

# COMP5310: Principles of Data Science

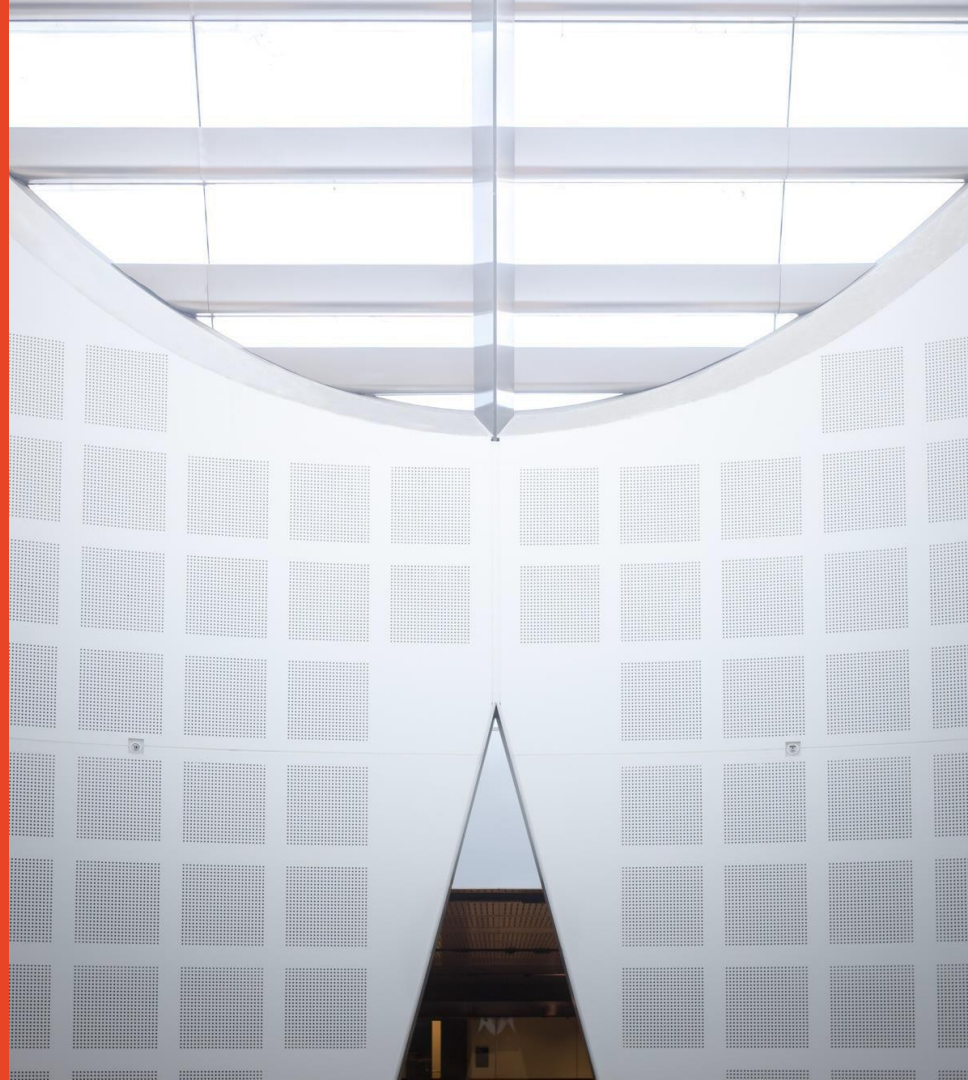
## W8: Clustering and Dimensionality Reduction

**Presented by**

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Based on slides by previous lecturers of this unit of study



# Last week: Association Rule Mining

## Objective

Learn techniques for unsupervised learning, with tools in Python.

## Lecture

- Association rule mining

## Readings

- Intro to Data Mining, Ch. 5  
[https://www-users.cse.umn.edu/~kumar001/dmbook/ch5\\_association\\_analysis.pdf](https://www-users.cse.umn.edu/~kumar001/dmbook/ch5_association_analysis.pdf)
- Data Science from Scratch, Ch. 11

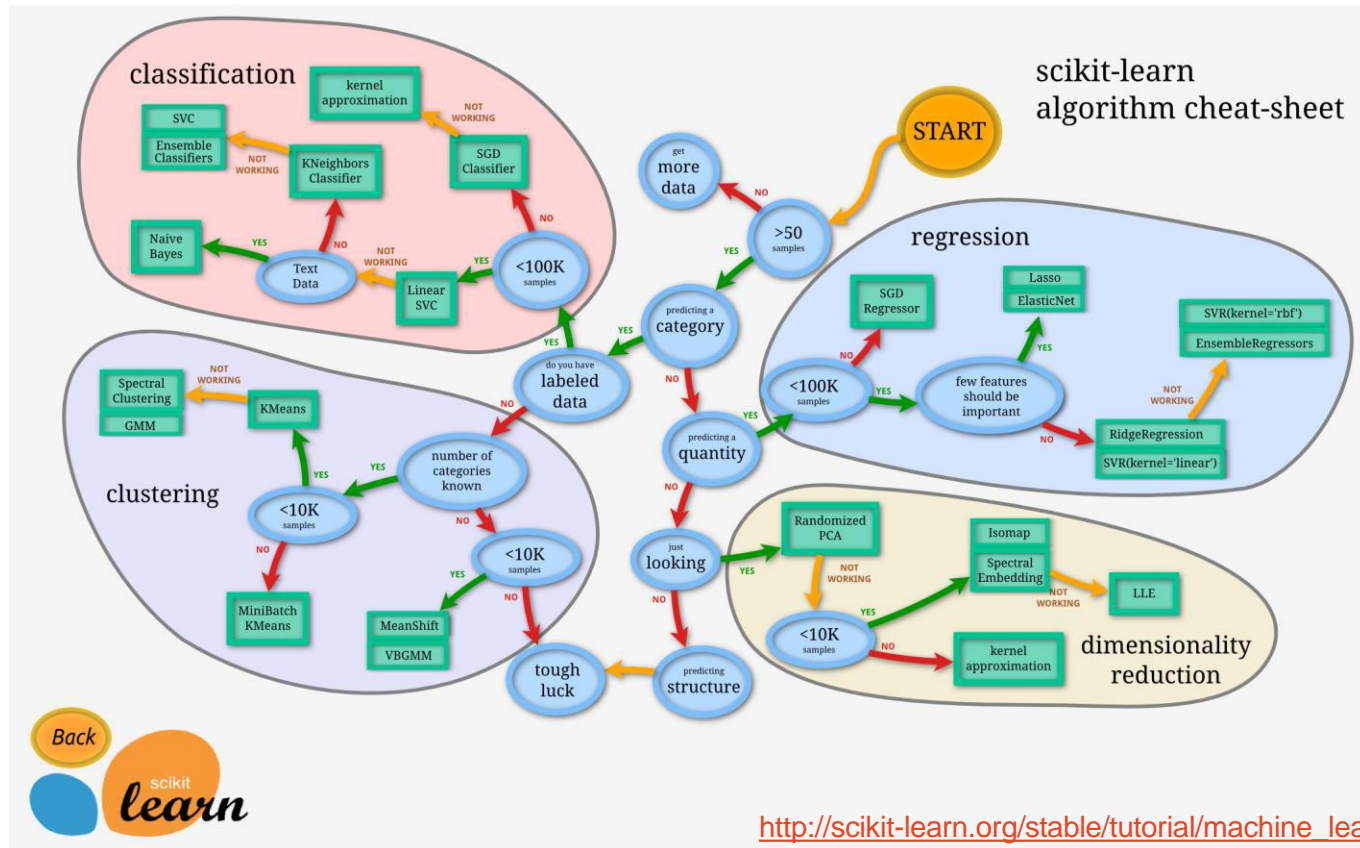
## Exercises

- Associations from scratch
- Associations using mlxtend
- Associations using pyfpgrowth

# Unsupervised Learning:

- We'll focus on **unsupervised** machine learning techniques
  - ☑ *Association rule mining*
  - **Clustering**
  - **Dimensionality reduction**
  - Outlier detection
  - Etc.

