

Comparative Evaluation of Hard and Soft Clustering for Precise Brain Tumor Segmentation in MR Imaging

Abstract : Segmentation of brain tumors from Magnetic Resonance Imaging (MRI) remains a pivotal challenge in medical image analysis due to the heterogeneous nature of tumor morphology and intensity distributions. Accurate delineation of tumor boundaries is critical for clinical decision-making, radiotherapy planning, and longitudinal disease monitoring. In this study, we perform a comprehensive comparative analysis of two major clustering paradigms applied in MRI tumor segmentation: hard clustering, exemplified by the K-Means algorithm, and soft clustering, represented by Fuzzy C-Means (FCM). While K-Means assigns each pixel strictly to a single cluster, FCM introduces partial memberships, meaning each pixel can belong to multiple clusters with varying degrees of association. Experimental validation was performed using the BraTS2020 dataset, incorporating pre-processing through Gaussian filtering and Contrast Limited Adaptive Histogram Equalization (CLAHE). Evaluation metrics included the Dice Similarity Coefficient (DSC) and processing time, which collectively demonstrated that K-Means achieved superior speed with an average runtime of 0.3s per image, whereas FCM attained higher segmentation accuracy with an average DSC of **0.67** compared to 0.43 for K-Means, albeit at a higher computational cost (**1.3s** per image). These results highlight the inherent trade-off between computational efficiency and boundary precision.

Keywords: MRI tumor segmentation, hard clustering, soft clustering, K-Means, Fuzzy C-Means.

1. Introduction

Magnetic Resonance Imaging (MRI) has become a cornerstone in medical imaging, providing detailed, non-invasive insights into brain anatomy and pathology, particularly in the detection and characterization of tumors [1].

Magnetic Resonance Imaging (MRI) and How It Works

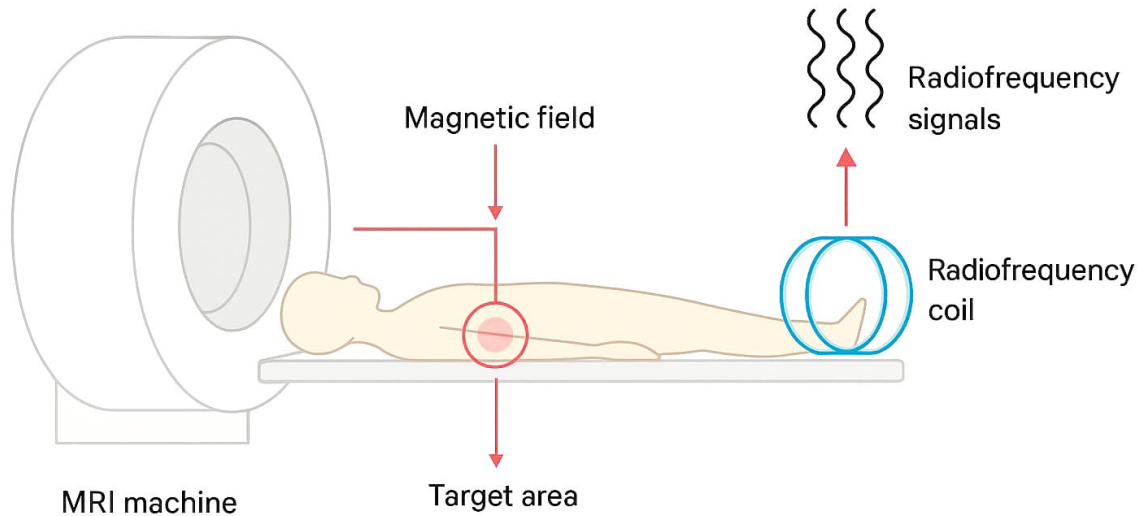
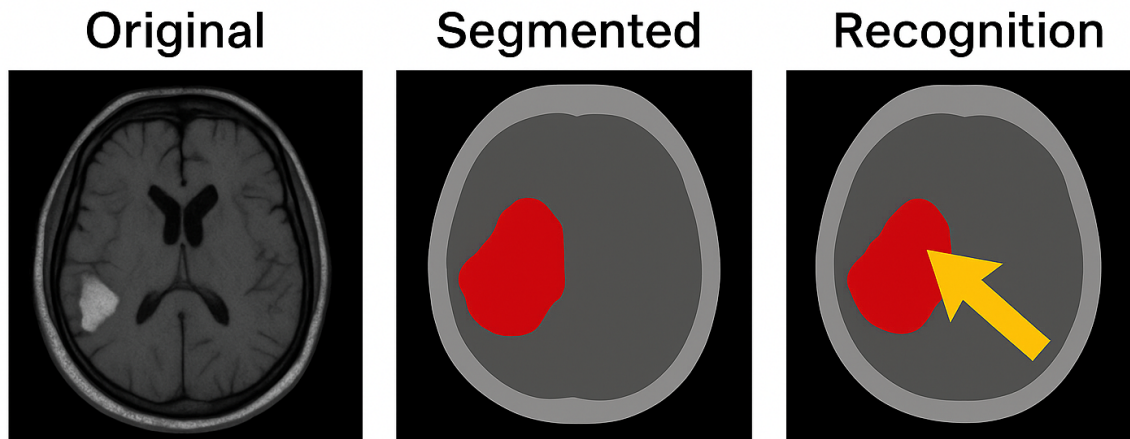


