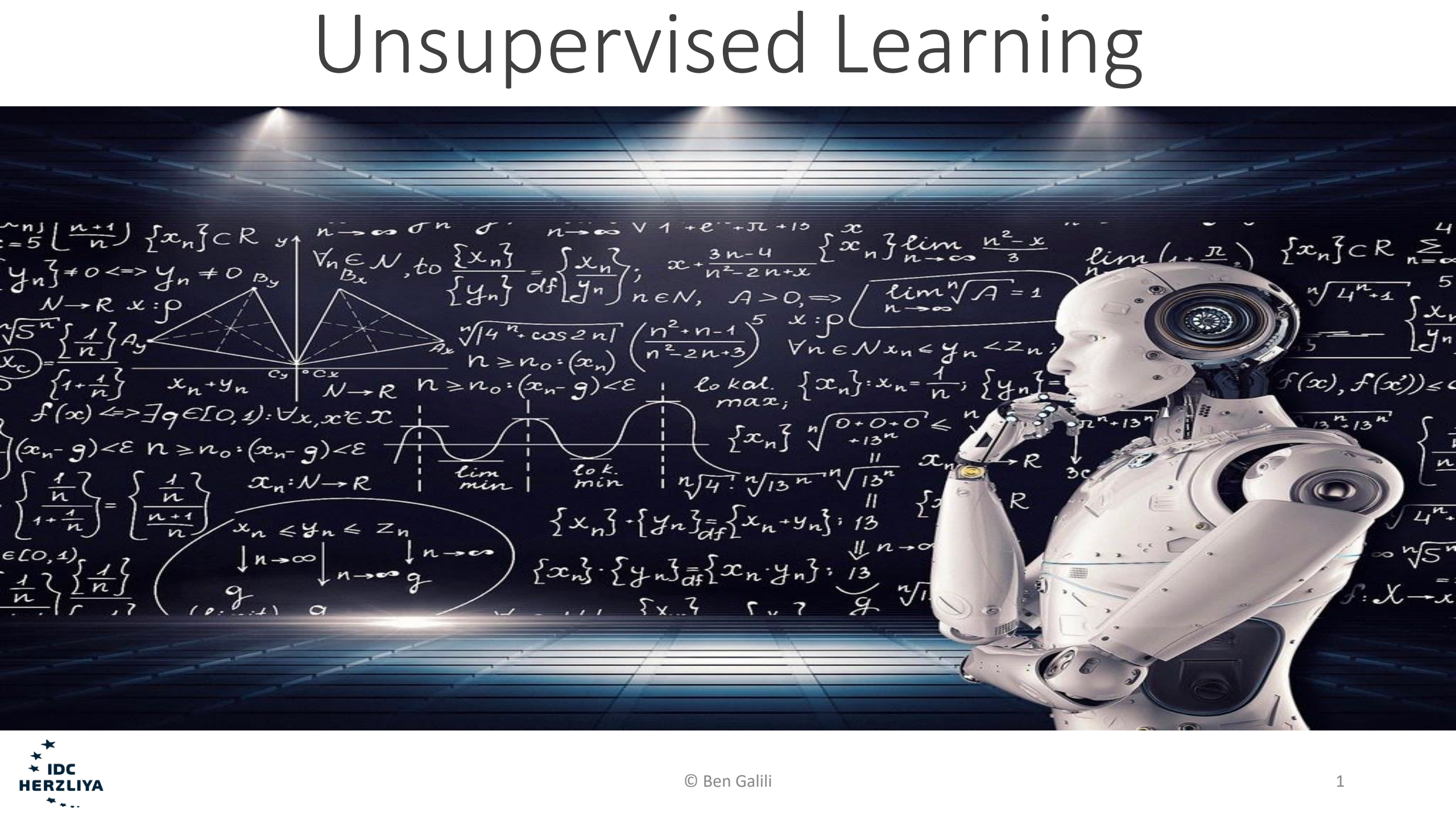


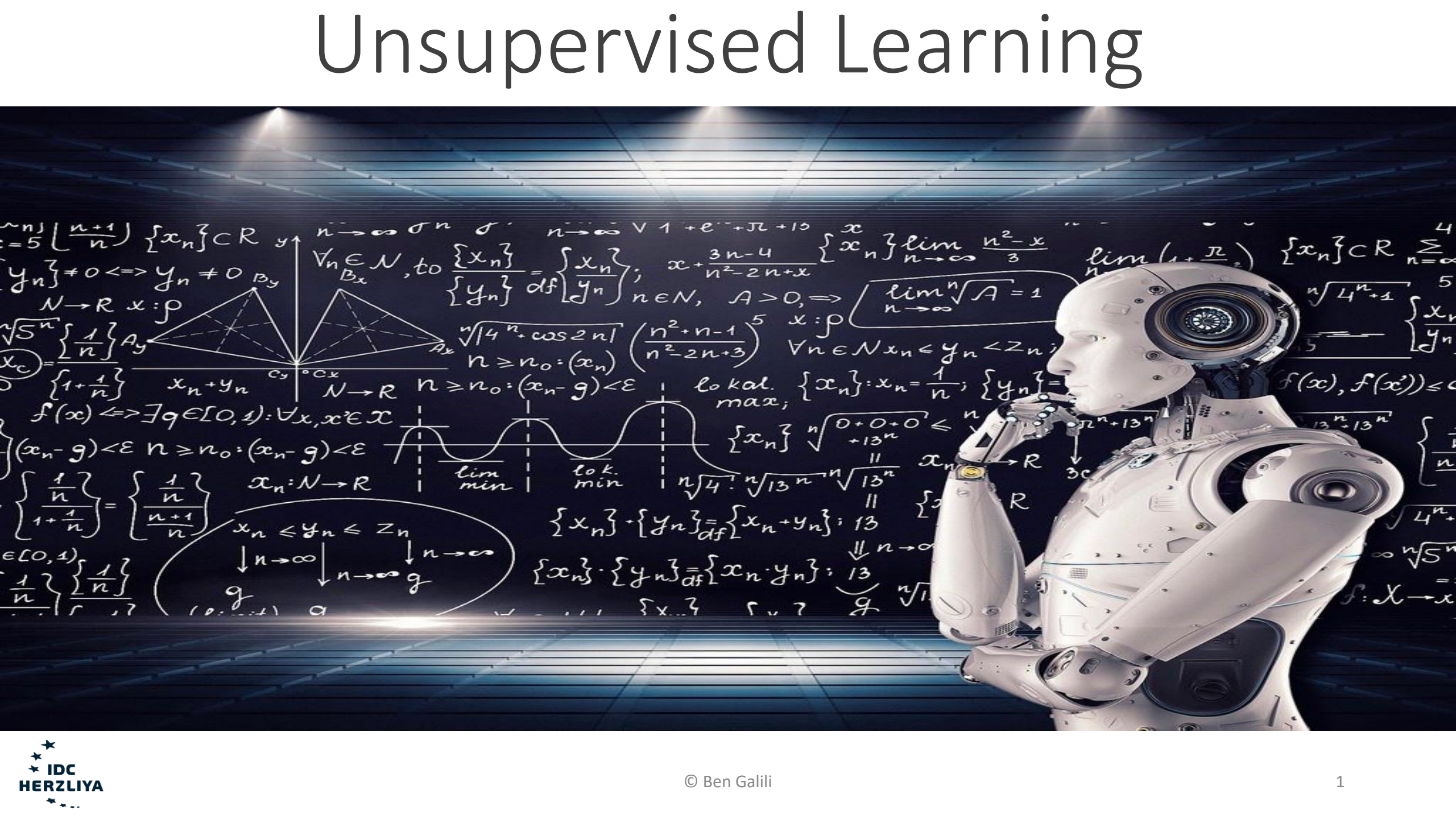
# Unsupervised Learning



The background is a dark, blue-toned space filled with glowing mathematical formulas and geometric diagrams. The formulas include various mathematical expressions such as sequences, limits, and set definitions. The robot is a futuristic, white and blue humanoid figure with a large, circular, glowing eye. It is standing in the foreground, looking towards the left, where the mathematical content is most dense. The overall scene suggests a theme of artificial intelligence and mathematics.