# Machine Learning Map from Scikit-learn



[http://scikit-learn.org/stable/tutorial/machine\\_learning\\_map/](http://scikit-learn.org/stable/tutorial/machine_learning_map/)

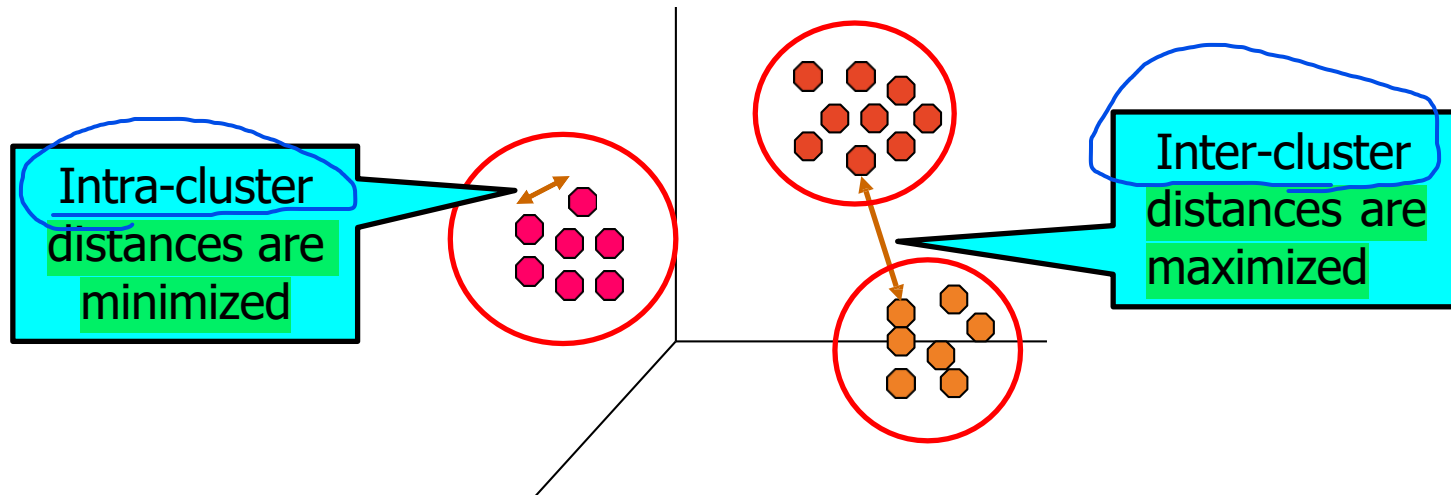
# Clustering

# Clustering for Understanding

- Group related documents for browsing
- Group genes, proteins, or cells that have similar functionality
- Group stocks with similar price fluctuations
- etc

# Clustering: Group Similar Objects

- Group data points into clusters such that
  - Data points in one cluster are more similar to one another.
  - Data points in separate clusters are less similar to one another.
  - Distance function specifies the “closeness” of two objects.



# Similarity and Dissimilarity Between Objects

- Distances are normally used to measure the similarity or dissimilarity between two data objects
- Some popular ones include: *Minkowski distance*:

$$d(i, j) = \sqrt[q]{|x_{i1} - x_{j1}|^q + |x_{i2} - x_{j2}|^q + \cdots + |x_{ip} - x_{jp}|^q}$$

where  $x_i = (x_{i1}, x_{i2}, \cdots, x_{ip})$  and  $x_j = (x_{j1}, x_{j2}, \cdots, x_{jp})$  are two  $p$ -dimensional data objects, and  $q$  is a positive integer

- If  $q = 1$ ,  $d$  is Manhattan distance

$$d(i, j) = |x_{i1} - x_{j1}| + |x_{i2} - x_{j2}| + \cdots + |x_{ip} - x_{jp}|$$



## Similarity and Dissimilarity Between Objects (Cont.)

- If  $q = 2$ ,  $d$  is Euclidean distance:

*L2 norm*

$$d(i, j) = \sqrt{|x_{i1} - x_{j1}|^2 + |x_{i2} - x_{j2}|^2 + \dots + |x_{ip} - x_{jp}|^2}$$

- Properties

- $d(i, j) \geq 0$
- $d(i, i) = 0$
- $d(i, j) = d(j, i)$
- $d(i, j) \leq d(i, k) + d(k, j)$

# Data Structures

## – Data matrix

n-observations with p-attributes (measurements).

## – Dissimilarity matrix $d(i, j)$ is the dissimilarity between objects i and j

– expresses the pairwise dissimilarities (distances) between observations in the data set

– the desired data input to some clustering algorithm

attributes/dimensions

	$x_{11}$	...	$x_{1f}$	...	$x_{1p}$
	...	...	...	...	...
	$x$		$if$		$ip$
	...	...	...	...	...
	$x_{n1}$	...	$x_{nf}$	...	$x_{np}$

tuples/objects

			objects	
	0			
	$d(2,1)$	0		
	$d(3,1)$	$d(3,$	0	
	:	(,1)	(	
	,2)	...	...	
				0

objects

# Types of Clusterings

Important distinction between **hierarchical** and **partitional** sets of clusters

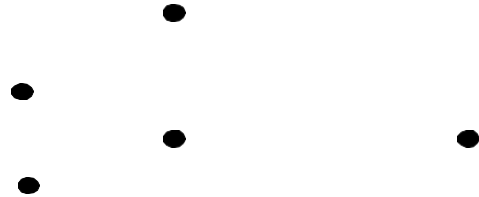
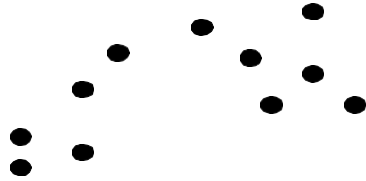
- ***Partitional clustering***

A division of data objects into non-overlapping subsets (clusters) such that each data object is in exactly one subset

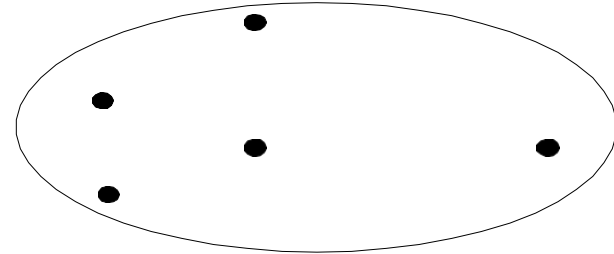
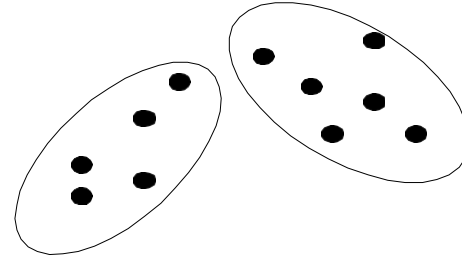
- ***Hierarchical clustering***

A method of cluster analysis which seeks to build a hierarchy of clusters. It produces a set of nested clusters organized as a hierarchical tree

# Partitional Clustering



Original Points



A Partitional Clustering

# Partitional Clustering: K-Means Clustering

- Number of clusters,  $k$ , must be specified
- Each cluster is associated with a centroid (center point)
- Each point is assigned to the cluster with the closest centroid
- The basic algorithm is very simple

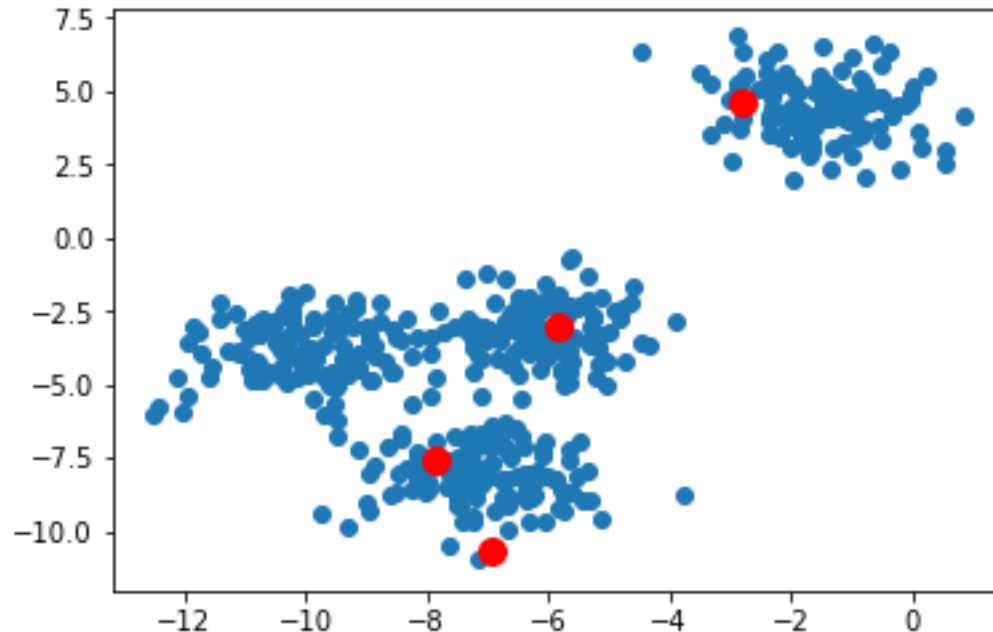
- 
- 1: Select  $K$  points as the initial centroids.
  - 2: **repeat**
  - 3:   Form  $K$  clusters by assigning all points to the closest centroid.
  - 4:   Recompute the centroid of each cluster.
  - 5: **until** The centroids don't change
-