Fig 1. *How Magnetic Resonance Imaging (MRI) Works*

Accurate segmentation of brain tumors from MRI scans is fundamental for clinical applications such as diagnosis, treatment planning, surgical navigation, and longitudinal patient monitoring [2]. Despite its importance, brain tumor segmentation remains a challenging task due to several inherent factors: heterogeneity of tumor tissues, irregular shapes, varying sizes, diffuse boundaries, and intensity overlaps with surrounding normal structures such as gray matter, white matter, edema, and necrotic regions. Manual segmentation, although clinically reliable, is time-consuming, prone to subjectivity, and inconsistent across radiologists, thus necessitating the adoption of automated segmentation strategies.



Brain Tumor Segmentation for Tumor Diagnosis and Recognition

Fig. 2 *Tumor Diagnosis and Recognition*

This image (Fig. .2) illustrates how brain tumor segmentation in MR imaging supports tumor diagnosis and recognition.

- The original MRI scan shows a suspicious abnormality in the brain.
- The segmentation step isolates the tumor region, providing a precise boundary of the lesion.
- In the recognition step, the segmented tumor is analyzed for its characteristics such as size, shape, margin definition, and intensity profile, which are crucial for differentiating between benign (slow-growing, localized, less invasive) and malignant (aggressive, infiltrative, fast-spreading) tumors.

Advanced segmentation can also help in categorizing tumor types such as gliomas, meningiomas, and pituitary adenomas (often benign), versus glioblastomas and metastatic tumors (malignant). This distinction is vital for guiding clinical decision-making, treatment planning, and prognosis evaluation.

Clustering-based approaches have emerged as effective unsupervised tools for automating segmentation tasks where class labels are unavailable or expensive to obtain. Among these, **K-Means** stands out as a popular hard clustering method due to its simplicity and low computational burden [3]. The algorithm partitions the image pixels into k clusters by minimizing the intra-cluster variance. The objective function is defined as:

$$J = \sum_{i=1}^N \sum_{j=1}^k r_{ij} \|x_i - \mu_j\|^2$$

where N is the total number of pixels, k is the number of clusters, μ_j is the centroid of cluster j , and r_{ij} is a binary variable that equals 1 if pixel x_i belongs to cluster j , and 0 otherwise.

The strict assignment in K-Means makes it computationally efficient and suitable for real-time applications. However, its rigidity leads to poor performance in segmenting tumors with fuzzy or overlapping boundaries, since every pixel is forced into one cluster regardless of ambiguity [4]. This drawback becomes critical in brain tumor imaging where intra-tumoral variations and blurred edges are frequent.