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# The goal

- We don't know the labels of the data
- What can we know about data with no labels?
  - Structure
  - Regularity
  - Grouping
- This means we can find the similarity between the instances
- This is called Unsupervised Learning

# Unsupervised Learning



- The task of inferring a function to describe hidden structure from unlabeled data
- This doesn't mean that there is no “guidance”
- There are several usages for this learning task

# Clustering



- Partition unlabeled examples into subsets of clusters
  - Patterns within a cluster are very similar
  - Patterns in different clusters are very different
- A cluster is a volume of high-density points separated from other clusters by a relatively low-density volumes
- Clustering is all about modeling the underlying structure of the feature space
  - As opposed to supervised learning which aims at minimizing the loss with respect to a specified target (e.g. label, value)

# Clustering



- A clustering algorithm will always find clusters, even if there are none ...
- There is no “best” clustering method
  - But we can tell how good is the solution it provides
- The various approaches may vary in the following
  - Data Representation
  - Similarity Measures
  - Hypotheses Space
  - Objective Function
  - Evaluation criteria for quality and validity of the solution



# Similarity

- How to decide if samples are similar or not?
- We first need to know how to measure similarity
- Distance – the closer the instances are, the more similar they are
  - Non-negativity:
    - $d(x_1, x_2) \geq 0$
  - Identity of indiscernible:
    - $d(x_1, x_2) = 0 \Leftrightarrow x_1 = x_2$
  - Symmetry:
    - $d(x_1, x_2) = d(x_2, x_1)$
  - Triangle inequality:
    - $d(x_1, x_2) \leq d(x_1, x_3) + d(x_3, x_2)$
- We already saw some different distance methods (Manhattan, Euclidean, Infinity Norm)

# Similarity



- How to use the similarity to create clusters?
- Simple approach:
  - Start from randomly selected un-clustered instance and insert it to a new cluster
  - Insert to the cluster all instances that have distance (the similarity measure) lower then some threshold to one of the instances in the cluster – repeat till no instance was added to the cluster
  - Repeat the 2 steps till all the instances were clustered



# Objective function

- We want to achieve 'good' clustering
- How can we know if the partition of the instances to some  $k$  clusters is good or not?
  - Maximize between classes
  - Minimize within classes



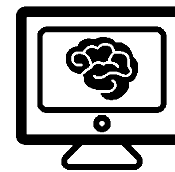
# K-Means



- Centroid-based clustering, clusters are represented by a central vector, which may not necessarily be a member of the data set
- Given a set of observations  $(\mathbf{x}_1, \dots, \mathbf{x}_n)$ , where each  $\mathbf{x}_i$  is a  $d$ -dimensional vector
- Centroid-based algorithms aim to partition the  $n$  observations into  $k$  ( $\leq n$ ) clusters  $\{C_1, \dots, C_k\}$  so as to minimize the within-cluster sum of squares (WCSS):

$$\sum_{i=1}^k \sum_{x \in C_i} \|x - c_i\|^2$$

where  $c_i$  is the cluster center



## Find the best solution

- How many possibility for partition n instances into k clusters?
- There are approximately  $\frac{k^n}{k!}$  ways to partition the n elements into k clusters
- And if we also searching for k

$$\sim \sum_{k=1}^n \frac{k^n}{k!}$$

- Finding the optimal solution to this optimization problem is NP-Hard even for  $k = 2$   
Thus, a variety of heuristic algorithms are generally used



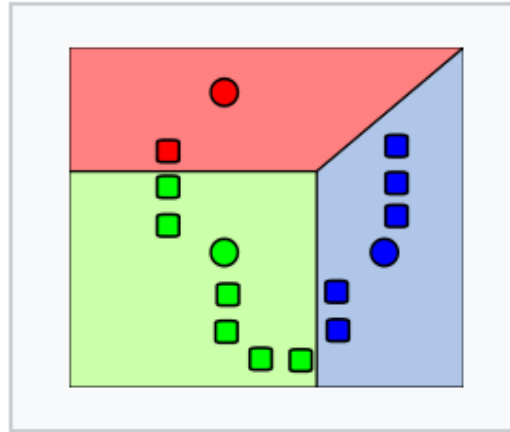
# K-Means

- Initialize randomly the k-means  $\mu_1, \dots, \mu_k$
  - Repeat
    - For each instance
      - Assign it to the nearest cluster w.r.t its mean  $\mu_i$
    - Re-computes  $\mu_i$  for each cluster
  - Until no change in  $\mu_1, \dots, \mu_k$  (or any other stopping condition)
  - Return  $\mu_1, \dots, \mu_k$
- \* Usually uses simple Euclidean distance in feature space

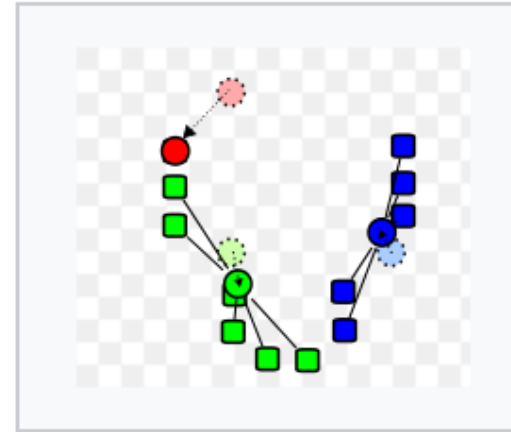
# K-Means Demonstration



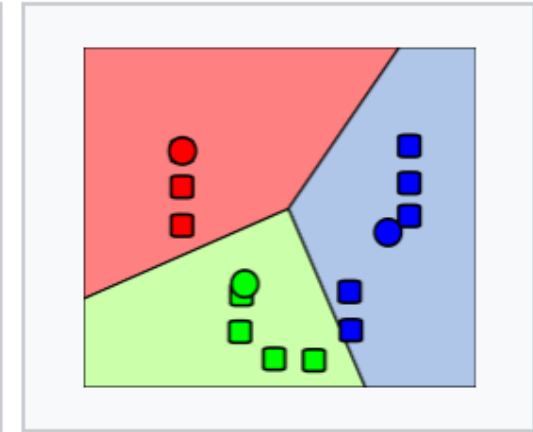
1.  $k=3$  initial "means" are randomly generated within the data domain



2.  $k$  clusters are created by associating every observation with the nearest mean



3. The centroid of each of the  $k$  clusters becomes the new mean



4. Steps 2 and 3 are repeated until convergence has been reached



# K-Means Clustering

- Let's start by generating some blobs:

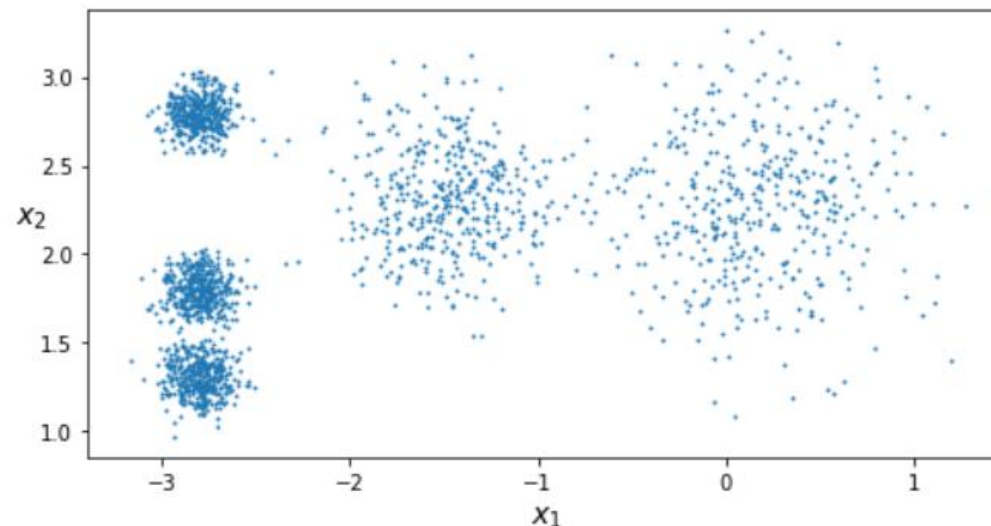
```
from sklearn.datasets import make_blobs

blob_centers = np.array(
    [[ 0.2, 2.3],
     [-1.5, 2.3],
     [-2.8, 1.8],
     [-2.8, 2.8],
     [-2.8, 1.3]])
blob_std = np.array([0.4, 0.3, 0.1, 0.1, 0.1])

X, y = make_blobs(n_samples=2000, centers=blob_centers,
                  cluster_std=blob_std)
```

```
def plot_clusters(X, y=None):
    plt.scatter(X[:, 0], X[:, 1], c=y, s=1)
    plt.xlabel("$x_1$", fontsize=14)
    plt.ylabel("$x_2$", fontsize=14, rotation=0)
```

```
plt.figure(figsize=(8, 4))
plot_clusters(X)
plt.show()
```





# K-Means Clustering

- Let's train a K-Means on this dataset
- It will try to find each blob's center and assign each instance to the closest blob:

```
from sklearn.cluster import KMeans

k = 5
kmeans = KMeans(n_clusters=k, random_state=0)
y_pred = kmeans.fit_predict(X)
y_pred

array([1, 4, 4, ..., 1, 1, 3])
```

- K-Means preserves the labels of the instances it was trained on
- The label of an instance is the index of the cluster that instance gets assigned to:

```
kmeans.labels_

array([1, 4, 4, ..., 1, 1, 3])
```

```
y_pred is kmeans.labels_

True
```



# K-Means Clustering

- The **cluster\_centroids\_** variable holds the 5 centroids (cluster centers):

```
kmeans.cluster_centers_
```

```
array([[-2.80379109,  1.30017997],  
       [ 0.17864202,  2.27506362],  
       [-2.80180006,  2.79464334],  
       [-1.46332098,  2.31083369],  
       [-2.80446936,  1.79959228]])
```

- Of course, we can predict the labels of new instances:

```
X_new = np.array([[0, 2], [3, 2], [-3, 3], [-3, 2.5]])  
kmeans.predict(X_new)
```

```
array([1, 1, 2, 2])
```

# Decision Boundaries

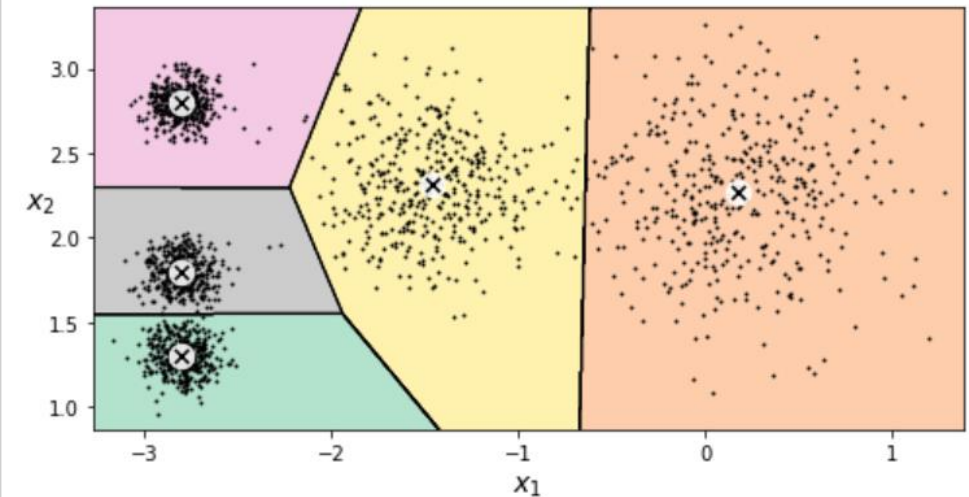


- Let's plot the model's decision boundaries. This gives us a *Voronoi diagram*:

```
def plot_decision_boundaries(clusterer, X, resolution=1000,
                             show_centroids=True):
    mins = X.min(axis=0) - 0.1
    maxs = X.max(axis=0) + 0.1
    xx, yy = np.meshgrid(np.linspace(mins[0], maxs[0], resolution),
                          np.linspace(mins[1], maxs[1], resolution))
    Z = clusterer.predict(np.c_[xx.ravel(), yy.ravel()])
    Z = Z.reshape(xx.shape)

    plt.contourf(Z, extent=(mins[0], maxs[0], mins[1], maxs[1]),
                 cmap='Pastel2')
    plt.contour(Z, extent=(mins[0], maxs[0], mins[1], maxs[1]),
                linewidths=1, colors='k')
    plot_data(X)
    if show_centroids:
        plot_centroids(clusterer.cluster_centers_)
    plt.xlabel("$x_1$", fontsize=14)
    plt.ylabel("$x_2$", fontsize=14, rotation=0)
```

```
plt.figure(figsize=(8, 4))
plot_decision_boundaries(kmeans, X)
plt.show()
```







