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# K-MEANS FROM SCRATCH

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SUMMER 2024

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## IMPLEMENTING K-MEANS CLUSTERING FROM SCRATCH

### History

The term "k-means" was first used by James MacQueen in 1967,<sup>[1]</sup> though the idea goes back to [Hugo Steinhaus](#) in 1956.<sup>[2]</sup> The standard algorithm was first proposed by Stuart Lloyd of [Bell Labs](#) in 1957 as a technique for [pulse-code modulation](#), although it was not published as a journal article until 1982.<sup>[3]</sup> In 1965, Edward W. Forgy published essentially the same method, which is why it is sometimes referred to as the Lloyd –Forgy algorithm.<sup>[4]</sup>

### Explanation

k-means clustering is one of the simplest and most commonly used clustering algorithms. It tries to find cluster centers that are representative of certain regions of the data. The algorithm alternates between two steps: assigning each data point to the closest cluster center, and then setting each cluster center as the mean of the data points that are assigned to it. The algorithm is finished when the assignment of instances to clusters no longer changes. The following example illustrates the algorithm on a synthetic dataset<sup>[5]</sup>:

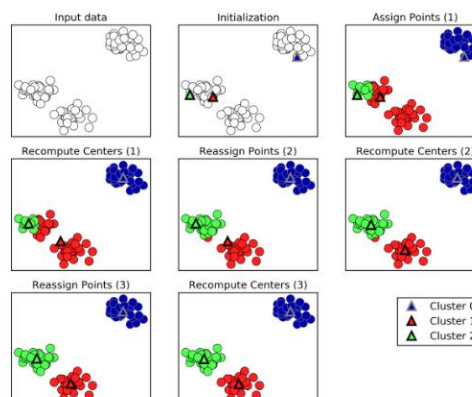


Figure 1 - Input data and three steps of the k-means algorithm

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### Code Example using scikit-learn<sup>[6]</sup>

```
from sklearn.cluster import KMeans
from sklearn.datasets import make_blobs
X, y = make_blobs([...]) # make the blobs: y contains the
cluster IDs, but we
# will not use them; that's what we want to predict
k = 3
kmeans = KMeans(n_clusters=k, random_state=42)
y_pred = kmeans.fit_predict(X)
```

### Implementing from scratch

The source code is also included in a separate python file<sup>[7]</sup>. Some steps of this algorithm are :

