### Key takeaways:

Implementing clustering methods

- Hierarchical clustering
- K- medoids clustering
- Spectral clustering

#### Hierarchical clustering

- Load data 'mtcars' available in R mydata <- mtcars</li>
- 2. Understand the summary of data
- 3. Remove the records with missing values in data
- 4. Standardize the data using 'scale' function
- 5. Hierarchical Clustering

```
#Ward Hierarchical Clustering
#First we need to compute the distance matrix
d<-dist(data2,method = "euclidean")
#To see the distances, we needto convert it to matrix
distances<-as.matrix(d)

#Now cluster
fit<-hclust(d,method="single")
plot(fit)

fit <- hclust(d, method="ward")
plot(fit) # display dendogram
groups <- cutree(fit, k=5) # cut tree into 5 clusters
groups
# draw dendogram with red borders around the 5 clusters
rect.hclust(fit, k=5, border="red")
```

#### K-medoids clustering

Please use the below R code as reference and then implement on 'Cereals' data set

# **Spectral Clustering**

Please use the below R code as reference and then implement on 'Cereals' data set

## Jaccard's Distance

Name	Gender	Fever	Cough	Test-1	Test-2	Test-3	Test-4
Jack	M	Y	N	P	N	N	N
Mary	F	Y	N	P	N	P	N
Jim	M	Y	P	N	N	N	N

Identify the symmetric and asymmetric attributes- (Hint: Asymmetric attributes are those categorical attributes in which one level is more important than the other)

Identify which two of the three are closer Jaccard's coefficient:

 $Dist = \frac{number\ of\ dissimilar\ attributes\ between\ the\ records}{number\ of\ dissimilar\ attributes\ +\ number\ of\ similar\ attributes\ (excluding\ records\ with\ 0.0)}$ 

	Data point j 1	Data point j 0
Data point i 1	a	b
0	С	d