# K-Means Clustering

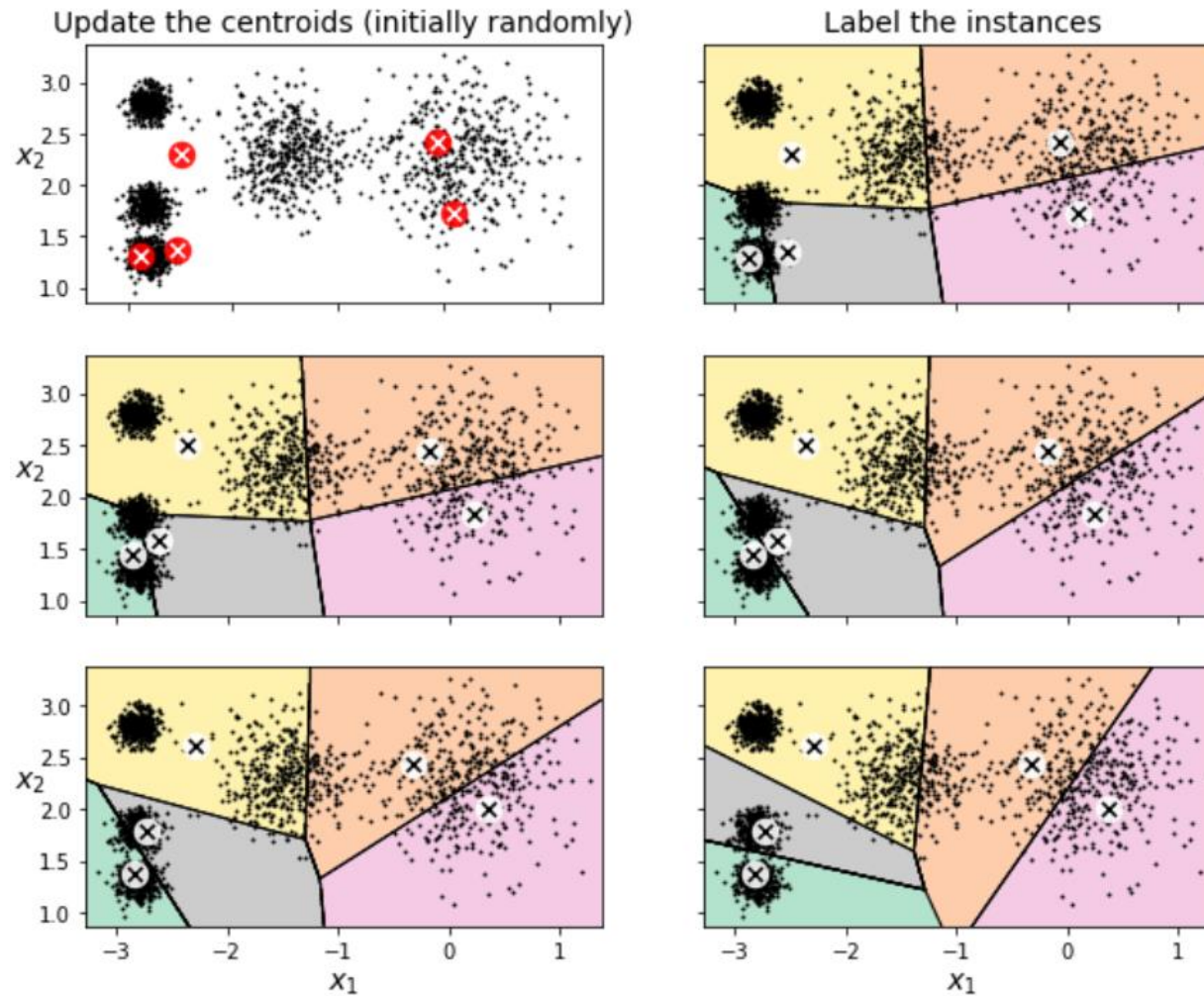
- Let's run the K-Means algorithm for 1, 2 and 3 iterations, to see how the centroids move around:

```
kmeans_iter1 = KMeans(n_clusters=5, init="random", n_init=1,  
                      algorithm="full", max_iter=1, random_state=0)  
kmeans_iter2 = KMeans(n_clusters=5, init="random", n_init=1,  
                      algorithm="full", max_iter=2, random_state=0)  
kmeans_iter3 = KMeans(n_clusters=5, init="random", n_init=1,  
                      algorithm="full", max_iter=3, random_state=0)  
  
kmeans_iter1.fit(X)  
kmeans_iter2.fit(X)  
kmeans_iter3.fit(X)
```

```
KMeans(algorithm='full', copy_x=True, init='random', max_iter=300,  
       n_clusters=5, n_init=1, n_jobs=None, precompute_distances='auto',  
       random_state=0, tol=0.0001, verbose=0)
```

- The K-Means class applies an optimized algorithm by default
- To get the original K-Means algorithm, you need to set `init="random"`, `n_init=1` and `algorithm="full"`

# K-Means Clustering





# K-Means

- Is this algorithm find the solution for the optimization problem?

$$\text{minimize} \sum_{i=1}^k \sum_{x \in D_i} \|x - \mu_i\|^2$$

- We can rewrite the function:

$$\text{minimize} \frac{1}{m} \sum_{i=1}^m \|x_i - \mu_{c_i}\|^2$$

Where  $\mu_{c_i}$  is the mean of the cluster that  $x_i$  belong to

# K-Means



- We can show that at each iteration the function  $\frac{1}{m} \sum_{i=1}^m \|x_i - \mu_{c_i}\|^2$  is reduced, why?
  - The assignment of  $x_i$  to a cluster:
    - If  $x_i$  doesn't change its cluster – stay the same
    - If  $x_i$  does change its cluster, it assign to the nearest cluster – reduce
  - Re-compute means:
    - The average will give the min square error – reduce

# K-Means Variability



- In the original K-Means algorithm, the centroids are just initialized randomly, and the algorithm simply runs a single iteration to gradually improve the centroids
- A problem with this approach is that if you run K-Means multiple times (or with different random seeds), it can converge to very different solutions (local minima problem):

```
def plot_clusterer_comparison(clusterer1, clusterer2, X,
                              title1=None, title2=None):

    clusterer1.fit(X)
    clusterer2.fit(X)

    plt.figure(figsize=(10, 3.2))

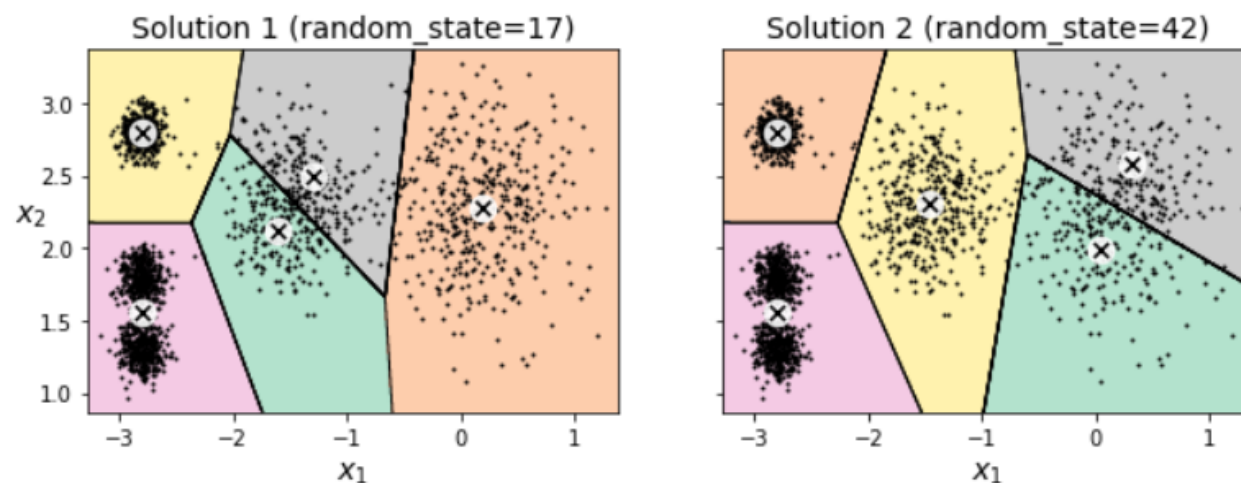
    plt.subplot(121)
    plot_decision_boundaries(clusterer1, X)
    if title1:
        plt.title(title1, fontsize=14)

    plt.subplot(122)
    plot_decision_boundaries(clusterer2, X, show_ylabels=False)
    if title2:
        plt.title(title2, fontsize=14)
```



# K-Means Variability

```
kmeans_rnd_init1 = KMeans(n_clusters=5, init="random", n_init=1,  
                           algorithm="full", random_state=17)  
kmeans_rnd_init2 = KMeans(n_clusters=5, init="random", n_init=1,  
                           algorithm="full", random_state=42)  
  
plot_clusterer_comparison(kmeans_rnd_init1, kmeans_rnd_init2, X,  
                          "Solution 1 (random_state=17)",  
                          "Solution 2 (random_state=42)")
```





# Inertia

- To select the best model, we will need a way to evaluate a K-Mean model's performance
- Unfortunately, clustering is an unsupervised task, so we do not have the targets
- But at least we can measure the distance between each instance and its centroid
- This is the idea behind the *inertia* metric:

```
kmeans.inertia_
```

```
210.90540191468097
```

- As you can easily verify, inertia is the sum of the squared distances between each training instance and its closest centroid:

```
X_dist = kmeans.transform(X)  
np.sum(X_dist[np.arange(len(X_dist)), kmeans.labels_]**2)
```

```
210.90540191468136
```