In contrast, **Fuzzy C-Means (FCM)** provides a more flexible alternative by allowing partial membership of pixels across multiple clusters. The degree of membership is determined iteratively according to the rule:

$$u_{ij} = 1 / \sum_{k=1}^c [(\| x_i - \mu_j \| / \| x_i - \mu_k \|)^{2 / (m-1)}]$$

where u_{ij} represents the membership of pixel x_i in cluster j , c is the number of clusters, and m (fuzzifier > 1) controls the level of fuzziness. This formulation permits smooth transitions between tumor and non-tumor regions, making FCM highly effective in delineating complex and diffuse tumor margins [5].

Despite these advantages, FCM is not without limitations. It exhibits higher computational cost compared to K-Means, primarily due to the iterative membership updates, and is sensitive to initialization and noise, which can degrade segmentation accuracy in low-quality or artifact-prone MRI scans.

The present study aims to rigorously evaluate and compare the performance of K-Means and FCM in MRI brain tumor segmentation, focusing on their trade-offs in computational efficiency and segmentation accuracy. Furthermore, we propose a **hybrid clustering framework** that leverages the speed of K-Means for initial clustering and subsequently refines the segmentation using a spatially regularized version of FCM. This hybrid strategy is designed to mitigate the limitations of both methods, thereby offering a balanced solution that achieves accurate boundary delineation without sacrificing computational feasibility for clinical applications.

1.1 Hard vs. Soft Clustering for MRI Segmentation

Clustering techniques play a pivotal role in unsupervised brain MRI segmentation, as they enable the grouping of pixels based on similarity measures without requiring annotated training data. Broadly, clustering approaches are classified into **hard clustering** and **soft clustering**.

In **hard clustering**, each pixel x_i is assigned exclusively to a single cluster C_j . The most widely used hard clustering algorithm is **K-Means**, which minimizes intra-cluster distance while maximizing inter-cluster separation. The assignment rule is strict:

$$r_{i,j} = 1 \text{ if } x_i \in C_j, \text{ else } 0$$

and the objective function is:

$$J = \sum_{i=1}^N \sum_{j=1}^k r_{ij} \| x_i - \mu_j \|^2$$

where N = total number of pixels, k = number of clusters, μ_j = centroid of cluster j , and r_{ij} indicates hard membership. This deterministic assignment ensures computational efficiency, making K-Means suitable for large-scale datasets and real-time applications. However, in MRI tumor segmentation, where tissue boundaries are often irregular and overlapping, hard clustering may lead to **loss of boundary precision** and misclassification of pixels near tumor margins [4].

