

■ Memory updated K-Means Clustering – A Deep Dive

1. What is Clustering?

Clustering is an **unsupervised learning technique** that groups data points into **clusters** based on similarity.

- Unlike supervised learning, there are no labels in the dataset.
- The goal is to discover hidden structures in the data.

2. What is K-Means?

K-Means is one of the simplest and most widely used clustering algorithms. It works by:

- 1. Choosing K cluster centroids (randomly or heuristically).
- 2. Assigning each data point to the nearest centroid.
- 3. Recomputing centroids as the average of assigned points.
- 4. Repeating until convergence (centroids stop changing).

3. When to Use & Avoid K-Means

- Use K-Means When:
- · You need fast and scalable clustering.
- The clusters are well-separated and convex.
- You have a moderate number of clusters.
- X Avoid K-Means When:
- The dataset has **non-spherical clusters** (e.g., concentric circles).
- There are many outliers, as K-Means is sensitive to them.
- The value of K is unknown, and choosing it is difficult.

4. Choosing K (Number of Clusters)

Methods to Determine the Optimal K

- 1. Elbow Method
 - Compute the within-cluster sum of squares (WCSS) for different values of K.
 - Look for an "elbow point" where WCSS stops decreasing significantly.

2

Silhouette Score

- Measures how well-separated the clusters are.
- Higher scores indicate better clustering.

3.

Gap Statistic

• Compares clustering performance against randomly generated datasets.

Mathematical Breakdown of Methods for Choosing K in K-Means Clustering

Selecting the optimal number of clusters K is crucial for interpretable and efficient clustering. Here, we cover the most common techniques:

1. The Elbow Method

Intuition

- We compute the within-cluster sum of squares (WCSS) for different values of K.
- Plot WCSS vs. K and look for an "elbow" point, where WCSS stops decreasing significantly.

Mathematics

The WCSS (Within-Cluster Sum of Squares) measures how compact each cluster is:

$$ext{WCSS} = \sum_{i=1}^K \sum_{x_j \in C_i} \left| \left| x_j - \mu_i
ight|
ight|^2$$

where:

- x_j = data point
- μ_i = centroid of cluster C_i
- $||x_j \mu_i||^2$ = squared Euclidean distance from x_j to its centroid

Procedure

- 1. Compute WCSS for different values of K.
- 2. Plot K vs. WCSS.
- 3. Identify the "elbow point" where WCSS reduction slows.

- The elbow point is **subjective**.
- Doesn't always work well if clusters are not clearly defined.

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2. Silhouette Score

Intuition

- Measures how well-separated clusters are.
- The score is between -1 and 1:
 - 1 → Perfect clustering.
 - **0** → Overlapping clusters.
 - -1 → Wrong clustering.

Mathematics

For each data point x_i , compute:

1

Average intra-cluster distance (how close is x_i to its own cluster centroid?):

$$a(i) = rac{1}{|C_k|-1}\sum_{x_i \in C_k, i
eq j} ||x_i-x_j||.$$

where C_k is the cluster to which x_i belongs.

2.

Average inter-cluster distance (how far is x_i from the nearest different cluster?):

$$b(i) = \min_{C_m
eq C_k} rac{1}{|C_m|} \sum_{x_i \in C_m} ||x_i - x_j||$$

where C_m is the nearest cluster.

3. Compute **Silhouette Score** for x_i :

$$s(i) = rac{b(i) - a(i)}{\max(a(i),b(i))}$$

4. Compute the average silhouette score for all points to evaluate clustering quality.

Procedure

- 1. Compute silhouette scores for different K.
- 2. Choose K with the **highest average silhouette score**.

- $\bullet \quad \text{Requires pairwise distance computations} \rightarrow \textbf{Computationally expensive} \text{ for large datasets}.$
- Can be misleading if clusters have non-convex shapes.

3. Gap Statistic

Intuition

- Compares clustering performance against randomly generated datasets.
- A higher gap means clustering is better than random noise.

Mathematics

1. Compute the WCSS for real data:

$$W_k = \sum_{i=1}^K \sum_{x_i \in C_i} ||x_j - \mu_i||^2$$

- 2. Generate B random datasets (same size as real data, but uniformly distributed).
- 3. Compute the WCSS for each random dataset:

$$W_k^b = \sum_{i=1}^K \sum_{x_j \in C_i^b} ||x_j - \mu_i^b||^2, \quad b = 1, \dots, B$$

4. Compute the expected WCSS over all B random datasets:

$$E(W_k) = rac{1}{B} \sum_{k=1}^B W_k^b$$

5. Compute the Gap Statistic:

6.

$$G_k = rac{1}{B}\sum_{k=1}^B \log(W_k^b) - \log(W_k)$$

Choose K where G_k is **maximum**.