- The score() method returns the negative inertia
- That's s because a predictor's score() method respects the "*great is better*" rule

```
kmeans.score(X)
```

```
-210.90540191468136
```



# Multiple Initializations

- One approach to solve the variability issue is to simply run the K-Means algorithm multiple times with different random initializations, and select the solution that minimizes the inertia
- For example, here are the inertias of the two "bad" models shown in the previous figure:

```
kmeans_rnd_init1.inertia_
```

```
238.48246617500146
```

```
kmeans_rnd_init2.inertia_
```

```
219.0489599322056
```

- As you can see, they have a higher inertia than the first "good" model we trained, which means they are probably worse



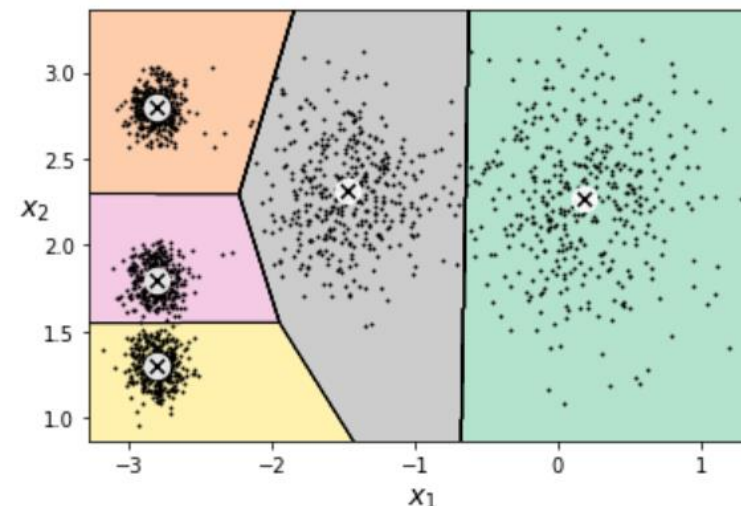


# Multiple Initializations

- When you set the `n_init` hyperparameter, Scikit-Learn runs the original algorithm `n_init` times, and selects the solution that minimizes the inertia
- By default, Scikit-Learn sets `n_init=10`

```
kmeans_rnd_10_inits = KMeans(n_clusters=5, init="random", n_init=10,  
                             algorithm="full", random_state=17)  
kmeans_rnd_10_inits.fit(X)  
print(kmeans_rnd_10_inits.inertia_)  
  
plot_decision_boundaries(kmeans_rnd_10_inits, X)  
plt.show()
```

210.9054019146808



- As you can see, we end up with the initial model, which is certainly the optimal K-Means solution (at least in terms of inertia)

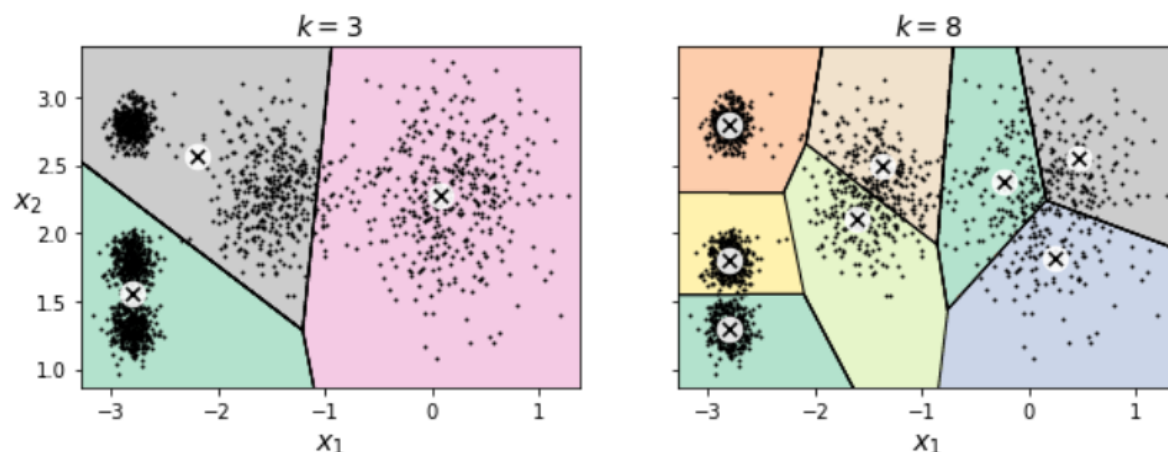


# Finding the Optimal Number of Clusters

- What if the number of clusters was set to a lower or greater value than 5?

```
kmeans_k3 = KMeans(n_clusters=3, random_state=0)
kmeans_k8 = KMeans(n_clusters=8, random_state=0)

plot_clusterer_comparison(kmeans_k3, kmeans_k8, X, "$k=3$", "$k=8$")
```



- These two models don't look great. What about their inertias?

```
print("k3 inertia:", kmeans_k3.inertia_)
print("k8 inertia:", kmeans_k8.inertia_)
```

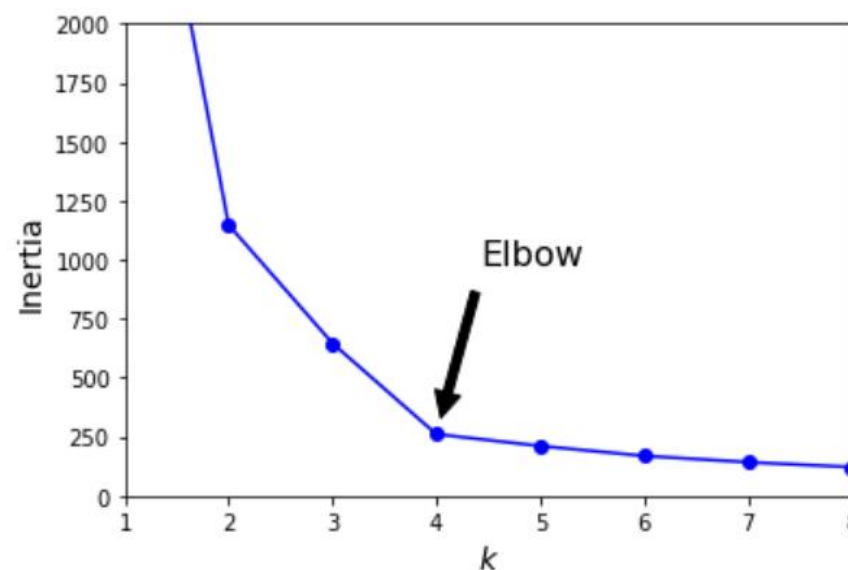
```
k3 inertia: 646.2252909343712
k8 inertia: 121.60198303182476
```



# Finding the Optimal Number of Clusters

- We cannot simply take the value of  $k$  that minimizes the inertia, since it keeps getting lower as we increase  $k$
- Indeed, the more clusters there are, the closer each instance will be to its closest centroid, and therefore the lower the inertia will be
- However, we can plot the inertia as a function of  $k$  and analyze the resulting curve:

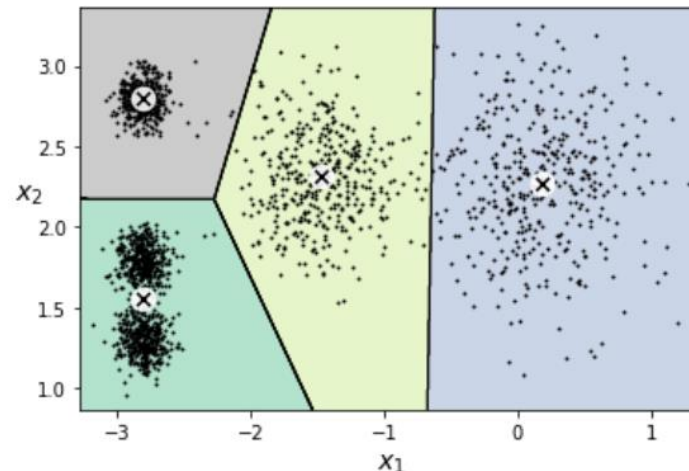
```
plt.plot(range(1, 10), inertias, "bo-")
plt.xlabel("$k$", fontsize=14)
plt.ylabel("Inertia", fontsize=14)
plt.annotate('Elbow',
             xy=(4, inertias[3]),
             xytext=(0.55, 0.55),
             textcoords='figure fraction',
             fontsize=16,
             arrowprops=dict(facecolor='black', shrink=0.1))
plt.axis([1, 8, 0, 2000])
plt.show()
```