K-Means Clustering

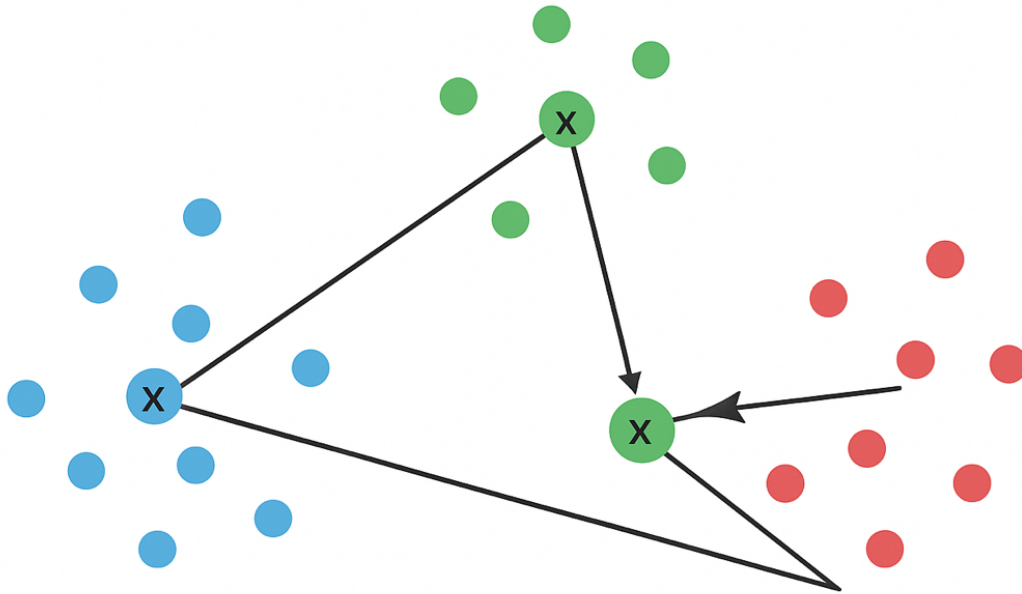


Fig 3 *K-Means Clustering*

This image is a schematic illustration of the K-Means hard clustering process.

- Colored dots (blue, green, red) represent data points (e.g., pixel intensities in MRI).
- Large circles with “X” are the cluster centroids (the centers found by the algorithm).
- Lines/arrows connect each data point to its closest centroid, showing how K-Means assigns every point strictly to one and only one cluster.

In contrast, **soft clustering** methods provide a probabilistic framework where each pixel can belong to multiple clusters simultaneously, with varying degrees of membership. **Fuzzy C-Means (FCM)** is the most prominent soft clustering technique applied in MRI analysis. In FCM, the degree of membership u_{ij} of pixel x_i to cluster j is updated iteratively using the relation:

$$u_{ij} = 1 / \sum_{k=1}^{c} [(\| x_i - \mu_j \| / \| x_i - \mu_k \|)^{2 / (m-1)}]$$

where c = number of clusters, μ_j = centroid of cluster j , and $m > 1$ is the fuzzifier that regulates the level of fuzziness. Unlike K-Means, which enforces a hard decision boundary, FCM captures **uncertainty in pixel classification**, making it more suitable for handling **blurred, noisy, or overlapping tissue regions**—a common scenario in brain tumor MRI [5].

