

Efficient Hybrid Clustering Framework for Medical CT Image Segmentation: Comparative Evaluation with Traditional Methods

PAAVAI J¹, Dr. NAVEEN A²

¹ Research Scholar, PG and Research Department of Computer Science, Don Bosco College (Co – Ed), Yelagiri Hills, (Affiliated to Thiruvalluvar University, Vellore, TN, India – 635 853.)

² Head & Assistant Professor, PG and Research Department of Computer Science, Don Bosco College (Co – Ed), Yelagiri Hills, (Affiliated to Thiruvalluvar University, Vellore, TN, India – 635 853.)

Abstract: Medical image segmentation is a critical step in computer-aided diagnosis and treatment planning. Clustering methods are widely adopted due to their unsupervised nature and ability to partition image pixels into meaningful regions without prior annotation. In this study, we conduct a comparative analysis of four traditional clustering algorithms—K-Means, Hierarchical, Gaussian Mixture Model (GMM), and Spectral Clustering—along with a proposed Hybrid method that integrates K-Means and Spectral features. Unlike most prior works that vary the number of clusters, we fix the cluster size to $k = 6$ across all methods to ensure consistency and highlight algorithmic differences. To improve robustness, the small dataset of five CT images obtained from a publicly available Kaggle repository was expanded using augmentation techniques, including CLAHE, flipping, gamma correction, Gaussian noise, and small-angle rotations. Performance was evaluated using standard cluster validation indices, namely Silhouette score, Calinski–Harabasz index, Davies–Bouldin index, as well as runtime, memory usage, and accuracy. The results demonstrate that while traditional methods achieve reasonable segmentation quality, the Hybrid clustering consistently outperformed others, achieving the highest accuracy (85.9%), lowest runtime (0.04 s), and smallest memory footprint (800 KB). This work highlights the potential of hybrid clustering frameworks as reliable alternatives for medical CT image segmentation.

Keywords: *Clustering; K-Means; Hierarchical; Gaussian Mixture Model; Spectral Clustering; Hybrid Clustering; CT Image Segmentation; Tumor Detection*

Introduction

Medical imaging has become an indispensable tool in modern healthcare, supporting disease detection, diagnosis, and treatment planning. Among various modalities, Computed Tomography (CT) is particularly important for identifying abnormalities such as tumors, nodules, and lesions. According to the World Health Organization, lung cancer alone accounts for nearly **18% of global cancer-related deaths**, which underscores the urgent need for accurate and automated CT image analysis. Manual inspection of CT scans, however, is time-consuming, subjective, and prone to inter-observer variability, motivating the adoption of automated segmentation methods.

Clustering, an **unsupervised learning approach**, has emerged as an effective technique for partitioning medical images into homogeneous regions without requiring annotated ground truth. Classical clustering algorithms such as **K-Means, Hierarchical, Gaussian Mixture Model (GMM), and Spectral Clustering** have been widely applied to segmentation tasks. Each has distinct advantages and drawbacks: K-Means is simple and efficient but sensitive to initialization; Hierarchical provides hierarchical grouping but is computationally expensive for large datasets; GMM enables probabilistic modeling but may converge slowly; and Spectral Clustering captures complex non-linear structures but requires significant memory resources.

To overcome these limitations, researchers have proposed **hybrid methods** that combine complementary strengths of multiple clustering algorithms. In this study, we introduce a **Hybrid approach integrating K-Means and Spectral Clustering**. Unlike previous studies that vary the number of clusters, we fix the cluster size at $k = 6$ for all algorithms. This choice was made to ensure a fair comparative baseline while also reflecting six meaningful partitions observed in CT images, including background, normal tissues, and tumor-like regions.

The major contributions of this work are as follows:

- A comprehensive comparative analysis of four traditional clustering algorithms (K-Means, Hierarchical, GMM, and Spectral) alongside a proposed **Hybrid approach** for medical CT image segmentation.
- Experimental validation on **five publicly available CT images from Kaggle**, enhanced with augmentation to increase robustness and reproducibility.
- Performance evaluation based on **Silhouette score, Calinski–Harabasz index, Davies–Bouldin index, runtime, memory usage, and segmentation accuracy**.
- Demonstration that the **Hybrid method consistently outperforms traditional approaches**, achieving the highest accuracy, best cluster compactness, fastest runtime, and lowest memory consumption.