# K-Means Clustering – Details

- Initial centroids are often chosen randomly
- Clusters produced vary from one run to another
- K-means will converge for common similarity measures
- Most of the convergence happens in the first few iterations
- Complexity is  $O(n \times k \times i \times d)$ 
  - $n$  = number of points,  $k$  = number of clusters,  
 $i$  = number of iterations,  $d$  = number of attributes (or dimensions)

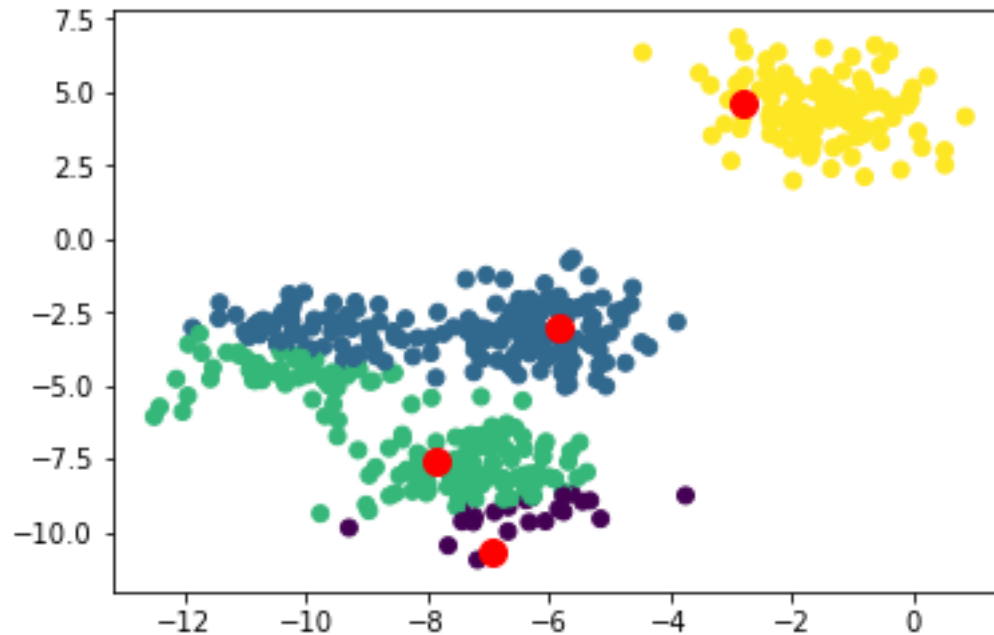
# K-Means Example

- Number of clusters:  $K = 4$
- Initialize 4 centroids randomly



## K-Means Example (Cont.)

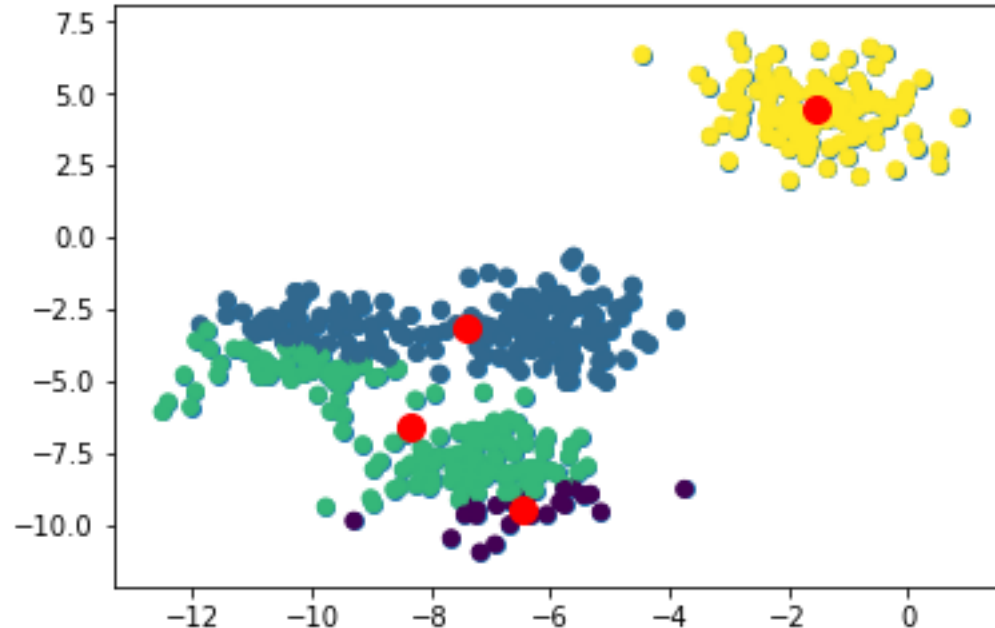
- Assigned each point to the cluster with the closest centroid





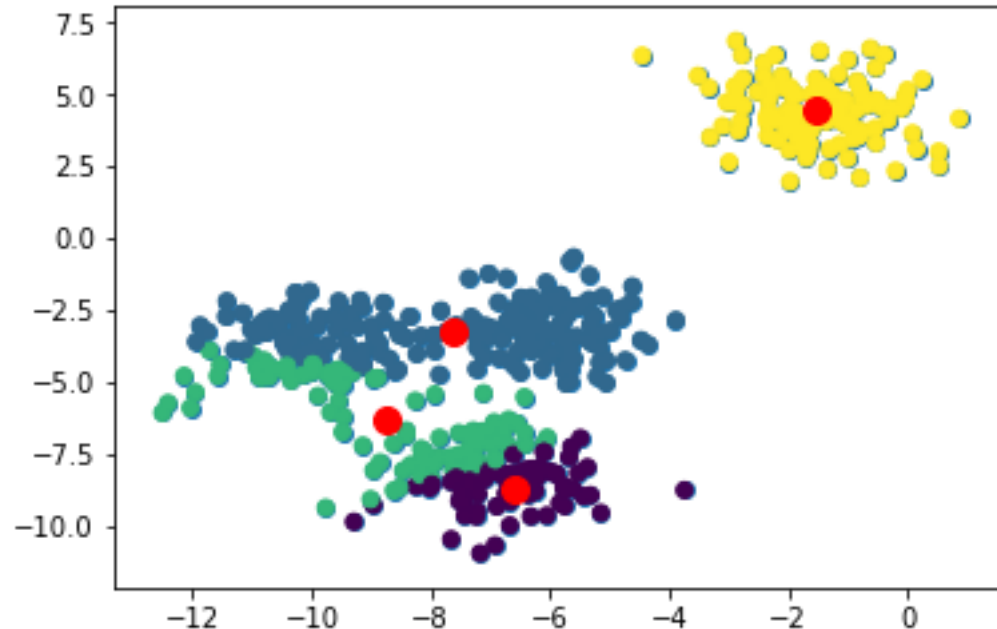
## K-Means Example (Cont.)

- Re-compute each cluster center to be the mean of the points previously assigned.



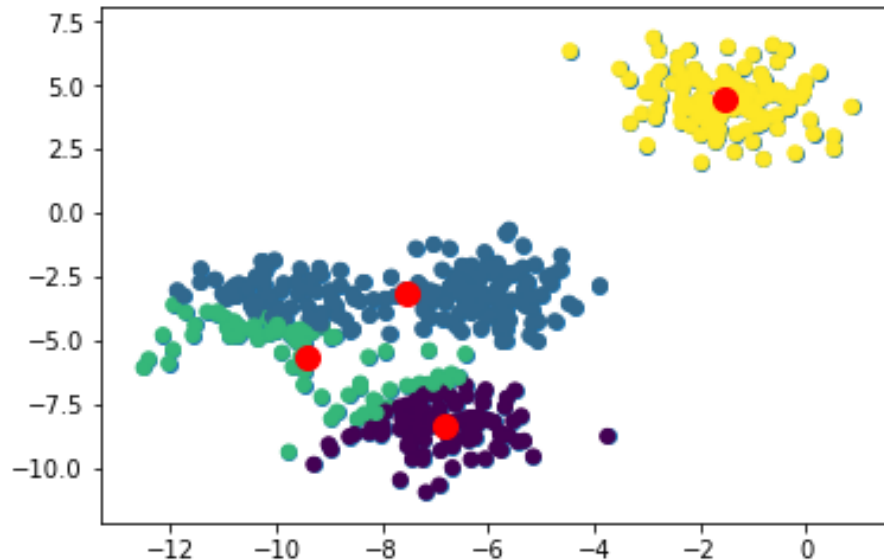
## K-Means Example (Cont.)