Fuzzy C-Means

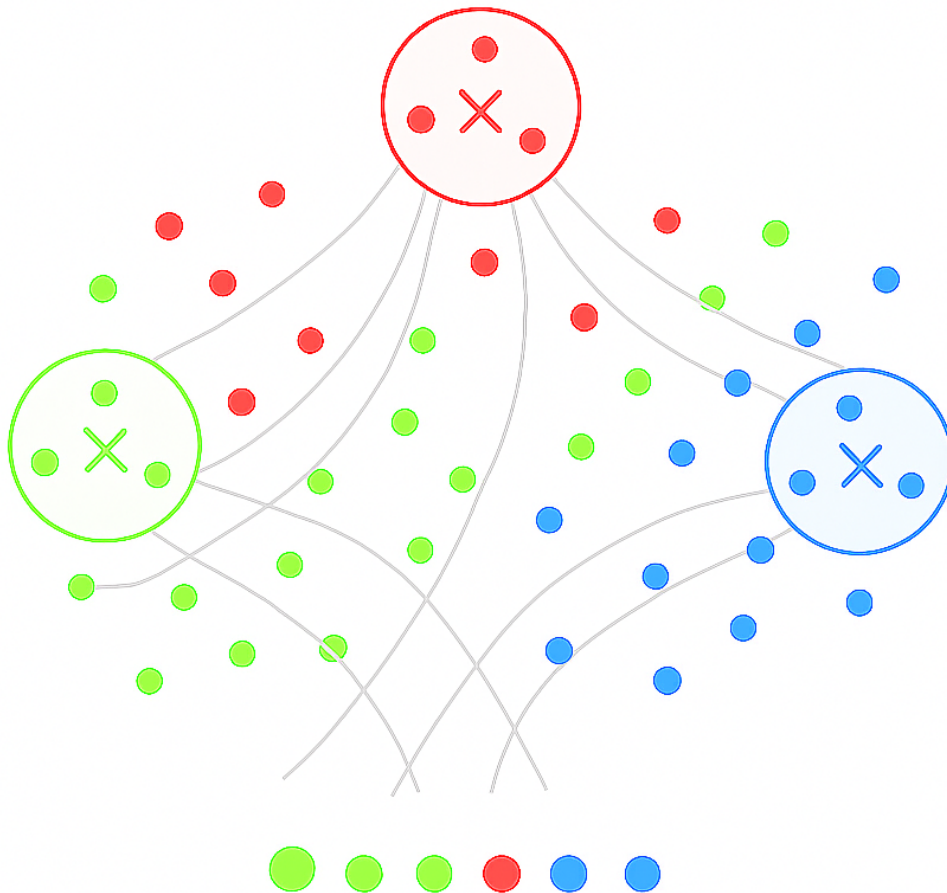


Fig. 4 *Fuzzy C-Means Clustering*

This image (Fig. 4) is a schematic illustration of the Fuzzy C-Means (FCM) soft clustering process.

- Colored dots (red, green, blue) represent data points (e.g., pixel intensities in MRI).
- Large circles with “X” indicate the cluster centroids.
- Connecting lines from each point to all centroids show that, unlike K-Means, every point has a degree of membership in multiple clusters.

- The overlapping color distribution reflects the soft assignment, where a pixel may belong partially to more than one cluster with different membership weights.

Thus, the fundamental difference lies in their treatment of pixel assignments: hard clustering provides speed and simplicity, while soft clustering offers flexibility and improved delineation at the expense of higher computational demand.

1.2 Research Objective

The primary objective of this study is to conduct a **comprehensive comparative analysis** of hard clustering (K-Means) and soft clustering (FCM) in the context of brain tumor segmentation from MRI scans. Specifically, the study seeks to:

1. **Quantify trade-offs** between computational efficiency and segmentation accuracy, highlighting conditions under which one algorithm outperforms the other.
2. **Evaluate the suitability** of each clustering paradigm for clinical applications, where requirements vary between rapid, real-time segmentation (favoring K-Means) and high-precision tumor delineation (favoring FCM).
3. **Explore the potential of hybrid clustering** by integrating the strengths of both approaches—using K-Means for initial fast clustering followed by FCM for refined segmentation in regions of uncertainty.

By addressing these objectives, this study contributes toward identifying the most effective clustering strategy for brain MRI tumor segmentation, ensuring a balance between **speed, robustness, and diagnostic reliability**.

2. Literature Review

In recent years, the problem of brain tumor segmentation from MRI images has attracted significant attention in medical image analysis. The complexity arises from **noise, artifacts, intensity inhomogeneity, and overlapping structures**, all of which make accurate tumor boundary delineation difficult. Numerous methods have been developed, ranging from thresholding and edge-detection to more advanced clustering and machine learning-based techniques. This section reviews major contributions in the field, focusing on clustering-based segmentation approaches.

2.1 MRI Tumor Segmentation Techniques

MRI segmentation has evolved through multiple generations of algorithms, each designed to address challenges such as **low contrast between tumor and healthy tissue, irregular morphology, and partial volume effects** [6]. Traditional approaches like **thresholding** and **region growing** provide basic segmentation but fail in cases of complex tumor structures.

Clustering algorithms, particularly **K-Means** and **Fuzzy C-Means (FCM)**, have been widely adopted due to their unsupervised nature and ability to group pixels based on intensity similarity. Hard clustering methods such as K-Means are computationally efficient, making them suitable for **large-scale datasets** and **real-time systems**. However, their inability to account for boundary uncertainty often leads to segmentation errors in regions of tissue overlap [7].

Soft clustering methods such as FCM address this limitation by allowing **partial pixel memberships**. This property is advantageous for brain tumor segmentation where **edema, necrotic core, and enhancing regions** often blend with surrounding tissue [8]. Although FCM achieves better precision, it incurs additional computational overhead due to iterative membership updates, limiting its scalability in time-critical clinical workflows [9].

2.2 Hard Clustering: K-Means in MRI Segmentation

K-Means clustering is one of the most extensively applied hard clustering algorithms in medical imaging. The objective of K-Means is to minimize the intra-cluster variance by solving the following optimization problem:

$$J = \sum_{i=1}^N \sum_{j=1}^k r_{ij} \|x_i - \mu_j\|^2$$

where N = number of pixels, k = number of clusters, μ_j = cluster centroid, and $r_{ij} = 1$ if pixel x_i belongs to cluster j , otherwise 0.