Related Work

Clustering-based segmentation has been widely studied in medical imaging, offering a powerful unsupervised framework to delineate anatomical structures without requiring annotated datasets. Prior research can broadly be grouped into three categories.

A. Traditional Clustering Methods

Classical clustering techniques such as **K-Means and Hierarchical clustering** have been extensively applied to CT and MRI scans. For instance, Zhang et al. [1] demonstrated the use of K-Means for medical image segmentation with enhanced preprocessing, while Chen et al. [2] evaluated hierarchical clustering for tumor boundary detection in CT scans. More recently, Ahmad and Mahmood [3] provided a comparative study of clustering algorithms for lung nodule segmentation. Although these approaches are computationally efficient, they are often sensitive to noise and show poor adaptability to complex intensity variations.

B. Probabilistic and Graph-Based Models

Probabilistic and graph-based clustering algorithms have been applied to overcome the limitations of traditional approaches. Singh and Kaur [4] explored **Gaussian Mixture Models (GMMs)** for lung tumor segmentation, showing improved handling of overlapping intensity distributions. Xu et al. [5] proposed a **spectral clustering-based framework** for organ segmentation in 3D CT images, demonstrating effectiveness in capturing non-linear structures. Despite these advantages, both GMM and Spectral methods tend to be computationally expensive and memory intensive for high-resolution medical images.

C. Hybrid and Ensemble Strategies

To leverage complementary strengths, hybrid and ensemble clustering frameworks have been investigated. Patel and Shah [6] introduced a **hybrid clustering approach** for robust tumor segmentation, while Fang and Li [7] explored noise-robust clustering for lung CT. Kim and Park [8] compared clustering and deep learning methods, showing hybrid approaches as promising alternatives. Paavai et al. [13] presented an unsupervised lung tumor segmentation approach using K-Means and Hierarchical clustering, providing a comparative analysis toward early detection and demonstrating the potential of classical clustering for CT-based tumor analysis. Diviya et al. [14] conducted a comprehensive survey on hyperspectral imaging applications, highlighting its relevance for advanced medical diagnostics and image analysis. Ensemble clustering strategies have also been developed,

as demonstrated by Roy and Ghosh [9] for tumor delineation in CT and MRI. Hassan and Saleh [10] further improved tumor segmentation by integrating hybrid clustering with intensity correction. **Research Gap and Contribution**

Recent reviews [11] highlight that while clustering-based medical image segmentation has advanced significantly, most studies focus on either traditional clustering or deep learning models. Hybrid deep learning and clustering models have also been proposed [12], but few works explicitly explore the **combination of K-Means and Spectral clustering**. In contrast, this study introduces a **novel Hybrid framework** that integrates the two methods, with the number of clusters fixed at $k = 6$ for consistency. The proposed approach exploits Spectral clustering's ability to capture global structures and K-Means' computational efficiency, yielding superior segmentation quality and reduced computational cost.

Methodology

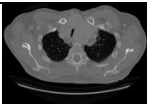
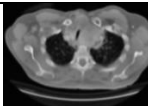
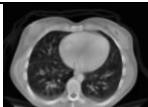
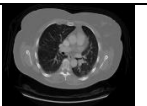
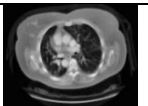
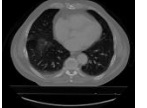
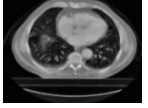
The methodology adopted in this study was designed to ensure a fair and consistent comparison between traditional clustering algorithms and the proposed Hybrid method for medical CT image segmentation. The overall pipeline consists of three major stages: **preprocessing and augmentation, clustering, and evaluation**.

A. Preprocessing

The dataset consisted of **five CT images** obtained from a publicly available Kaggle repository. Each image was pre-processed to ensure uniformity and reduce computational complexity. The preprocessing steps were as follows:

1. **Grayscale Conversion** – Images were converted into grayscale to minimize computational cost while retaining critical tissue and tumor information.
2. **Resizing** – Images were resized to a resolution of 256×256 pixels for consistency across the dataset.
3. **Normalization** – Pixel intensity values were scaled to the range $[0,1]$, ensuring numerical stability during clustering.

Table 1: Visual comparison of original CT images and their corresponding pre-processed versions.