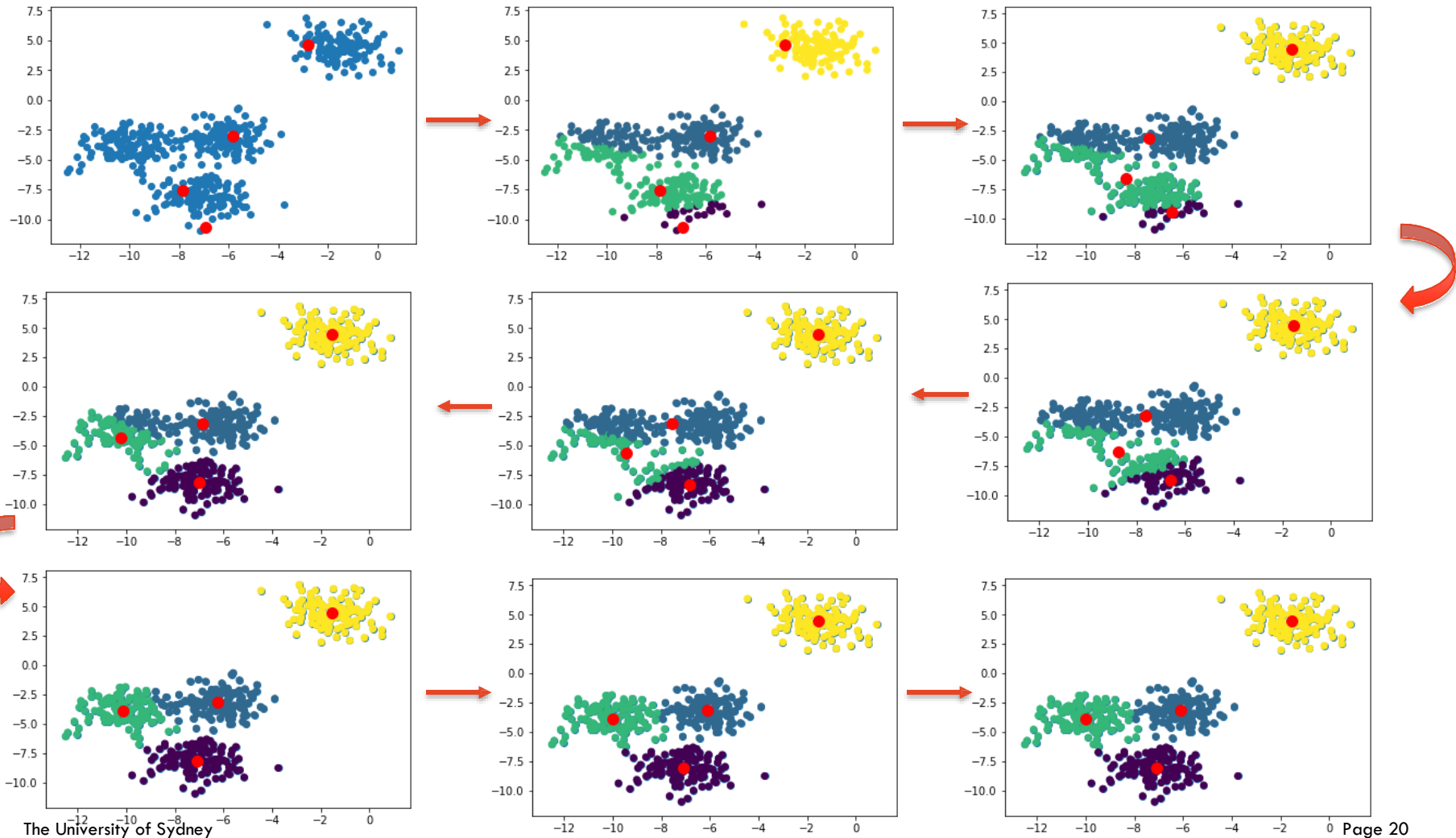
- Assigned each point to the cluster with the closest centroid



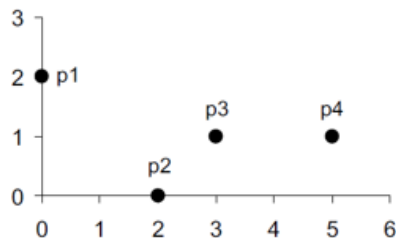
## K-Means Example (Cont.)

- Re-compute each cluster center
- Centroid changed?
  - Assigned each point to the cluster with the closest centroid
  - Re-compute each cluster center





point	x	y
p1	0	2
p2	2	0
p3	3	1
p4	5	1



Pairwise Euclidean Distances:

1. p1-p2

$$\sqrt{(2-0)^2 + (0-2)^2} = \sqrt{4+4} = \sqrt{8} \approx 2.83$$

4. p2-p3

$$\sqrt{(3-2)^2 + (1-0)^2} = \sqrt{1+1} = \sqrt{2} \approx 1.41$$

2. p1-p3

$$\sqrt{(3-0)^2 + (1-2)^2} = \sqrt{9+1} = \sqrt{10} \approx 3.16$$

5. p2-p4

$$\sqrt{(5-2)^2 + (1-0)^2} = \sqrt{9+1} = \sqrt{10} \approx 3.16$$

3. p1-p4

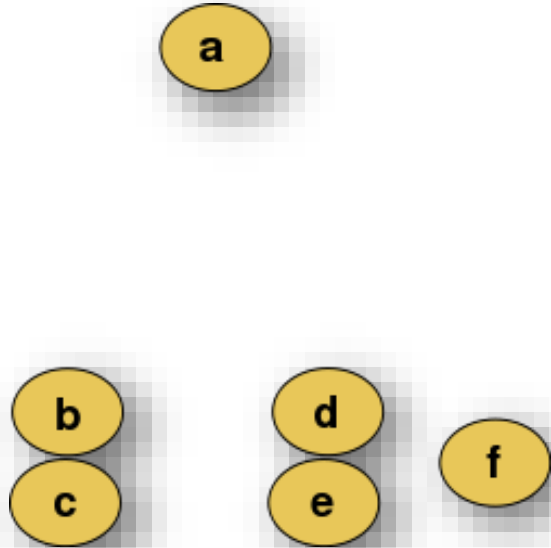
$$\sqrt{(5-0)^2 + (1-2)^2} = \sqrt{25+1} = \sqrt{26} \approx 5.10$$

6. p3-p4

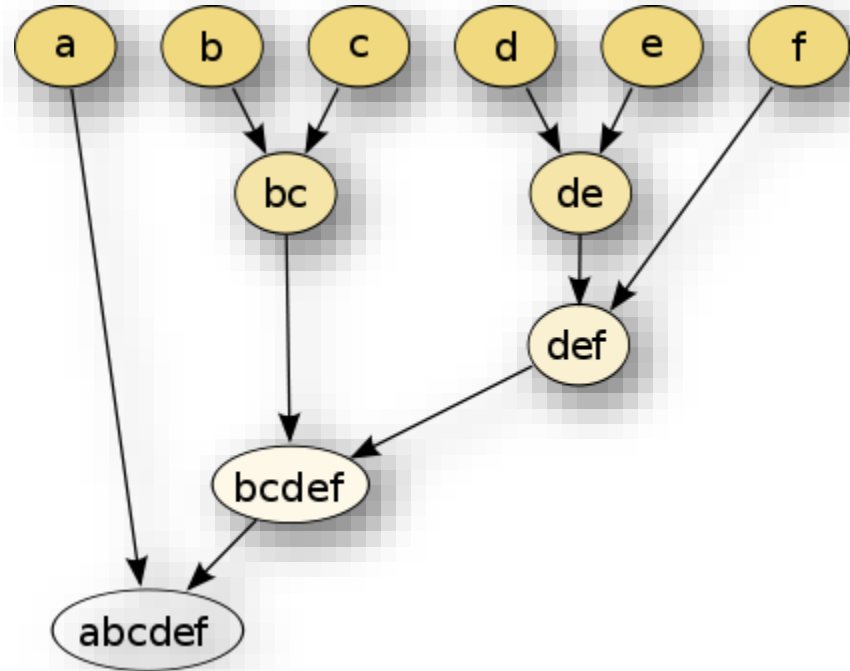
$$\sqrt{(5-3)^2 + (1-1)^2} = \sqrt{4+0} = \sqrt{4} = 2.00$$

L2	p1	p2	p3	p4
p1	0	2.828	3.162	5.099
p2	2.828	0	1.414	3.162
p3	3.162	1.414	0	2
p4	5.099	3.162	2	0