# Finding the Optimal Number of Clusters



- As you can see, there is an elbow at  $k = 4$ , which means that less clusters than that would be bad, and more clusters would not help much and might cut clusters in half
- So  $k = 4$  is a pretty good choice
- In this example it is not perfect since it means that the two blobs in the lower left will be considered as just a single cluster, but it's a pretty good clustering nonetheless





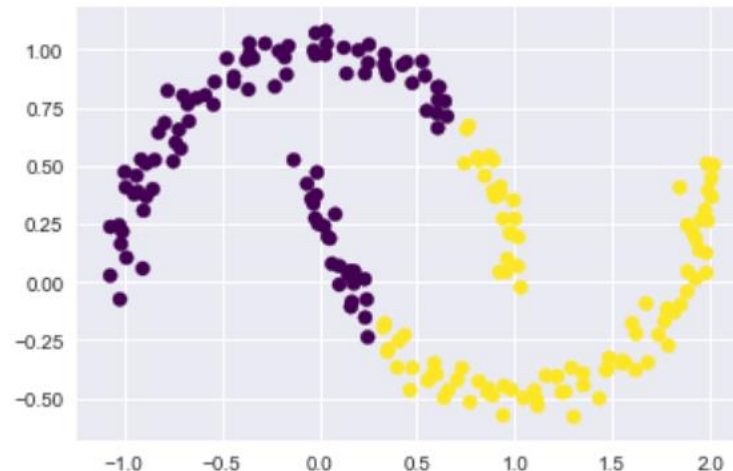
# Hard Clustering vs. Soft Clustering

- Hard – assumes that each instance is given a “hard” assignment to exactly one cluster
- Soft – gives probabilities that an instance belongs to each one of the clusters
- How can we use it in k-means?
  - With distance
  - For example:
    - For each instance calculate a distance vector from all means
    - Normalized the vector
    - Use weighted average to calculate the new means

## Another problem...



- Another caveat of  $k$ -means is that its assumption that points will be closer to their own cluster center than to others means that the boundaries between  $k$ -means clusters will always be linear
- Thus, the  $k$ -means method is not suitable for discovering clusters with nonconvex shapes or clusters of very different size
- Moreover, it is sensitive to noise and outlier data points because a small number of such data can substantially influence the mean value



# Hierarchical Clustering



- The two main approaches to hierarchical clustering are **agglomerative** and **divisive** hierarchical clustering
- In agglomerative clustering, we start with each sample as an individual cluster and merge the closest pairs of clusters until only one cluster remains
- In divisive hierarchical clustering, we start with one cluster that encompasses all our samples, and we iteratively split the cluster into smaller clusters until each cluster only contains one sample.

# Agglomerative Clustering



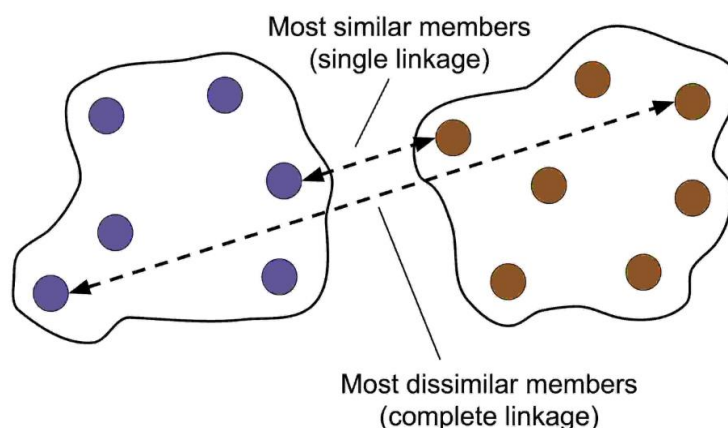
- Agglomerative hierarchical clustering is an iterative procedure that can be summarized by the following steps:
  - Compute the distance matrix of all samples
  - Represent each data point as a singleton cluster
  - Merge the two closest clusters based on the chosen linkage criterion
  - Update the similarity matrix
  - Repeat steps 2-4 until one single cluster remains





# Linkage Measures

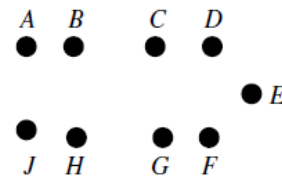
- The linkage criterion determines which distance to use between sets of observation
- The clustering algorithm will merge the pairs of clusters that minimize this criterion
- Common linkage measures:
  - **Single linkage** uses the minimum of the distances between all observations of the two sets
  - **Complete linkage** uses the maximum distances between all observations of the two sets
  - **Ward** minimizes the variance of the clusters being merged
  - **Average** uses the average of the distances of each observation of the two sets



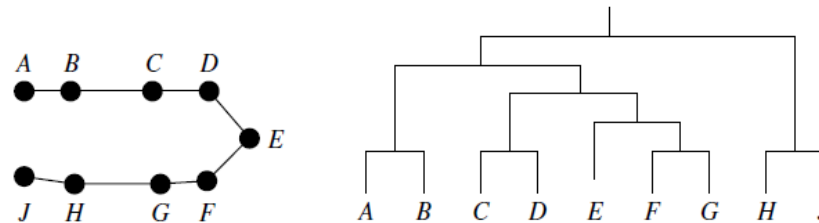
# Dendrogram



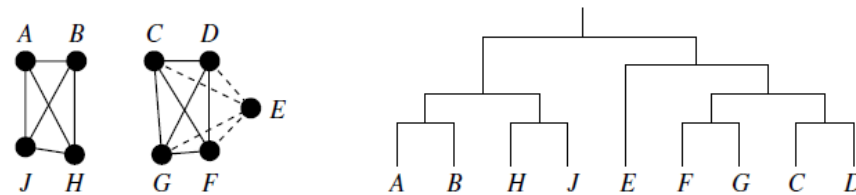
- The main output of Hierarchical Clustering is a *dendrogram*, which shows the hierarchical relationship between the clusters:



(a) Data set



(b) Clustering using single linkage



(c) Clustering using complete linkage



# Example

- You have the following points in your dataset:  
 $\{(1,2), (4,8), (3,9), (7,3), (4,3), (2,4), (5,2), (3,5), (2,5), (6,6)\}$
- We'll run an agglomerative hierarchical clustering on this dataset
- Use a Manhattan distance metric and the single linkage criterion