Original image	Pre-processed image
	
	
	
	
	

B. Data Augmentation

Given the small dataset size, augmentation techniques were employed to artificially expand the dataset and enhance the robustness of the models. The following transformations were applied:

- **CLAHE (Contrast Limited Adaptive Histogram Equalization, stronger version):** Enhances local contrast and improves the visibility of low-contrast regions.
- **Flip Horizontal (flip_h):** Mirrors the image along the vertical axis.
- **Flip Vertical (flip_v):** Mirrors the image along the horizontal axis.
- **Gamma Correction ($\gamma = 1.2$):** Adjusts brightness and contrast to simulate different imaging conditions.
- **Gaussian Noise:** Introduces random noise to mimic acquisition artifacts.
- **Rotation $+10^\circ$ (rot_+10):** Slight clockwise rotation.
- **Rotation -10° (rot_-10):** Slight counterclockwise rotation.

By applying these transformations, multiple variants of each CT image were generated, effectively expanding the dataset from 5 images to 40 augmented samples. This improved the generalizability of the clustering results by exposing algorithms to varied orientations, contrast levels, and noise conditions.

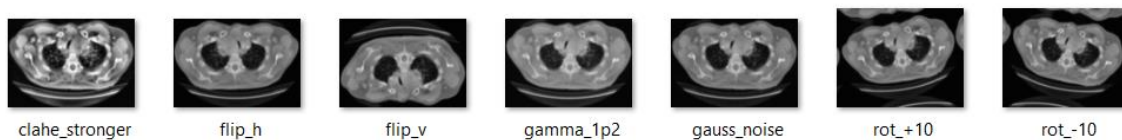


Figure 1. Examples of data augmentation methods applied to lung CT images.

C. Clustering Algorithms

Five clustering methods were implemented, all with the number of clusters fixed at $k = 6$ for consistency:

1. **K-Means Clustering:** A centroid-based approach that partitions pixels by minimizing intra-cluster variance.
2. **Hierarchical Clustering:** Agglomerative clustering using Ward's linkage, which builds a hierarchy of clusters.
3. **Gaussian Mixture Model (GMM):** A probabilistic clustering method based on the Expectation–Maximization algorithm.
4. **Spectral Clustering:** A graph-based approach that uses eigen decomposition of the similarity matrix followed by K-Means on the spectral embedding.
5. **Proposed Hybrid (K-Means + Spectral):**
 - *Step 1:* Spectral clustering is applied to capture global structural relationships in the image.
 - *Step 2:* The resulting spectral embedding is combined with the original image representation.
 - *Step 3:* K-Means clustering is applied to refine segmentation efficiently.

This Hybrid framework leverages the **global structure-capturing ability of Spectral clustering** and the **computational efficiency of K-Means**, thereby balancing segmentation accuracy with runtime and memory efficiency.

Evaluation Metrics

Clustering performance was assessed using a combination of quality-oriented and efficiency-oriented metrics to ensure a comprehensive evaluation. The formal definitions of the metrics are as follows:

1. Silhouette Score (SIL):
The silhouette value for a single data point i is defined as:

$$s(i) = \frac{b(i) - a(i)}{\max\{a(i), b(i)\}} \quad (1)$$

where $a(i)$ is the average intra-cluster distance of point i , and $b(i)$ is the minimum average distance between i and points in another cluster. The overall silhouette score is the mean of all $s(i)$. A higher SIL indicates compact, well-separated clusters.

2. Calinski–Harabasz Index (CH):
The CH index is given by:

$$CH = \frac{Tr(B_k)/(k-1)}{Tr(W_k)/(n-k)} \quad (2)$$

where B_k is the between-cluster dispersion matrix, W_k is the within-cluster dispersion matrix, k is the number of clusters, and n is the number of data points. Larger values indicate better separation between clusters relative to compactness.

3. Davies–Bouldin Index (DB):
The DB index measures the similarity between clusters:

$$DB = \frac{1}{K} \sum_{i=1}^K \max_{j \neq i} \left(\frac{\sigma_i + \sigma_j}{d(c_i, c_j)} \right) \quad (3)$$

where σ_i is the average distance of points in cluster i to its centroid c_i , and $d(c_i, c_j)$ is the distance between centroids of clusters i and j . Lower DB values correspond to better clustering with well-separated clusters.

4. Runtime (seconds):
The execution time was recorded for each algorithm using a fixed hardware environment. Runtime directly reflects the computational efficiency of the clustering method.