# Hierarchical Clustering



Original Data Items



Hierarchical Clustering

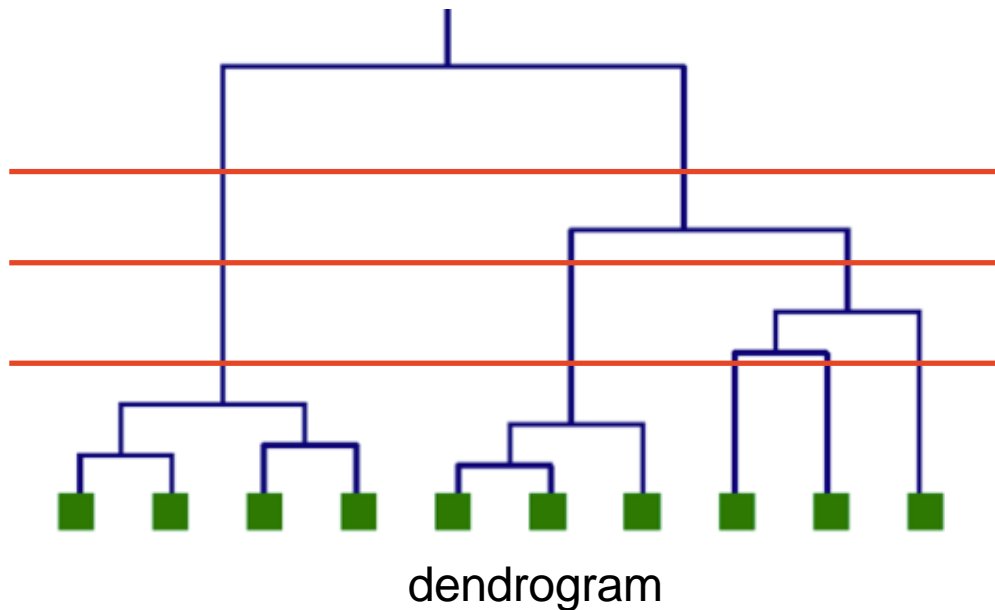
# Hierarchical Clustering

Strategies for hierarchical clustering generally fall into two types:

- **Agglomerative:** This is a "bottom up" approach: each object starts in its own cluster, and pairs of clusters are merged as one moves up the hierarchy.
- **Divisive:** This is a "top down" approach: all objects start in the same cluster, and splits are performed recursively as one moves down the hierarchy.

# Hierarchical Clustering: e.g. Agglomerative

- Initial
  - Each point in its own cluster
- Repeat
  - Find closest pair of clusters
    - Min-distance between any two points
  - Merge them into one cluster
  - Recompute distances between new cluster and others
- Until
  - Desired number of clusters remaining e.g. single cluster

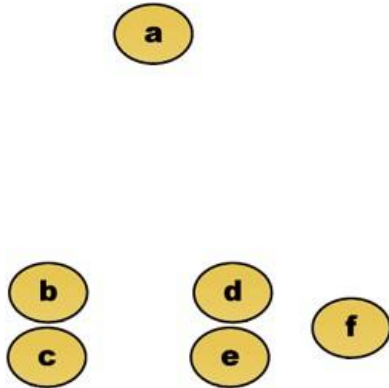




# Hierarchical Algorithm

## Steps in Hierarchical Algorithm:

- The first step generates the distance calculation matrix for each data item as shown in table below, in this case: {a}, {b}, {c}, {d}, {e}, {f}.



	a	b	c	d	e	f
a	0	184	222	177	216	231
b	184	0	45	123	128	200
c	222	45	0	129	121	203
d	177	123	129	0	46	83
e	216	128	121	46	0	83
f	231	200	203	83	83	0

# Hierarchical Algorithm

- Next step is to merge the closest data items.
  - In this case: {b , c} are merged.
  - Therefore, the first clustering process generates: {a}, {b, c}, {d},{e},{f}.

	a	b	c	d	e	f
a	0	184	222	177	216	231
b	184	0	45	123	128	200
c	222	45	0	129	121	203
d	177	123	129	0	46	83
e	216	128	121	46	0	83
f	231	200	203	83	83	0



	a	b,c	d	e	f
a	0	?	177	216	231
b,c	?	0	?	?	?
d	177	?	0	46	83
e	216	?	46	0	83
f	231	?	83	83	0

# Hierarchical Algorithm

## Distance Calculation between **two clusters**:

- single linkage:
  - The minimum distance between elements of the two clusters
- complete linkage:
  - The maximum distance between elements of the two clusters
- average linkage: i.e. mean distance calculation.

# Hierarchical Algorithm with Single Linkage

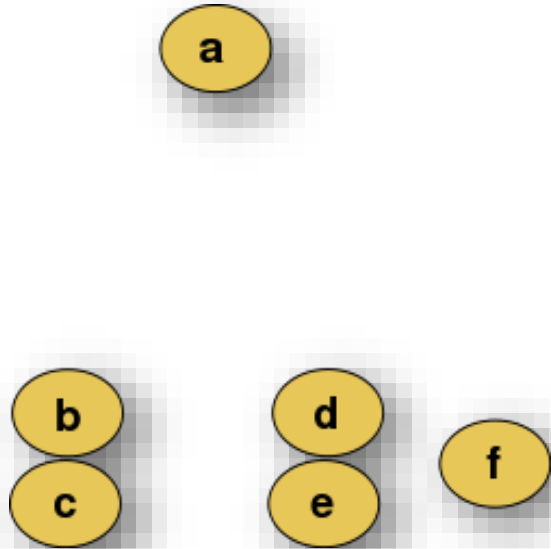
- Repeat the distance calculation process based on single linkage
- Apply merging process based on previous merged results.
  - In this case: {d, e} are merged.
- The final results are: {a}, {b, c} {d, e} {f} → {a}, {b, c}, {d, e, f} → {a}, {b, c, d, e, f} → {a, b, c, d, e, f}

	a	b	c	d	e	f
a	0	184	222	177	216	231
b	184	0	45	123	128	200
c	222	45	0	129	121	203
d	177	123	129	0	46	83
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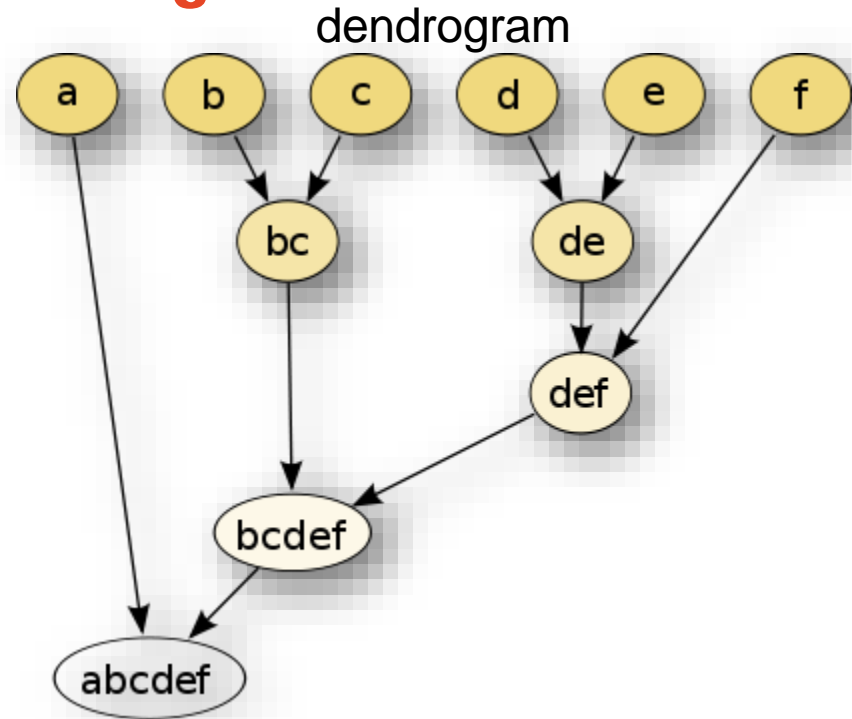


	a	b, c	d	e	f
a	0	184	177	216	231
b, c	184	0	123	121	200
d	177	123	0	46	83
e	216	121	46	0	83
f	231	200	83	83	0

# Resultant Hierarchical Clustering



Original Data Items



Hierarchical Clustering

# Evaluating Clustering

# Cluster Validity

- For supervised classification, we have a variety of measures to evaluate how good our model is (accuracy, precision, recall) –
- For cluster analysis, the analogous question is how to evaluate the “goodness” of the resulting clusters.
- While clusters are in the eye of the beholder, we may still want to evaluate them...
  - To avoid finding patterns in noise
  - To compare clustering algorithms
  - To compare two sets of clusters
- <https://scikit-learn.org/stable/modules/clustering.html#clustering-performance-evaluation>

# Measures of Cluster Validity

Numerical measures that are applied to judge various aspects of cluster validity, are classified into the following three types.