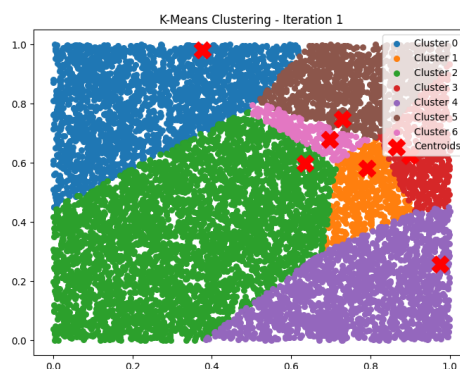


Figure 2 - step 1

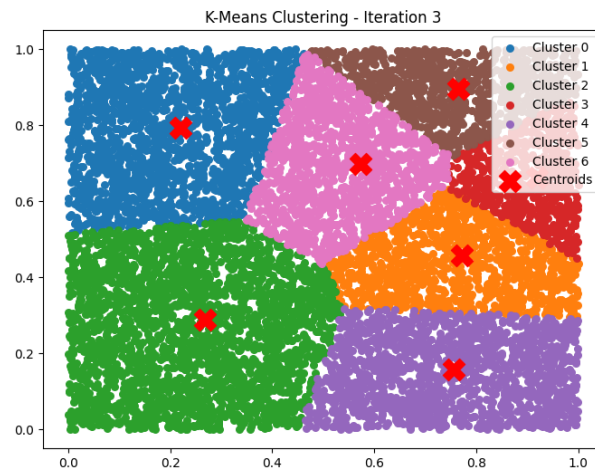


Figure 3 - step 3

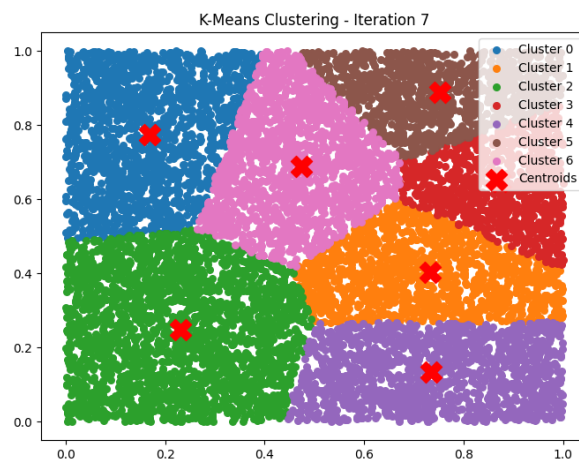


Figure 4 - step 7

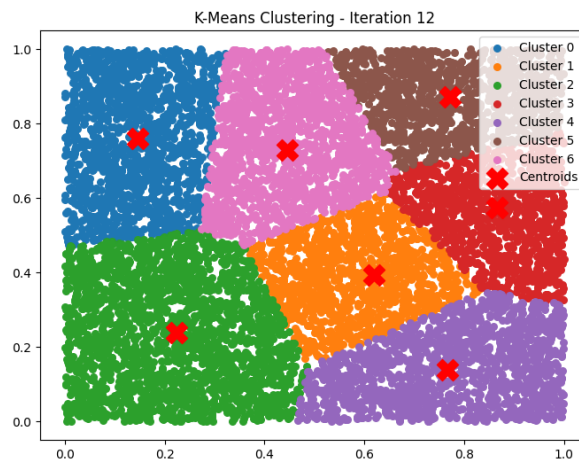


Figure 5 - step 12

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### IMAGE COMPRESSING USING K-MEANS

By changing the code and preparing it for loading images, we can use it to transform RGB images to 16-color images (so called compressing them). The source code is available in attached files. The outputs are shown in following pictures (iterations are limited to avoid very long time of execution) :



*Figure 6 - original image*

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*Figure 7 - compressed image*

Execution Time : 1min 36s

Max Iterations : 300

L2 Norm : 3412782.115732

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*Figure 8 - original image*



*Figure 9 - compressed image*

Execution Time : 42s, Iterations : 300, L2 Norm : 4562158.853435

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### OPTIMIZATION

There are a lot of ways that we can improve the execution time or quality of the this algorithm, however it is important to note that sometimes it is a trade-off between these two. Some optimization techniques are as follows:

- **Initialization Techniques**
  - E.g. : K-Means++: A smarter initialization method that spreads out initial cluster centers. This significantly improves the convergence speed and accuracy.<sup>[8]</sup>
- **Distance Measures**
  - E.g. : Euclidean Distance: The default, but other distance measures can be used depending on the data.<sup>[9]</sup>
- **Efficient Computation**
  - E.g. : Elkan's Algorithm: This optimizes the distance computation by using the triangle inequality, which reduces the number of distance calculations.<sup>[10]</sup>
- **Cluster Updating**
  - E.g. : Mini-Batch K-Means: Processes a small random subset of data in each iteration, leading to faster convergence and scalability to larger datasets.<sup>[11]</sup>
- **Stopping Criteria**
  - Fixed Iterations: Run for a set number of iterations.
  - Convergence Threshold: Stop when the centroids no longer move significantly (i.e., the change in centroid positions is below a threshold).
  - Centroid Convergence: Stop when a certain percentage of centroids do not change between iterations.<sup>[12]</sup>
- **Dimensionality Reduction**
  - Principal Component Analysis (PCA): Reduces the dimensionality of the data while preserving as much variance as possible.
  - t-SNE: For non-linear dimensionality reduction, often used in visualizing clusters in high-dimensional data.<sup>[13]</sup>



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- **Parallel and GPU Computation**
    - **Parallel Processing:** Distribute the computation across multiple processors.
    - **GPU Acceleration:** Leverage GPUs for parallel computation to accelerate K-Means clustering.<sup>[14]</sup>
  - **Avoiding Local Minima**
    - **Multiple Runs:** Run K-Means multiple times with different initializations and choose the best result.
    - **Simulated Annealing:** Combine K-Means with simulated annealing to escape local minima.
    - **Genetic Algorithms:** Use genetic algorithms to optimize the selection of centroids.<sup>[15][16]</sup>
  - **Post-Processing**
    - **Refining Clusters:** Post-process clusters to merge or split them based on additional criteria.
    - **Cluster Refinement via Hierarchical Clustering:** After initial K-Means clustering, refine clusters by applying hierarchical clustering techniques.<sup>[17]</sup>
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## OPTIMIZED IMPLEMENTATION

Now let's implement the optimized version of K-means, using max iterations and K-means++ optimization. However remember that in small data, the difference won't be that much different.

Using K-means++ we choose the initial centroids in a way that it converges better, so the final L2 Norm will improve, hence we get better image quality. Compare the following pictures with previous ones :

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*Figure 10 - lena  
optimized K-means*

Execution Time : 36s  
Max Iterations : 100  
L2 Norm : 3415795.502945



*Figure 11 - peppers optimized K-means*

Execution Time : 36s  
Max Iterations : 100  
L2 Norm : 4650520.628046

As you can see the L2 Norm for pictures has not changed a lot even though the iterations are reduced to 100 only, instead of 300.

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