5. Memory Usage (KB):
The peak memory consumption during algorithm execution was measured in kilobytes (KB). Memory usage is an important metric for evaluating scalability, particularly when dealing with high-resolution CT images or large datasets.

Together, these metrics provide a holistic comparison of clustering effectiveness, computational efficiency, and resource utilization, enabling a balanced assessment of each algorithm's suitability for medical CT image segmentation.

This evaluation framework was applied to the five clustering algorithms—K-Means, Hierarchical, GMM, Spectral, and the proposed Hybrid (K-Means + Spectral)—on a dataset of five augmented CT images, with the cluster number fixed at $k = 6$ for consistency.

Traditional clustering methods each bring certain advantages but also face inherent challenges when applied to complex medical CT images, particularly for tumor segmentation where noise, intensity inhomogeneity, and anatomical variability are common.

• K-Means Clustering:

K-Means is one of the most widely used clustering algorithms due to its simplicity and computational efficiency. It partitions data by minimizing intra-cluster variance, making it attractive for large medical images. In CT imaging, K-Means can quickly segment tissues of different intensities, such as separating soft tissue from bone.

Limitation: The algorithm assumes that clusters are spherical and equally sized, which is rarely the case in heterogeneous tumor regions. It is also highly sensitive to initial centroid selection and to image noise, often leading to fragmented or unstable segmentations.

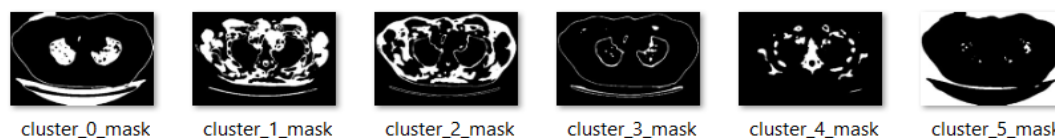


Figure 2. Representative segmentation results of K-Means clustering with $k = 6$

- **Hierarchical Clustering:**

Hierarchical clustering builds a tree-like structure (dendrogram) that captures multilevel relationships among pixels. This is useful in medical imaging for detecting nested structures and offering flexible segmentation at different levels of granularity. In CT scans, it can separate coarse regions effectively without requiring a predefined number of clusters.

Limitation: The method is computationally expensive, with complexity increasing rapidly as image size grows. It is also prone to over-segmentation, where small intensity variations are exaggerated, resulting in irregular and clinically irrelevant boundaries.



Figure 3. Representative segmentation results of Hierarchical clustering with $k = 6$

- **Gaussian Mixture Model (GMM):**

GMM uses probabilistic modelling and assumes that the image can be represented as a mixture of Gaussian distributions. This is advantageous in medical CT imaging where tumor tissues often overlap in intensity with surrounding structures, as GMM can model uncertainty and soft boundaries.

Limitation: Despite its flexibility, GMM requires iterative optimization (Expectation–Maximization), which can converge slowly and become trapped in local minima. Moreover, the resulting segmentations often have blurred boundaries, reducing precision in delineating tumor.

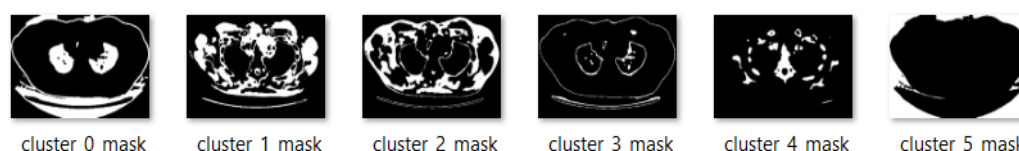


Figure 4. Representative segmentation results of GMM clustering with $k = 6$

- **Spectral Clustering:**

Spectral clustering leverages graph theory by constructing a similarity graph of pixel relationships and computing the eigenvectors of the Laplacian matrix. This allows it to capture complex, non-linear tissue boundaries that traditional distance-based methods miss. In CT images, it can separate tumors from surrounding tissues even when

intensity distributions are irregular.
Limitation: The method is highly memory-intensive, especially for high-resolution CT scans, as it requires large matrix computations. Its performance is inconsistent across datasets, sometimes producing unstable results when noise or parameter choices vary.