- **External Index:** Measure the extent to which cluster labels match externally supplied class labels (e.g., accuracy, precision, recall, F1-score)
- **Internal Index:** Measure the goodness of a clustering structure *without* respect to external information (e.g., Sum of Squared Error)
- **Relative Index:** Compare two different clusterings or clusters (often an external or internal index is used)



# External Evaluation Measures

- **Homogeneity** ranges from 0 to 1, preferring each cluster contains only members of a single class.  
(analogous to precision,  $P = TP / (TP+FP)$  )
- **Completeness** ranges from 0 to 1, preferring all members of a given class are assigned to the same cluster  
(analogous to recall,  $R = TP / (TP+FN)$  )
- **V-measure** is the harmonic mean of homogeneity and completeness  
(analogous to F1 score =  $2PR / (P+R)$ )
- <http://scikit-learn.org/stable/modules/clustering.html#homogeneity-completeness-and-v-measure>

## Internal: Sum of Squared Error (SSE)

- For each point, the error is the distance to the nearest cluster
- To get SSE, we square these errors and sum them.

$$SSE = \sum_{i=1}^K \sum_{x \in C_i} dist^2(x, m_i)$$

- $x$  is a data point in cluster  $C_i$  and  $m_i$  is the centroid point (mean) for cluster  $C_i$

## SSE Example

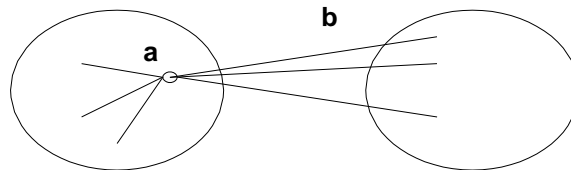
- Suppose we have 3 clusters:
  - Cluster 1: [2, 4] with centroid at 3
  - Cluster 2: [5, 6, 7] with centroid at 6
  - Cluster 3: [8, 10, 12] with centroid at 10
- Squared error for each cluster:
  - $SE1 = (2-3)^2 + (4-3)^2 = 1 + 1 = 2$
  - $SE2 = (5-6)^2 + (7-6)^2 = 1 + 1 = 2$
  - $SE3 = (8-10)^2 + (12-10)^2 = 4 + 4 = 8$
- $SSE = SE1 + SE2 + SE3 = 12$

# Internal: Silhouette Coefficient

- For an individual point  $x$ 
  - Calculate  $a$  = average distance of  $x$  to points in its cluster
  - Calculate  $b$  = average distance of  $x$  to points in the next nearest cluster
  - The silhouette coefficient for a point is then given by

$$s = 1 - a/b \quad \text{if } a < b, \quad (\text{or } s = b/a - 1 \quad \text{if } a \geq b, \text{ not the usual case})$$

- The closer to 1 the better



- Silhouette coefficient for dataset is average across all *data points*

# Silhouette Coefficient Example

- Suppose we have 3 clusters:
  - Cluster 1 = [ [1,0], [1,1] ]
  - Cluster 2 = [ [1,2], [2,3], [2,2], [1,2] ],
  - Cluster 3 = [ [3,1], [3,3], [2,1] ]
- Take a point [1,0] in cluster 1
- Calculate its average distance to all other points in its cluster, i.e. cluster 1
- So  $a_1 = \sqrt{(1-1)^2 + (0-1)^2} = \sqrt{0+1} = 1$

## Silhouette Coefficient Example (Cont.)

- Now for the point  $[1,0]$  in cluster 1 calculate its average distance from all the points in cluster 2 and cluster 3.
- Of these take the minimum average distance.
- So for cluster 2:
  - $[1,0] \rightarrow [1,2]$ , distance  $= \sqrt{(1-1)^2 + (0-2)^2} = \sqrt{0+4} = 2$
  - $[1,0] \rightarrow [2,3]$ , distance  $= \sqrt{(1-2)^2 + (0-3)^2} = \sqrt{1+9} = 3.16$
  - $[1,0] \rightarrow [2,2]$ , distance  $= \sqrt{(1-2)^2 + (0-2)^2} = \sqrt{1+4} = 2.24$
  - $[1,0] \rightarrow [1,2]$ , distance  $= \sqrt{(1-1)^2 + (0-2)^2} = \sqrt{0+4} = 2$
- Therefore, the average distance of point  $[1,0]$  in cluster 1 to all the points in cluster 2  $= (2+3.16+2.24+2)/4 = 2.35$

## Silhouette Coefficient Example (Cont.)

- Similarly, for cluster 3.
  - $[1,0] \rightarrow [3,1]$ , distance  $= \sqrt{(1-3)^2 + (0-1)^2} = \sqrt{4+1} = 2.24$
  - $[1,0] \rightarrow [3,3]$ , distance  $= \sqrt{(1-3)^2 + (0-3)^2} = \sqrt{4+9} = 3.61$
  - $[1,0] \rightarrow [2,1]$ , distance  $= \sqrt{(1-2)^2 + (0-1)^2} = \sqrt{1+1} = 1.41$
- Therefore, the average distance of point  $[1,0]$  in cluster 1 to all the points in cluster 3  $= (2.24+3.61+1.41)/3 = 2.42$
- Now, the minimum average distance of the point  $[1,0]$  in cluster 1 to the other clusters 2 and 3 is,  
 $b_1 = 2.35 \text{ (} 2.35 < 2.42 \text{)}$

## Silhouette Coefficient Example (Cont.)

- So the silhouette coefficient of point [1,0] in cluster 1

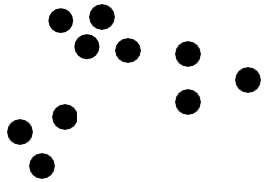
$$s_1 = 1 - (a_1 / b_1) = 1 - (1 / 2.35) = 1 - 0.43 = 0.57$$

- In a similar fashion you need to calculate the silhouette coefficient for each data point in each cluster
- Then we average them to calculate the overall silhouette coefficient to evaluate the resultant clusters
- The closer to 1 the better

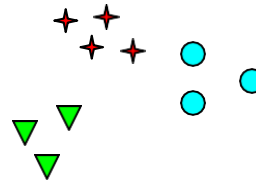
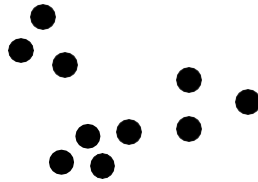


# Choosing $k$

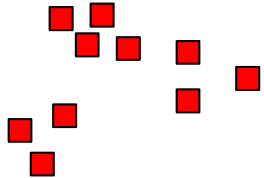
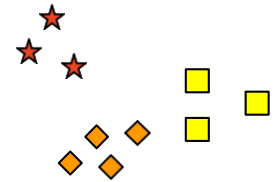
# Notion of a Cluster can be Ambiguous



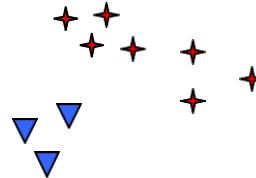
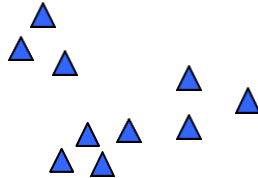
How many clusters..?



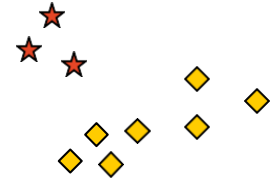
Maybe six clusters



Two clusters?



