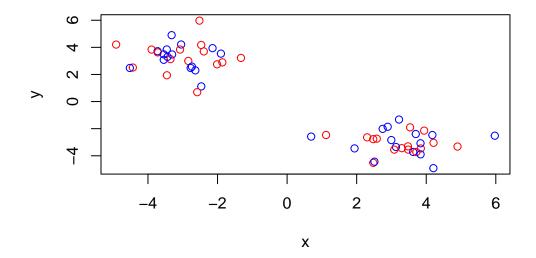
the function in base R for kmeana

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

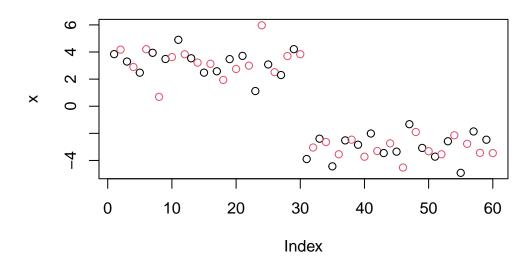
Q. print out the cluster membership vector (i.e. our main answer)

```
km$cluster
```

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

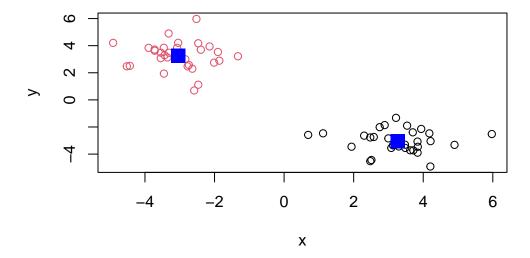


### plot(x, col=c(1,2))



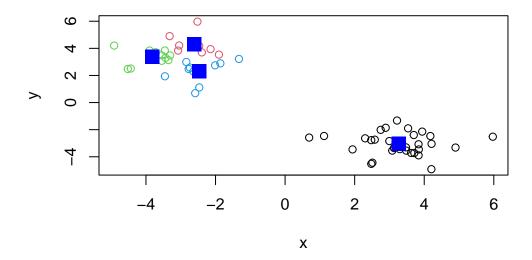
plot with clustering center

```
plot(z, col= km$cluster)
points(km$centers, col = "blue", pch=15, cex=2)
```



Q. can you cluster our data in  ${\tt z}$  into 4 clusters?

```
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 hierarachical 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 data.

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

Call:

hclust(d = d)

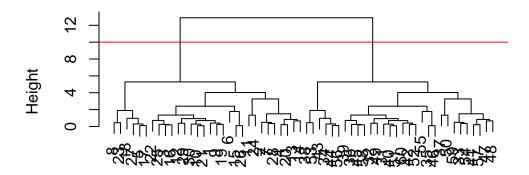
Cluster method : complete
Distance : euclidean

Number of objects: 60

there is a specific hclust plot() method..

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

## **Cluster Dendrogram**



### d hclust (\*, "complete")

the longer the cluster bar the larger the distance and the more space to scoare a difference between the clusters

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

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

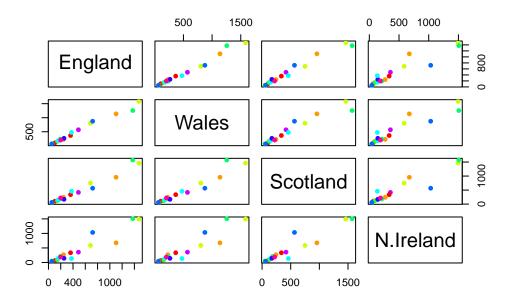
# **Principal Component Analysis**

reduce the features dimensionality while only losing a small amount of info (follows the best fit line through points)

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

	England	Wales	${\tt Scotland}$	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

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



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

 $\mathbf{t}()$  function is trnapose to switch the x axis to make it y axis

### t(x)

	CI)	a		0.1		n. 1			a
	Cheese	Carcass	_meat	Utner_	meat	Fish	Fats_and	_oiis	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_p	potatoes	Fres	h_Veg	Other	_Veg	Processed	d_pota	toes
England		720	0	253		488			198
Wales		874	4	265		570			203
Scotland		560	6	171		418			220
N.Ireland		1033	3	143		355			187
	Process	sed_Veg	Fresh	_fruit	Cere	als	Beverages	Soft_	drinks
England		360		1102	2	1472	57		1374
Wales		365		1137	•	1582	73		1256
Scotland		337		957	•	1462	53		1572
N.Ireland		334		674		1494	47		1506
	Alcohol	lic_drin	ks Co	nfectio	nery				
England		;	375		54				

Wales	475	64
Scotland	458	62
N.Ireland	135	41

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

#### 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
```

#Proportion variance is how much each PC captured (i.e., PC1 captured 67% of the data 0.67)

#cumulative proportion you add PC1 to PC2 (0.67 + 0.29)

let's see what us 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	-4.894696e-14
Wales	-240.52915	-224.646925	-56.475555	5.700024e-13
Scotland	-91.86934	286.081786	-44.415495	-7.460785e-13
N.Ireland	477.39164	-58.901862	-4.877895	2.321303e-13