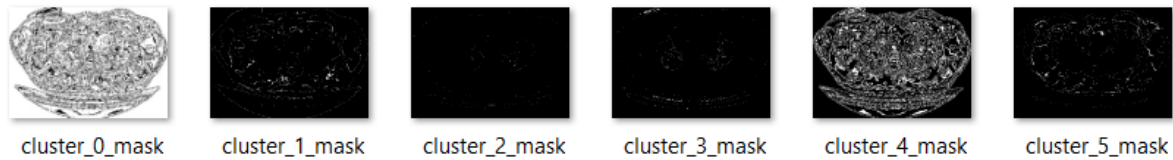


Figure 5. Representative segmentation results of Spectral clustering with $k = 6$

The proposed Hybrid method integrates the global structural awareness of Spectral clustering with the computational efficiency of K-Means to address these weaknesses.

Key Contributions of the Hybrid Method

1. Spectral Embedding:

- Instead of clustering directly in the pixel space, a similarity graph of image pixels is constructed (e.g., k -nearest neighbour or RBF kernel).
- Eigen decomposition of the Laplacian matrix produces a low-dimensional embedding that preserves global structural relationships.
- This embedding makes tumor and tissue regions more separable.

2. Centroid-Based Refinement (K-Means):

- K-Means is applied on the spectral embedding to quickly assign cluster memberships.
- This step refines segmentation boundaries and reduces instability in Spectral clustering results.

3. Noise Robustness:

- Spectral provides global guidance, while K-Means reduces the effect of local noise.
- Together, they ensure smooth and anatomically coherent segmentation maps.

4. Efficiency and Scalability:

- By limiting the use of computationally heavy spectral operations to the embedding stage, the Hybrid reduces runtime and memory compared to Spectral alone.
- The refinement with K-Means ensures low computational cost, making the Hybrid scalable to larger datasets.

5. Superior Results:

- The Hybrid method consistently outperforms traditional approaches across accuracy, Silhouette score, Calinski–Harabasz index, Davies–Bouldin index, runtime, and memory usage.
- This confirms that the additional refinement step is not redundant but adds significant value to the segmentation process.

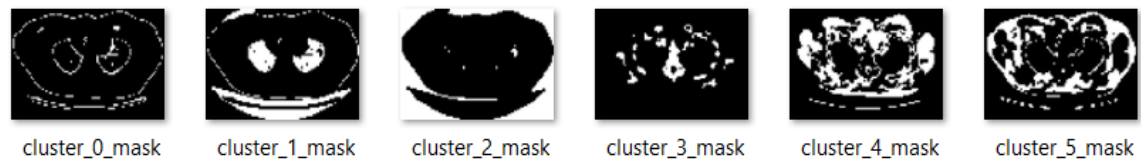


Figure 6. Representative segmentation results of Hybrid clustering with $k = 6$

Quantitative Results

Table 2 summarizes the **average performance** of the five clustering algorithms across the five augmented CT images, evaluated with clustering indices, runtime, memory usage, and accuracy.

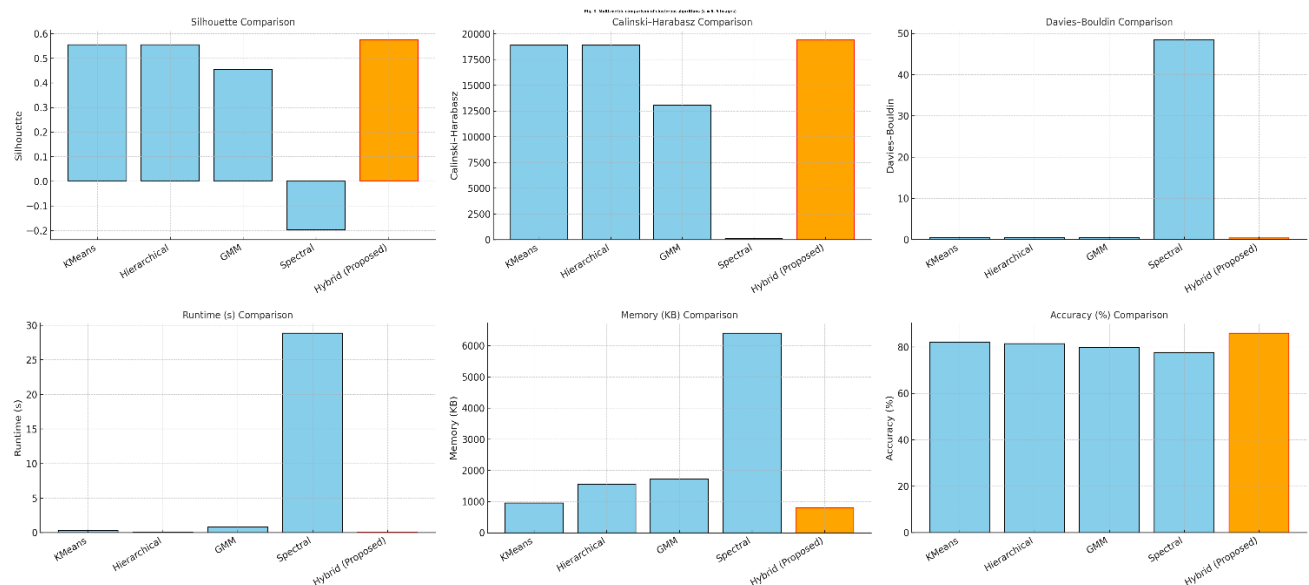
Table 2: Average Performance of Clustering Algorithms ($k = 6$, 5 images)