Or four clusters

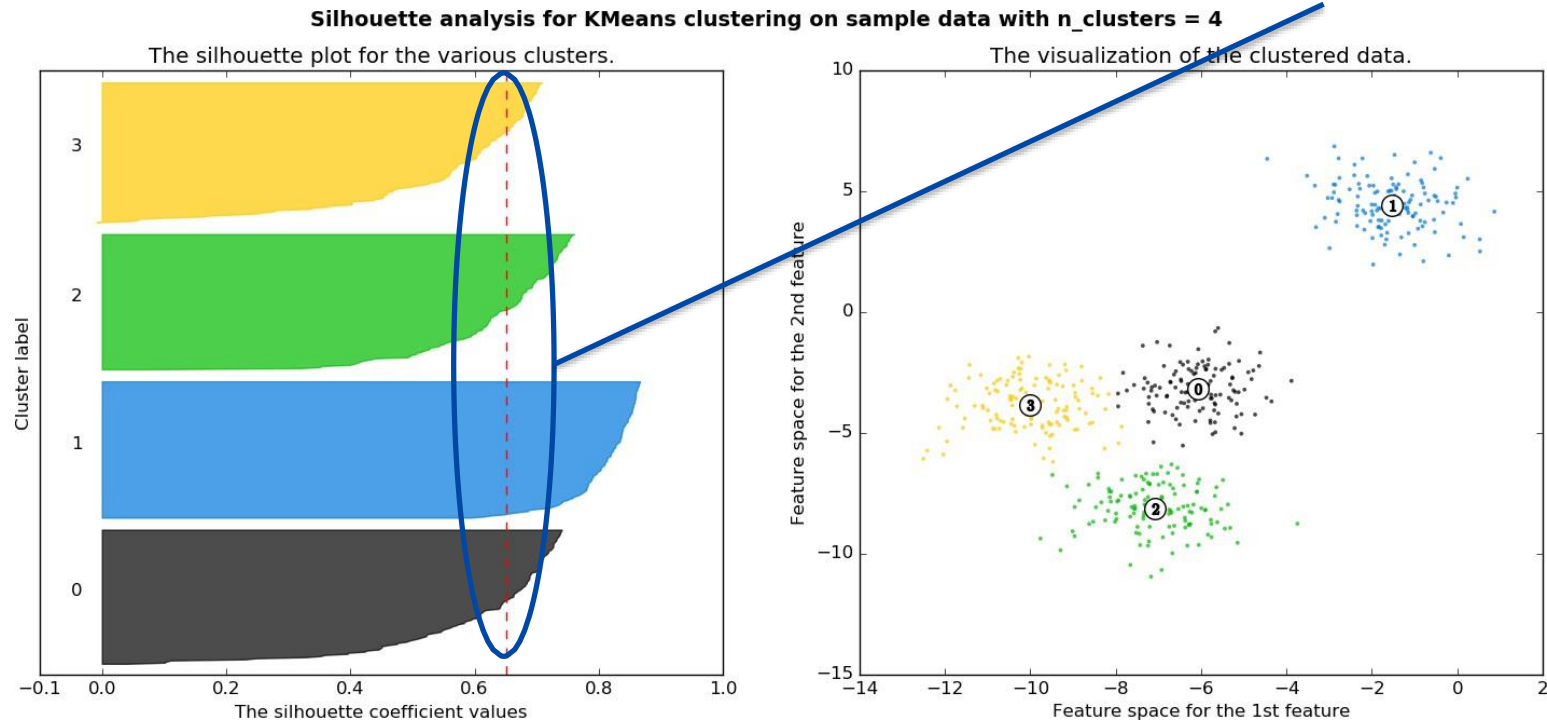


## Choosing $k$

- Often we don't know the number of clusters in our data
- Selecting  $k$  is generally an interactive process
- There are some approaches to aid interactive selection, and sometimes automate it

# Using Silhouettes to choose $k$

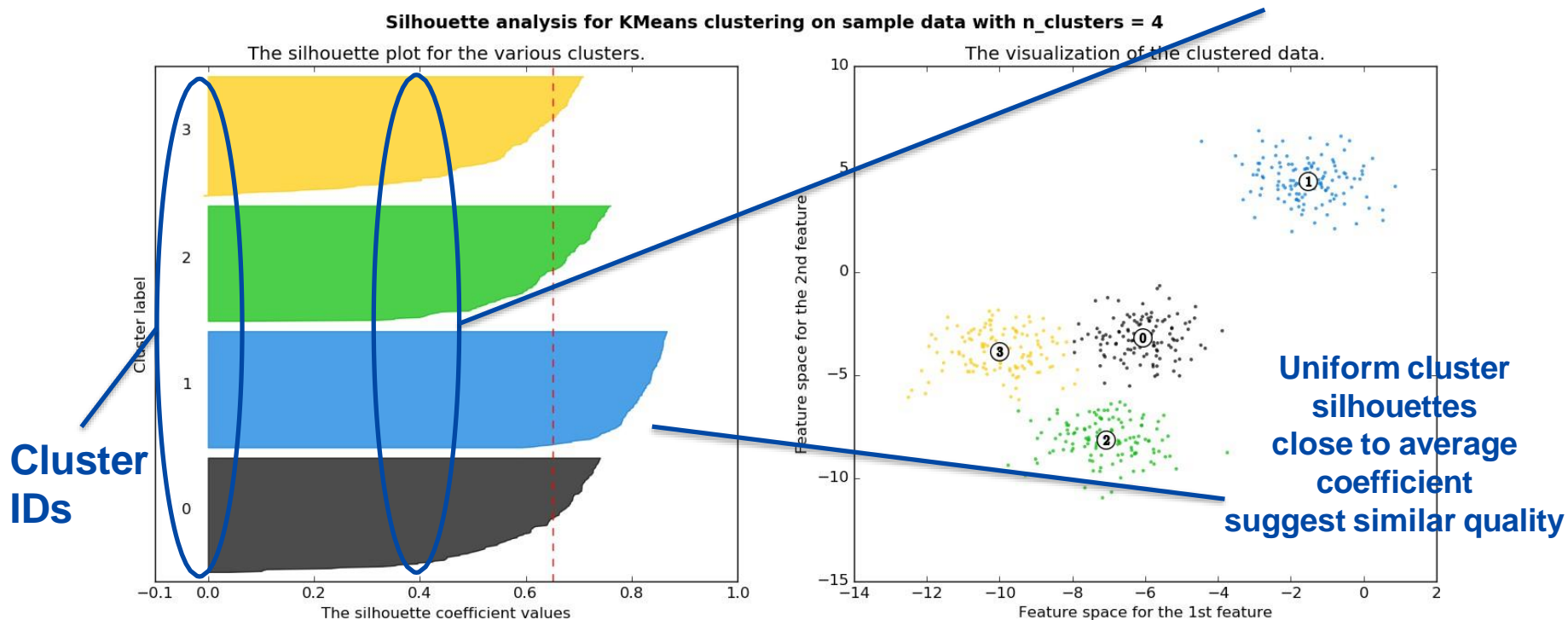
High average silhouette indicates points far away from neighbouring clusters



[http://scikit-learn.org/stable/auto\\_examples/cluster/plot\\_kmeans\\_silhouette\\_analysis.html](http://scikit-learn.org/stable/auto_examples/cluster/plot_kmeans_silhouette_analysis.html)

# Using Silhouettes to choose $k$

Bar chart showing silhouette values for each item grouped by cluster



[http://scikit-learn.org/stable/auto\\_examples/cluster/plot\\_kmeans\\_silhouette\\_analysis.html](http://scikit-learn.org/stable/auto_examples/cluster/plot_kmeans_silhouette_analysis.html)

# Pre-Processing for Clustering

We only looked at choosing  $k$ , but more pre-processing needed

- Data Cleansing
- Data Transformation
- **Data Normalisation**
- **Dimensionality Reduction** / choice or projection of dimensions
  - closely related to choice of **distance metric**
  - we used Euclidean Metric so far ( $L_2$ -Norm)
  - but others possible too, eg. Manhattan Distance ( $L_1$ -Norm)
  - "Curse of high dimensionality"; cf Aggarwal et al.: "On the Surprising Behavior of Distance Metrics in High Dimensional Space", 2001.

# Principal Component Analysis

# Principal Components Analysis

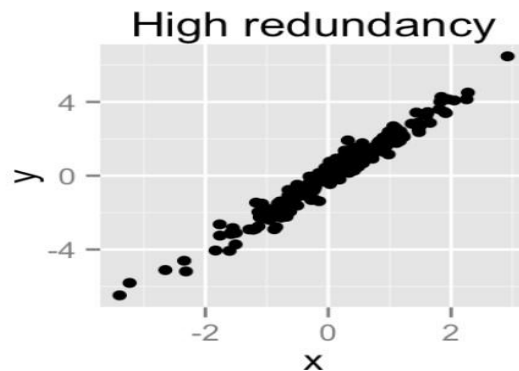
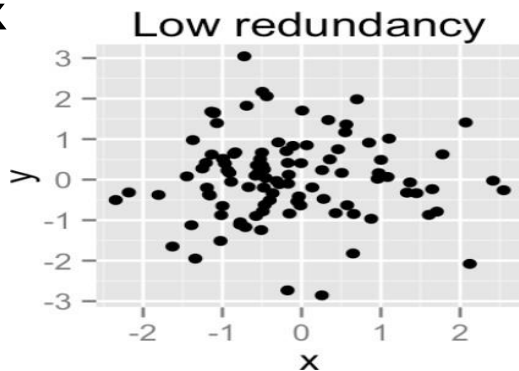
- Aims to transform the original data from high dimensional space into lower dimensional space.
- The new variables in the lower dimensional space corresponds to a linear combination of the originals and are called **principal components (PC)**
- PCA helps in
  - **Visualization.** Using the right variables to plot items will give more insights.
  - **Uncovering Clusters.** With good visualizations, hidden categories or clusters could be identified.
  - **Dimensionality reduction.** Reduce number of dimensions in data



# Principal Components Analysis

- PCA method is particularly useful when the variables within the data set are **highly correlated**.
  - **Correlation** indicates that there is redundancy in the data.
  - Correlation is captured by the **covariance matrix**<sup>1</sup>.
- PCA is traditionally performed on **covariance** matrix or correlation matrix

<sup>1</sup>covariance matrix is a square **matrix** that contains the variances and **covariances** associated with several variables.



# Covariance Matrix

- Representing Covariance between dimensions as a matrix e.g for three attributes (x,y,z):

$$C = \begin{pmatrix} \text{cov}(x, x) & \text{cov}(x, y) & \text{cov}(x, z) \\ \text{cov}(y, x) & \text{cov}(y, y) & \text{cov}(y, z) \\ \text{cov}(z, x) & \text{cov}(z, y) & \text{cov}(z, z) \end{pmatrix}$$

**Variances**

- The covariance between one dimension and itself is the variance
  - Diagonal is the variances of x, y and z
- $\text{cov}(x, y) = \text{cov}(y, x)$  hence matrix is symmetrical about the diagonal
- N-dimensional data will result in NxN covariance matrix

# Covariance Matrix Example

- Below is the covariance matrix of some 3 variables.
- Their variances are on the diagonal, and the sum of the 3 values (3.448) is the overall variability

1.343730	-.1601522	.1864702
-.1601522	.61920562	-.1266842
.1864702	-.1266842	1.485549

- In the covariance table above, the off-diagonal values are different from zero. This indicates the presence of redundancy in the data.
- In other words, there is a certain amount of correlation between variables.