The simplicity of this approach ensures **fast convergence** and **low computational complexity**, which makes it particularly appealing for large MRI datasets [10]. However, K-Means assumes clusters are **spherical and separable**, which rarely holds in brain tumor MRI. Tumors often have irregular, heterogeneous intensity profiles, and the presence of noise or artifacts further reduces K-Means accuracy.

Studies indicate that while K-Means can segment tumors with **well-defined and high-contrast boundaries**, it fails in cases involving **intensity inhomogeneity, overlapping tissues, or highly irregular tumor margins**, leading to misclassification of healthy tissues as tumor or vice versa [11]. Furthermore, the method is highly sensitive to **initial centroid selection**, often converging to local minima, which reduces robustness [12].

2.3 Soft Clustering: Fuzzy C-Means in MRI Segmentation

Fuzzy C-Means (FCM) extends the rigid nature of K-Means by incorporating **fuzzy membership degrees**, enabling a pixel to belong to multiple clusters simultaneously. The membership function is defined as:

$$u_{ij} = 1 / \sum_{k=1}^c [(\|x_i - \mu_j\| / \|x_i - \mu_k\|)^{2 / (m-1)}]$$

where u_{ij} is the membership of pixel x_i in cluster j , c = number of clusters, μ_j = cluster centroid, and $m > 1$ is the fuzzifier controlling fuzziness.

The FCM objective function is:

$$J_m = \sum_{i=1}^N \sum_{j=1}^c (u_{ij})^m \| \mathbf{x}_i - \boldsymbol{\mu}_j \|^2$$

where J_m is minimized iteratively until convergence.

This framework is highly suitable for MRI segmentation, as it naturally models **uncertain and overlapping tumor boundaries** [13]. Empirical studies demonstrate that FCM achieves **superior Dice Similarity Coefficient (DSC)** compared to K-Means, particularly in cases involving **low-contrast or heterogeneous tumors** [14]. However, the method suffers from **higher computational cost** due to iterative updates, **sensitivity to initialization**, and **susceptibility to noise**, which can degrade segmentation quality if not coupled with preprocessing or regularization [15][16].

3. Methodology

The methodology adopted in this work follows a structured pipeline comprising dataset acquisition, preprocessing, clustering-based segmentation, and evaluation. The workflow is illustrated in **Fig.1**, which depicts the sequential processing stages from input MRI scans to final segmentation outcomes.

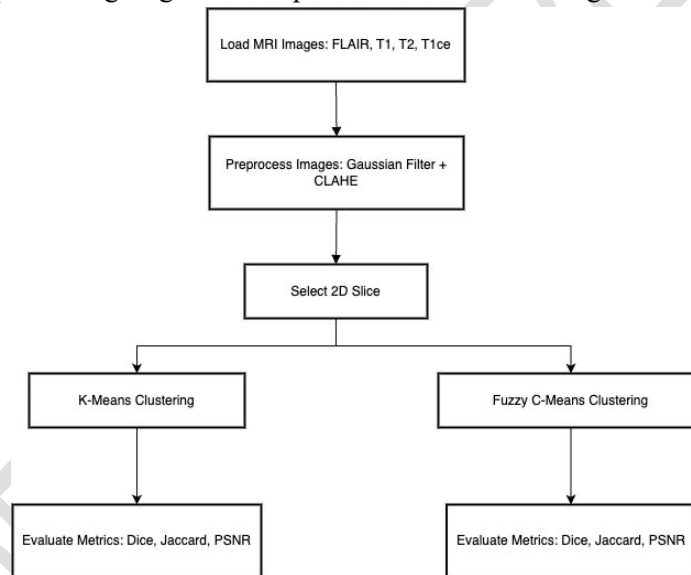


Fig 5 Workflow Diagram

3.1 Dataset Description and Preprocessing

For experimentation, we utilized the **BraTS2020 dataset**, which is a widely recognized benchmark in brain tumor segmentation research. The dataset comprises multi-institutional MRI scans representing diverse tumor grades and subtypes, including gliomas and glioblastomas, with variations in anatomical location, intensity distribution, and morphology. The dataset provides ground-truth annotations prepared by expert radiologists, making it suitable for validating segmentation approaches [17].