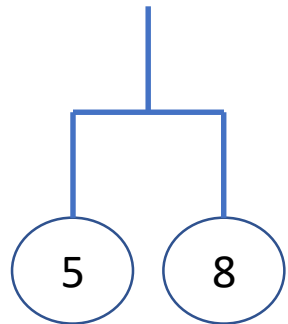
# Example



Point	X1	X2
0	1	2
1	4	8
2	3	9
3	7	3
4	4	3
5	2	4
6	5	2
7	3	5
8	2	5
9	6	6

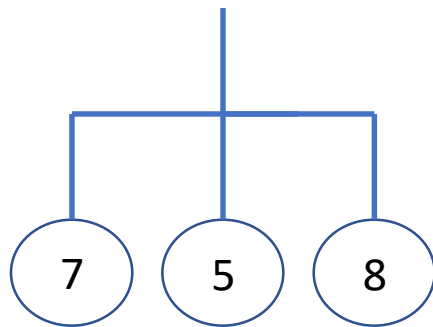
Point	Dist 0	Dist 1	Dist 2	Dist 3	Dist 4	Dist 5	Dist 6	Dist 7	Dist 8	Dist 9
0										
1	9									
2	9	2								
3	7	8	10							
4	4	5	7	3						
5	3	6	6	6	3					
6	4	7	9	3	2	5				
7	5	4	4	6	3	2	5			
8	4	5	5	7	4	1	6	1		
9	9	4	6	4	5	6	5	4	5	

# Example



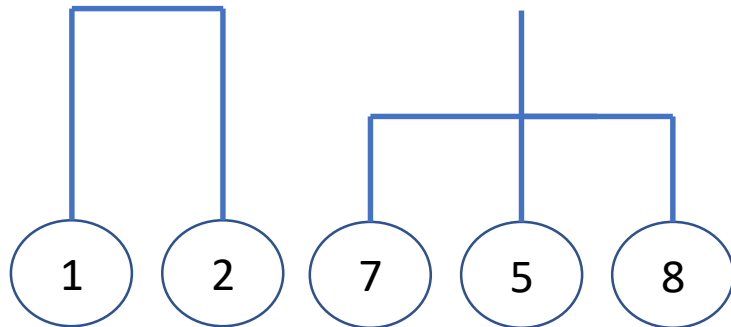
	Dist 0	Dist 1	Dist 2	Dist 3	Dist 4	Dist 5,8	Dist 6	Dist 7	Dist 9
0									
1	9								
2	9	2							
3	7	8	10						
4	4	5	7	3					
5,8	3	5	5	6	3				
6	4	7	9	3	2	5			
7	5	4	4	6	3	1	5		
9	9	4	6	6	5	5	5	4	

# Example



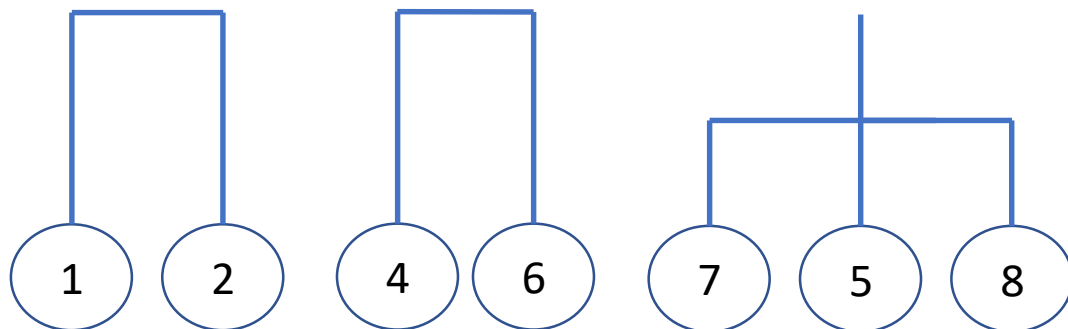
	Dist 0	Dist 1	Dist 2	Dist 3	Dist 4	Dist 7,5,8	Dist 6	Dist 7
0								
1	9							
2	9	2						
3	7	8	10					
4	4	5	7	3				
7,5,8	3	4	4	6	3			
6	4	7	9	3	2	5		
9	9	4	6	6	5	4	5	

# Example



	0	1,2	3	4	7,5,8	6	9
0							
1,2	9						
3	7	8					
4	4	5	3				
7,5,8	3	4	6	3			
6	4	7	3	2	5		
9	9	4	6	5	4	5	

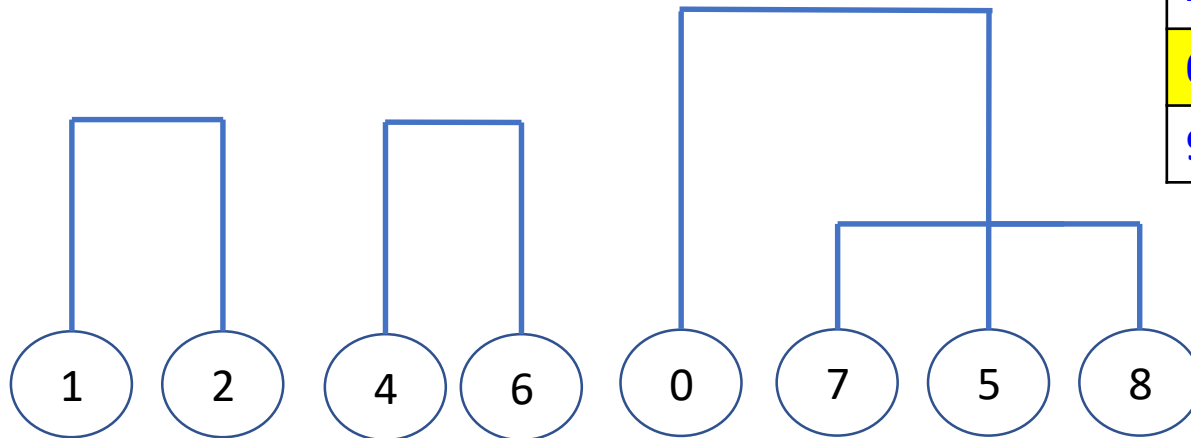
# Example



	0	1,2	3	4,6	7,5,8	9
0						
1,2	9					
3	7	8				
4,6	4	5	3			
7,5,8	3	4	6	3		
9	9	4	6	5	4	