# PCA Example

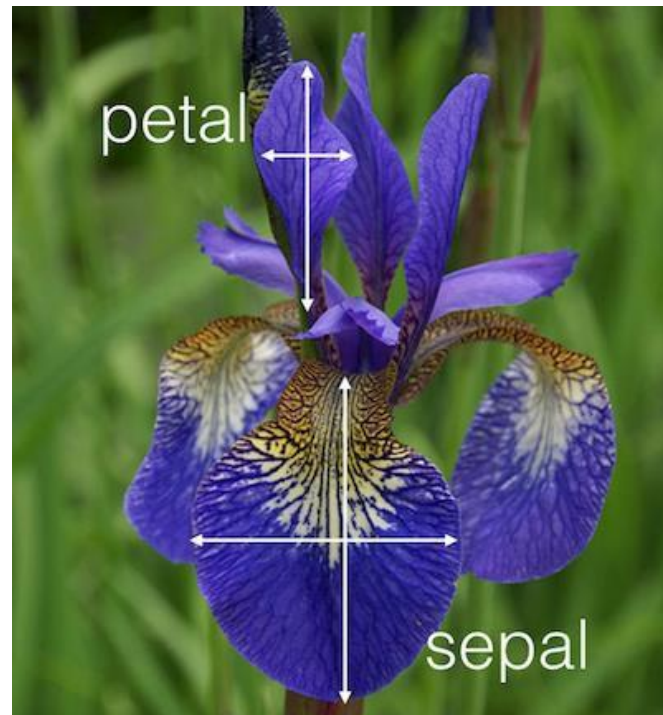
- PCA creates uncorrelated PC variables (called eigenvectors) having zero covariations and variances (called eigenvalues) sorted in decreasing order.
- The first PC captures the greatest variance, the second greatest variance is the second PC, and so on.
- By eliminating the later PCs we can achieve dimensionality reduction.
  - The 1st PC accounts for or "explains"  $1.651/3.448 = 47.9\%$  of the overall variability;
  - the 2nd one explains 35.4% of it; the 3rd one explains 16.7% of it.

1.65135	.000000	.000000
.000000	1.220288	.000000
.000000	.0000000	.576843

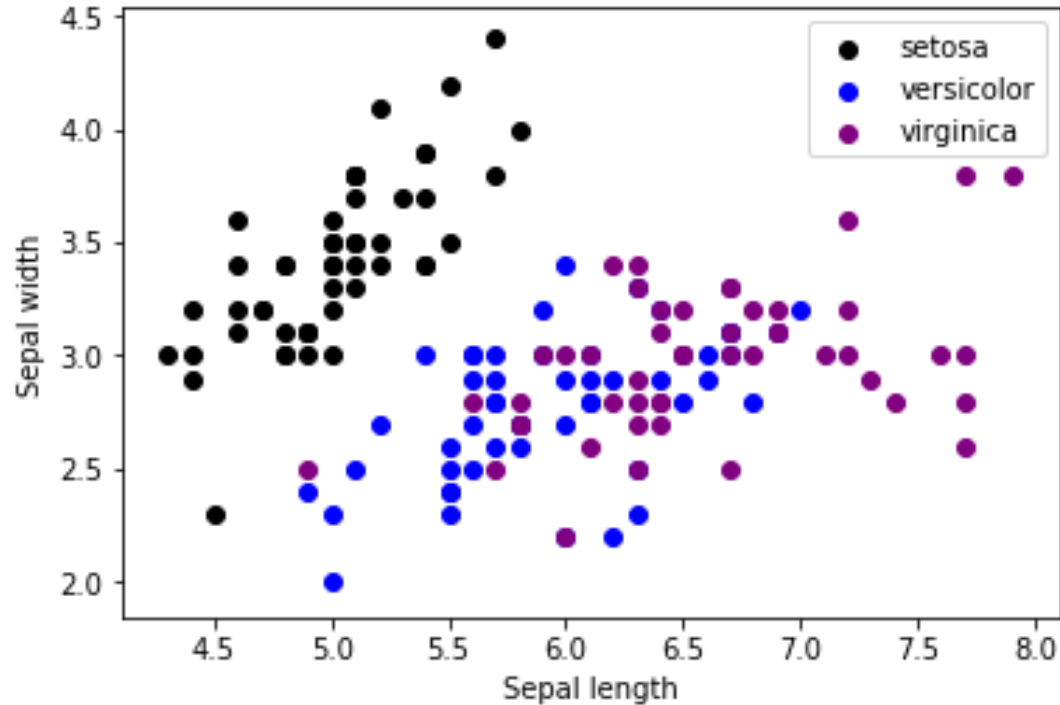
The covariance matrix  
between the principal  
components

# PCA on Iris Dataset

- Iris data has 150 observations equally distributed among three species:  
Setosa, Versicolor and Verginica.
- It has four variables:
  - Sepal length and width
  - Petal length and width
- Which variables can I use to plot the data in two dimensional space?
- Let's try using the two features:  
Sepal length VS. Sepal width



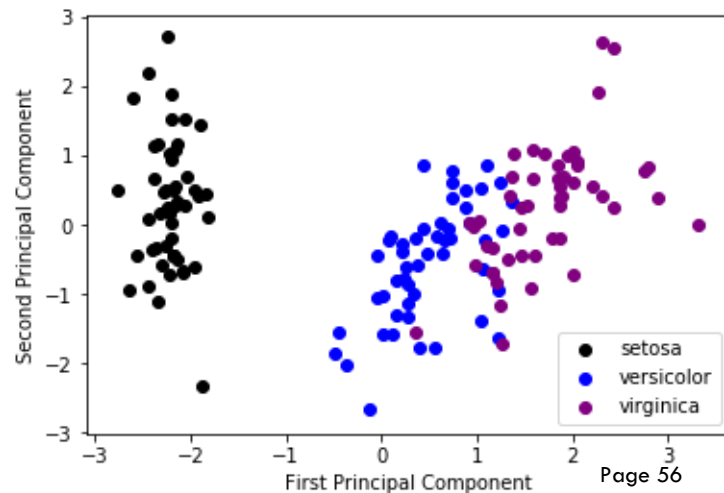
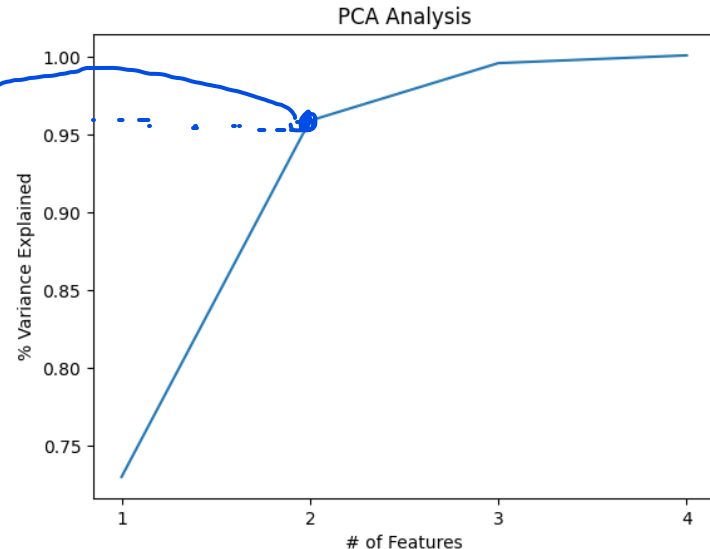
# Plotting the data points using Sepal Length vs Sepal Width



# PCA on IRIS Dataset

- Let's now choose the best variables using PCA and then plot the data
- The eigenvalues are:  
[ 0.728 0.230 0.037 0.005]
- The first two PCs represent 95.8% of the variance of the data
- Which means we can reduce the data into two dimensional spaces by eliminating PC3 and PC4

$$0.728 + 0.230$$
$$0.728 + \dots + 0.005$$



# Review



# W8 review: Clustering and Dimensionality Reduction

## Objective

Learn techniques for unsupervised learning, with tools in Python.

## Lecture

- Clustering algorithms
- Evaluating clustering
- Choosing k
- Principal Component Analysis

## Readings

- Intro to Data Mining, Ch. 7  
[https://www-users.cse.umn.edu/~kumar001/dmbook/ch7\\_clustering.pdf](https://www-users.cse.umn.edu/~kumar001/dmbook/ch7_clustering.pdf)
- Data Science from Scratch, Ch. 20

## Exercises

- sklearn: clustering and PCA