Class07

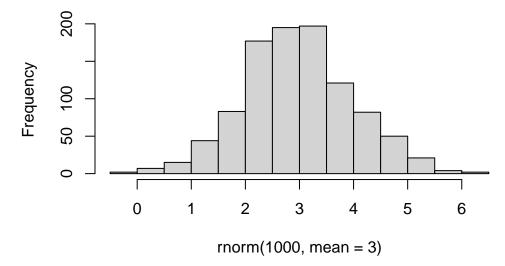
Nicholas Thiphakhinkeo

rnorm

```
rnorm(10)
```

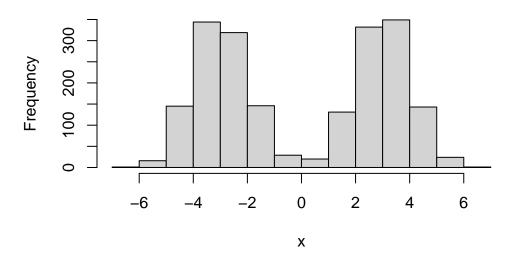
hist(rnorm(1000, mean=3))

Histogram of rnorm(1000, mean = 3)



```
n <- 1000
x <- c(rnorm(n,-3),rnorm(n,+3))
hist(x)</pre>
```

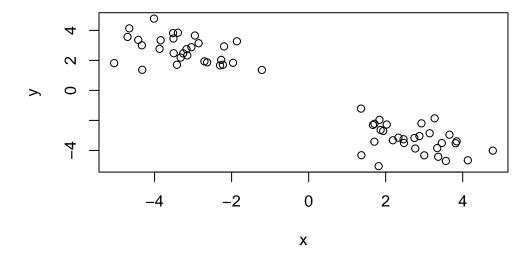
Histogram of x



```
n<-30
x<-c(rnorm(n,-3), rnorm(n,+3))
y <- rev(x)
z <- cbind(x,y)
head(z)</pre>
```

```
x y
[1,] -3.256146 2.464787
[2,] -1.963510 1.838160
[3,] -1.214137 1.361263
[4,] -2.300530 1.668796
[5,] -2.226912 1.707903
[6,] -3.043440 2.876707
```

plot(z)



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

Cluster means:

Clustering vector:

Within cluster sum of squares by cluster:

[1] 48.39342 48.39342 (between_SS / total_SS = 91.7 %)

Available components:

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

km\$size

[1] 30 30

Cluster Assignment

km\$cluster

Cluster Center

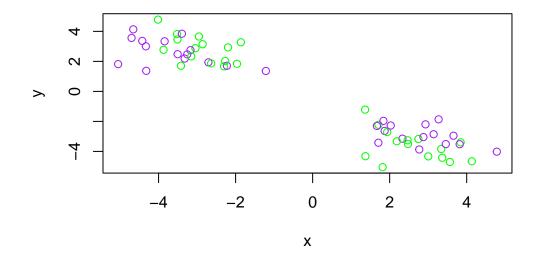
km\$centers

```
1 2.715122 -3.256493
2 -3.256493 2.715122
```

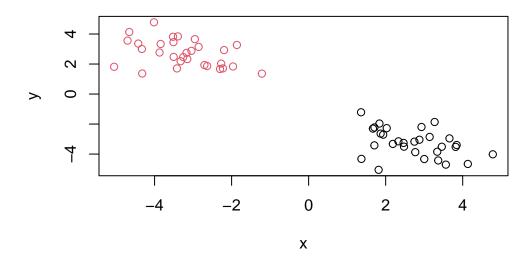
Plot z color colored by kmeans cluster assignment and add cluster centers as blue points

R recycles shorter color vector to be the same length as the longer (number of data points) in ${\bf z}$

```
plot(z, col=c("purple", "green"))
```

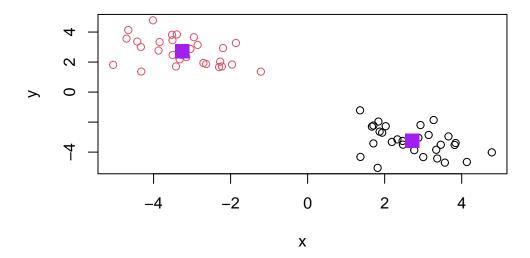


plot(z, col=km\$cluster)



use points() function to add new points to an existing plot... like a cluster plot