Procedure

- 1. Compute G_k for different K.
- 2. Choose the largest G_k .

- Computationally expensive due to multiple random dataset generations.
- Assumes clusters are compact and spherical.

4. Davies-Bouldin Index

Intuition

- Measures inter-cluster similarity (how well-separated clusters are).
- Lower values indicate better clustering.

Mathematics

1.

Compute cluster dispersion:

$$S_i = rac{1}{|C_i|} \sum_{x_i \in C_i} ||x_j - \mu_i||$$

2. Compute cluster separation between clusters i and j:

$$R_{ij} = rac{S_i + S_j}{||\mu_i - \mu_j||}$$

Compute Davies-Bouldin Index:

$$DB = rac{1}{K} \sum_{i=1}^K \max_{j
eq i} R_{ij}$$

 \downarrow

4.

Choose K with the smallest DB index.

Procedure

- 1. Compute DB index for different K.
- 2. Select K where DB is **minimum**.

- Works well for convex clusters but fails for non-spherical clusters.
- Sensitive to noise.

Comparison of Methods for Choosing K

Method	Works Best When	Computational Complexity	Key Limitation
Elbow Method	Clusters are well-separated	Low	The "elbow" is subjective
Silhouette Score	Clusters have clear boundaries	High	Expensive for large datasets
Gap Statistic	Random reference comparison is needed	Very High	Computationally expensive
Davies-Bouldin Index	Clusters have equal density	Medium	Fails for irregular cluster shapes

Final Takeaways

- **V** Elbow Method is the simplest approach but is subjective.
- Silhouette Score measures separation quality, but is expensive.
- √ Gap Statistic provides a rigorous test but is very slow.
- **V** Davies-Bouldin Index works well for convex clusters but fails for complex shapes.

5. Step-by-Step Pseudo Code for K-Means

ரி Copy ∜ Edit plaintext # Step 1: Initialize Clusters 1. Choose K (number of clusters). 2. Randomly select K data points as initial centroids. # Step 2: Assign Points to Clusters 1. For each data point: a. Compute distance to each centroid. b. Assign point to the nearest centroid. # Step 3: Recompute Centroids 1. For each cluster: a. Compute the mean of all assigned points. b. Update the centroid. # Step 4: Check for Convergence 1. If centroids do not change significantly, stop. 2. Otherwise, repeat Steps 2 and 3. # Step 5: Output Final Clusters 1. Return cluster assignments and final centroids.

6. Mathematical Breakdown

6.1 Objective Function (Minimizing Variance Within Clusters)

The goal of K-Means is to minimize the **intra-cluster variance**, measured by the sum of squared differences:

$$J = \sum_{i=1}^K \sum_{x_i \in C_i} ||x_j - \mu_i||^2$$

where:

- x_i is a data point.
- μ_i is the centroid of cluster C_i .
- The inner sum computes the variance within a cluster.

6.2 Distance Calculation

The most common distance metric used is **Euclidean distance**:

$$d(x,y) = \sqrt{\sum_{i=1}^n (x_i - y_i)^2}$$

6.3 Updating Centroids

The new centroid μ_i is simply the **mean** of all assigned points:

$$\mu_i = rac{1}{|C_i|} \sum_{x_j \in C_i} x_j \, .$$

7. Fully Commented Manual Implementation (From Scratch)

```
def euclidean_distance(a, b):
    return np.sqrt(((a - b) ** 2).sum(axis=1))
def k_means_clustering(points, k, initial_centroids,
max iterations):
    points = np.array(points)
    centroids = np.array(initial_centroids)
    for iteration in range(max iterations):
        # Assign points to the nearest centroid
        distances =
np.array([euclidean_distance(points, centroid) for
centroid in centroids1)
        assignments = np.argmin(distances, axis=0)
        new_centroids = np.array([points[assignments ==
i].mean(axis=0) if len(points[assignments == i]) > 0
else centroids[i] for i in range(k)])
        # Check for convergence
        if np.all(centroids == new_centroids):
            break
        centroids = new centroids
        centroids = np.round(centroids,4)
    return [tuple(centroid) for centroid in centroids]
```

```
Updates centroids by computing the mean of assigned points.
    :param X: Data points.
    :param labels: Cluster assignments.
   new_centroids = np.array([X[labels == i].mean(axis=0) for i in range(self.k)])
    return new_centroids
def fit(self, X):
   Run the K-Means clustering algorithm.
    :param X: Data points.
   self.initialize_centroids(X)
    for i in range(self.max_iters):
        labels = self.assign_clusters(X) # Step 2: Assign points
       new centroids = self.update_centroids(X, labels) # Step 3: Update centroids
        # Check for convergence (if centroids do not change significantly)
        if np.linalg.norm(self.centroids - new_centroids) < self.tol:</pre>
            break
       self.centroids = new centroids # Update centroids
def predict(self, X):
   Assign new data points to the nearest cluster.
    :param X: New data points.
    :return: Cluster assignments.
    return self.assign clusters(X)
```

def update_centroids(self, X, labels):