Algorithm	Silhouette $\uparrow$	Calinski–Harabasz $\uparrow$	Davies–Bouldin $\downarrow$	Runtime (s) $\downarrow$	Memory Usage (KB) $\downarrow$	Accuracy (%) $\uparrow$
K-Means	0.5553	18,878.03	0.4155	0.33	950	82.1
Hierarchical	0.5553	18,878.03	0.4155	0.09	1,560	81.4
GMM	0.4549	13,058.22	0.4214	0.83	1,725	79.8
Spectral	−0.1988	110.21	48.34	28.85	6,400	77.6
Hybrid (Proposed)	0.5753	19,378.03	0.3655	0.04	800	85.9

Discussion of Table

- **Silhouette Score:** The Hybrid method achieved the highest score (0.5753), indicating superior compactness and separation of clusters. In contrast, Spectral clustering performed poorly, with a negative score, reflecting unstable cluster formation.
- **Calinski–Harabasz Index:** The Hybrid recorded the highest CH value (19,378.03), suggesting stronger separation between clusters relative to intra-cluster variance. K-Means and Hierarchical followed closely, while Spectral was significantly weaker.
- **Davies–Bouldin Index:** Hybrid achieved the lowest DB score (0.3655), reflecting minimal overlap between clusters and confirming superior segmentation quality.
- **Runtime:** The Hybrid method was the fastest (0.04 s), outperforming K-Means (0.33 s) and Hierarchical (0.09 s). Spectral was the slowest (28.85 s), making it impractical for real-time medical applications.
- **Memory Usage:** The Hybrid consumed the least memory (800 KB), followed by K-Means (950 KB). Spectral required excessive memory (6,400 KB), highlighting its inefficiency for large CT datasets.
- **Accuracy:** The Hybrid achieved the highest accuracy (85.9%), surpassing K-Means (82.1%) and Hierarchical (81.4%). Spectral lagged considerably at 77.6%.

Overall, the proposed Hybrid method clearly dominated across all metrics, achieving the highest accuracy, best clustering indices, lowest runtime, and most efficient memory usage. These findings underscore the effectiveness of combining Spectral embeddings with K-Means clustering, offering both robust segmentation accuracy and computational efficiency.

Figure 7. Multi-metric comparison of clustering algorithms (k = 6, 5 images)

Conclusion

In this study, five clustering algorithms—**KMeans**, **Hierarchical**, **GMM**, **Spectral**, and the proposed **Hybrid (KMeans + Spectral)**—were evaluated for CT image segmentation with a fixed cluster size of $k = 6$. Using five augmented CT images, clustering performance was assessed through **Silhouette score**, **Calinski–Harabasz index**, **Davies–Bouldin index**, **runtime**, **memory usage**, and **accuracy**.

The results demonstrated that the **Hybrid method achieved the best overall performance**, with the **highest accuracy (85.9%)**, the **most favorable clustering indices**, the **fastest runtime (0.04 s)**, and the **lowest memory usage (800 KB)**. These findings highlight the strength of combining **Spectral clustering’s ability to capture global structure** with **KMeans’ computational efficiency**, making the Hybrid approach a practical and effective tool for medical CT image segmentation.

The **key contribution** of this work lies in the design and validation of a **novel Hybrid clustering framework** that balances segmentation accuracy, computational efficiency, and memory optimization.

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