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



Q. Run kmeans and ask for 4 clusters and plot results

```
km2 <- kmeans(z, centers=4)
km2</pre>
```

K-means clustering with 4 clusters of sizes 30, 17, 2, 11

Cluster means:

```
x y
1 2.715122 -3.256493
2 -2.653050 2.267015
3 -4.685379 1.593931
```

```
4 -3.929289 3.611503
```

```
Clustering vector:
```

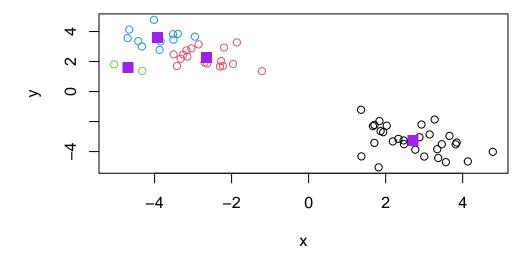
Within cluster sum of squares by cluster:

[1] 48.3934250 11.8945093 0.3656591 6.1139684 (between_SS / total_SS = 94.3 %)

Available components:

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

```
plot(z, col=km2$cluster)
points(km2$centers, col="purple", pch=15, cex=1.5)
```



Hierarchical Clustering

#need distance matrix of data to be clustered

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

Call:

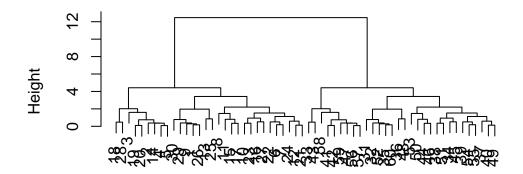
hclust(d = d)

Cluster method : complete
Distance : euclidean

Number of objects: 60

plot(hc)

Cluster Dendrogram



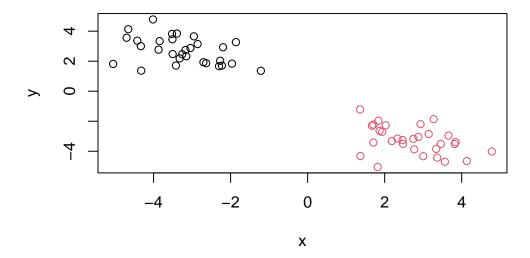
d hclust (*, "complete")

#Cluster Membership by cutting tree with cutree()

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

Plot "z" colored by hclust

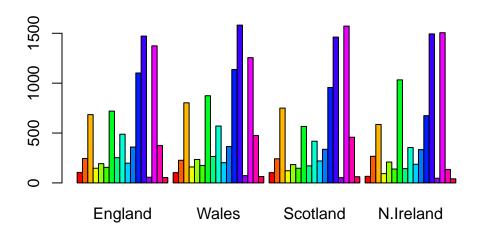
```
plot(z, col=grps)
```



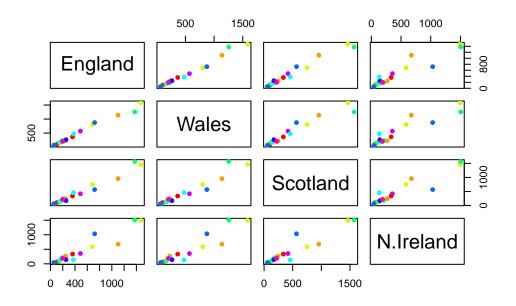
PCA Uk Foods Data

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

	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



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

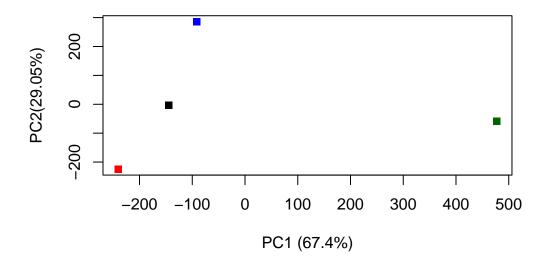


Using PCA for Larger Data Sets

```
pca <- prcomp(t(x))</pre>
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
attributes(pca)
$names
[1] "sdev"
             "rotation" "center"
                                     "scale"
$class
[1] "prcomp"
pca$x
                 PC1
                             PC2
                                        PC3
```

```
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

plot(pca$x[,1],pca$x[,2], col=c("black","red","blue","darkgreen"), pch=15, xlab="PC1 (67.4%)
```



Colored Country Plot

```
plot(pca$x[,1], pca$x[,2], xlab="PC1(67.4%)", ylab="PC2(29.05%)", xlim=c(-270,500))
text(pca$x[,1], pca$x[,2], colnames(x),col=c("yellow","red","blue","darkgreen"),pch=0, cex=1
```