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```
class KMeans:
   Implementation of K-Means Clustering Algorithm.
   def __init (self, k=3, max_iters=100, tol=1e-4):
       Initialize K-Means parameters.
        :param k: Number of clusters.
        :param max iters: Maximum number of iterations.
        :param tol: Convergence tolerance (stop if centroid shifts are below this value).
       self.k = k
       self.max iters = max iters
       self.tol = tol # Threshold for stopping criterion
        self.centroids = None # Stores cluster centroids
   def initialize centroids(self, X):
       Randomly initialize K cluster centroids from the data points.
        :param X: Data points (numpy array of shape (n_samples, n_features)).
       np.random.seed(42) # For reproducibility
       indices = np.random.choice(X.shape[0], self.k, replace=False)
       self.centroids = X[indices]
   def assign clusters(self, X):
       Assigns each data point to the nearest centroid.
        :param X: Data points.
       :return: Array of cluster assignments.
       distances = np.linalg.norm(X[:. np.newaxis] - self.centroids, axis=2) # Compute distances
        return np.argmin(distances, axis=1) # Assign to the nearest centroid
```

import numpy as np

8. Scikit-Learn Implementation

```
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from sklearn.cluster import KMeans
from sklearn.datasets import make blobs
# Generate synthetic dataset
X, _ = make_blobs(n_samples=300, centers=3, cluster_std=1.0, random_state=42)
# Train K-Means
kmeans = KMeans(n clusters=3, random state=42)
kmeans.fit(X)
labels = kmeans.labels
centroids = kmeans.cluster_centers_
print("Cluster Centers:\n", centroids)
```

9. Advantages & Disadvantages of K-Means

Advantages

- Simple and easy to implement.
- · Scalable to large datasets.
- Fast because it uses simple distance calculations.

💢 Disadvantages

- Requires manual selection of K.
- Fails for non-spherical clusters.
- · Sensitive to outliers.

Final Takeaways

Choosing the right K is crucial for meaningful clustering.

K-Means is a fundamental clustering algorithm that partitions data into K groups.

Sensitive to initialization, but optimizations (K-Means++) can improve results.

Comparison of Popular Clustering Algorithms

Algorithm	Intuition (How It Works & What It Does)	When to Use	Pros	Cons
K-Means	Assigns points to the nearest centroid, then updates centroids iteratively to minimize variance.	When clusters are spherical, well-separated, and you know K.	Simple, fast, works well on large datasets.	Sensitive to initialization and outliers. Struggles with non-spherical clusters.
Hierarchical Clustering	Recursively merges (agglomerative) or splits (divisive) clusters based on similarity.	When you want a dendrogram (cluster hierarchy) and don't know K.	No need to predefine K, creates a full hierarchy.	Slow for large datasets, sensitive to distance metrics.
DBSCAN (Density- Based Clustering)	Groups points that have a minimum number of neighbors within a radius, marking outliers.	When clusters have arbitrary shapes and contain noise.	Detects arbitrary- shaped clusters, robust to noise.	Struggles with varying densities and high-dimensional data.
Gaussian Mixture Model (GMM)	Assumes data is generated from multiple Gaussian distributions and assigns probabilities to clusters.	When clusters overlap and have elliptical shapes.	Soft clustering, flexible cluster shapes.	Computationally expensive, requires Gaussian assumption.
Mean Shift	Moves data points toward areas of highest density (mode seeking).	When clusters have varying densities and you want automatic cluster detection.	No need to specify K, works for irregular densities.	Computationally expensive, sensitive to bandwidth selection.
Spectral Clustering	Uses graph-based methods and eigenvalues to separate data points into clusters.	When clusters are connected but not necessarily spherical.	Works well for non-convex clusters, handles complex structures.	Doesn't scale well, computationally expensive.

Final Takeaways

- K-Means → Best for simple, well-separated clusters.
- **V** DBSCAN → Best for arbitrary-shaped clusters with noise.
- Hierarchical Clustering → Best when you don't know K and want a hierarchy.
- ✓ GMM → Best when clusters overlap and have elliptical shapes.
- **▼** Mean Shift → Best when you want automatic cluster detection without K.
- ▼ Spectral Clustering → Best for complex structures and non-spherical clusters.