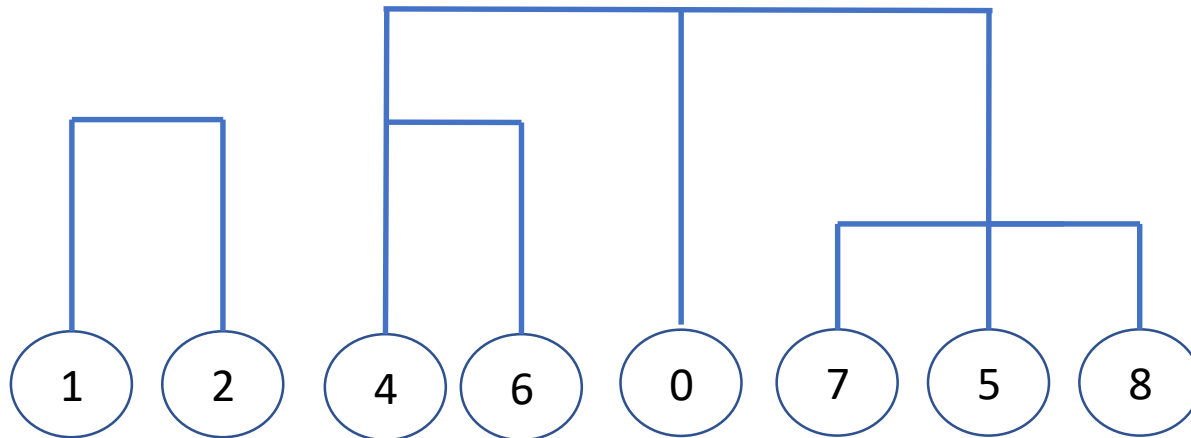


# Example



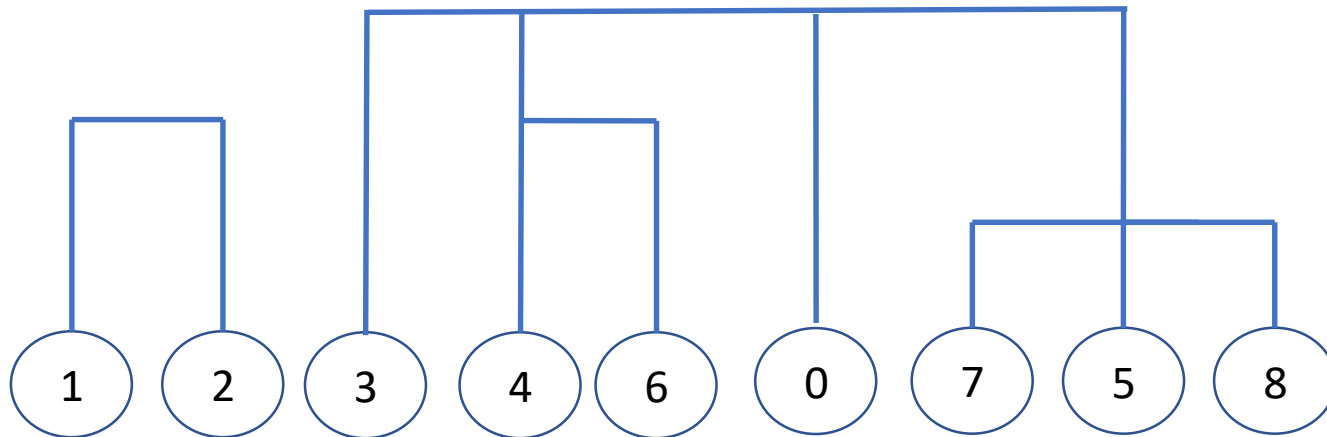
	1,2	3	4,6	0,7,5,8	9
1,2					
3	8				
4,6	5	3			
0,7,5,8	4	6	3		
9	4	6	5	4	

# Example



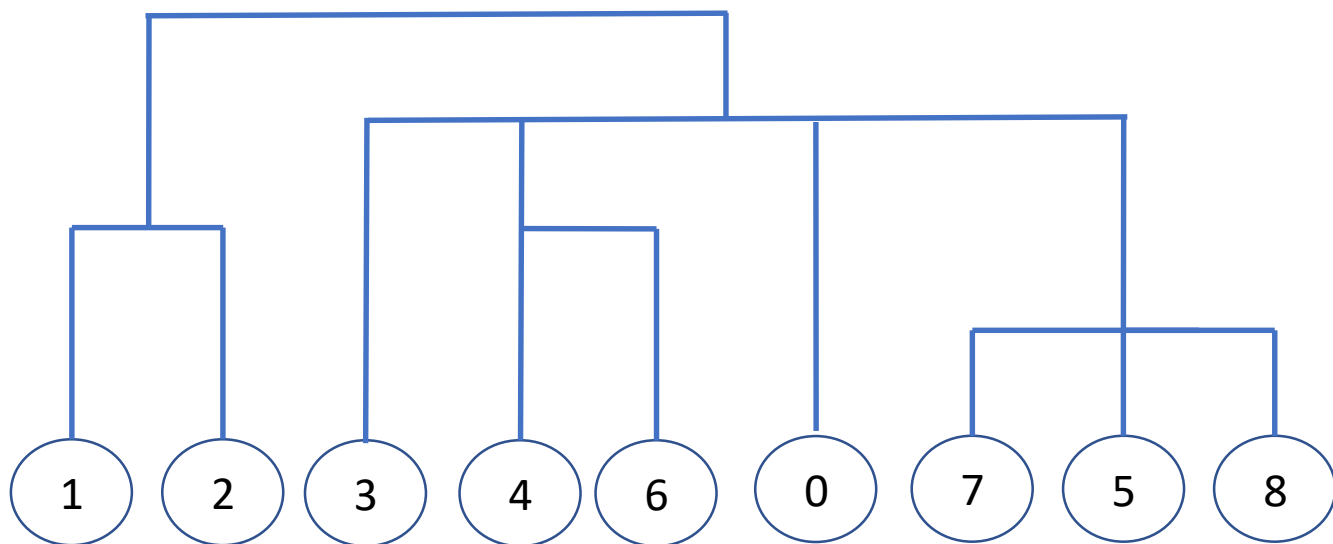
	1,2	3	4,6,0,7, 5,8	9
1,2				
3	8			
4,6,0,7, 5,8	4	3		
9	4	6	4	

# Example



	1,2	3,4,6,0, 7,5,8	9
1,2			
3,4,6,0, 7,5,8	4		
9	4	4	

# Example

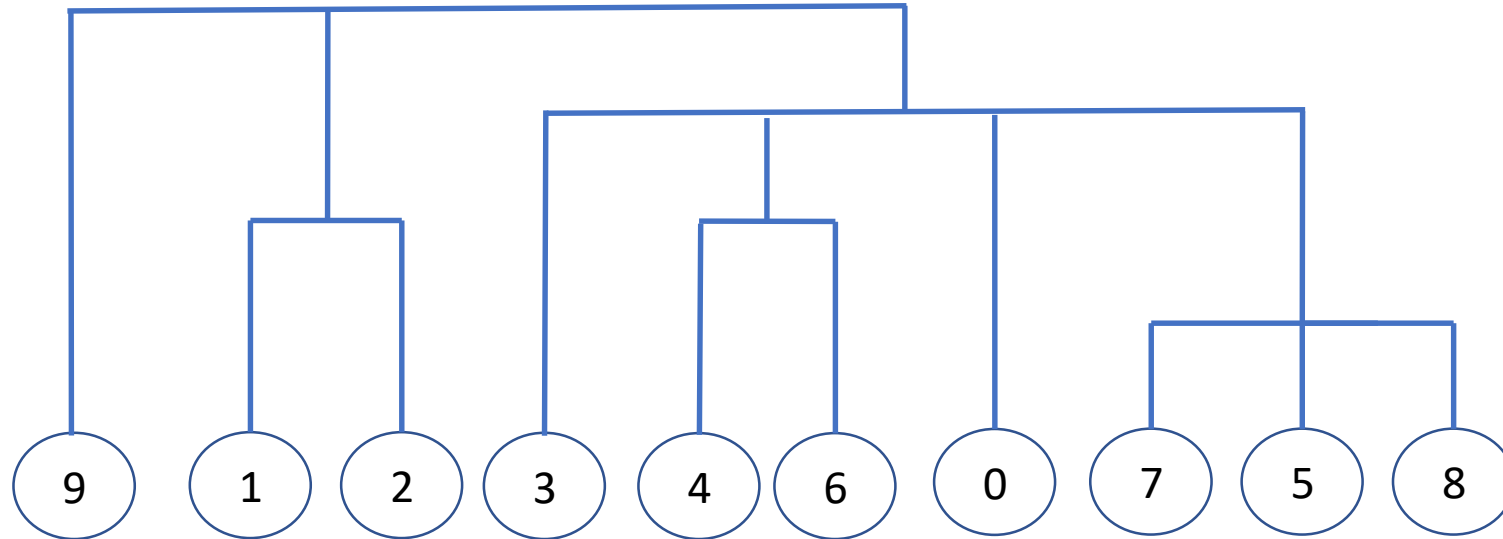


	1,2,3,4,6 ,0,7,5,8	9
1,2,3,4,6 ,0,7,5,8		
9	4	

# Example



- The final dendrogram is:



# Unsupervised Learning – Summary



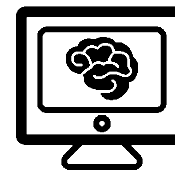
*“The validation of clustering structures is the most difficult and frustrating part of cluster analysis.*

*Without a strong effort in this direction, cluster analysis will remain a black art accessible only to those true believers who have experience and great courage.”*

Algorithms for Clustering Data, Jain and Dubes, 1988



# Example – Image Compression



# Questions