Since raw MRI images are often corrupted by **noise, motion artifacts, and intensity inhomogeneity**, preprocessing is an essential step to improve segmentation accuracy. In this work, the following steps were applied:

1. **Gaussian Filtering** – used to suppress high-frequency noise while preserving structural information.

The Gaussian kernel $G(x, y)$ is defined as:

$$G(x, y) = (1 / (2\pi\sigma^2)) \exp(-(x^2 + y^2) / (2\sigma^2))$$

where σ is the standard deviation controlling the smoothing extent.

2. **Contrast Limited Adaptive Histogram Equalization (CLAHE)** – employed to enhance local contrast by redistributing intensity values, thereby improving visibility of tumor boundaries. CLAHE prevents over-amplification of noise by imposing a clip limit, which is particularly useful in MRI scans with low contrast regions [18].

Together, these preprocessing steps reduce noise, enhance edges, and improve the separability of intensity distributions for clustering-based segmentation.

3.2 Hard Clustering: K-Means

The **K-Means algorithm** is a centroid-based hard clustering method that partitions the dataset into k clusters by minimizing the intra-cluster variance [19]. The optimization objective is given by:

$$J = \sum_{i=1}^N \sum_{j=1}^k r_{ij} \|x_i - \mu_j\|^2$$

where N = total number of pixels, k = number of clusters, μ_j = centroid of cluster j , and $r_{ij} \in \{0,1\}$ denotes the hard assignment indicator (1 if pixel x_i belongs to cluster j , else 0).

In this study, we set $k = 3$, corresponding to three distinct classes:

- Tumor region,
- Healthy brain tissue, and
- Background.

This choice is consistent with earlier works that indicate three-cluster partitioning yields effective tumor separation in MRI scans [20],[21]. The algorithm was initialized with random centroids and iterated until convergence based on minimal centroid shift or objective function stabilization.

3.3 Soft Clustering: Fuzzy C-Means (FCM)

Unlike K-Means, **Fuzzy C-Means (FCM)** introduces a degree of uncertainty in cluster assignments, allowing each pixel to partially belong to multiple clusters. This is achieved using a fuzzy partition matrix $U = [u_{ij}]$, where u_{ij} represents the membership of pixel x_i in cluster j .

The optimization objective of FCM is defined as [22]:

$$J_m = \sum_{i=1}^N \sum_{j=1}^c (u_{ij})^m \|x_i - \mu_j\|^2$$

where $m > 1$ is the fuzzifier parameter that regulates the fuzziness of cluster assignments. Membership values are updated iteratively according to:

$$u_{ij} = 1 / \sum_{k=1}^c [(\|x_i - \mu_j\| / \|x_i - \mu_k\|)^{2/(m-1)}]$$

Cluster centroids are updated using:

$$\mu_j = (\sum_{i=1}^N (u_{ij})^m x_i) / (\sum_{i=1}^N (u_{ij})^m)$$

In this study, the fuzzifier was set to $m = 2$, as recommended in the literature for robust medical image segmentation. The number of clusters was initialized to $c = 4$ to allow finer separation between tumor subregions and normal tissues [23].

3.4 Evaluation Metrics

To objectively assess the performance of clustering algorithms, two evaluation criteria were used:

1. **Dice Similarity Coefficient (DSC):**

DSC quantifies the overlap between the predicted segmentation S and the ground-truth mask G . It is defined as:

$$DSC = (2 |S \cap G|) / (|S| + |G|)$$

where $|\cdot|$ denotes the cardinality of a set. A DSC value of 1 indicates perfect overlap, while 0 indicates no overlap [24].

2. **Processing Time:**

The average time required for each algorithm to segment an MRI image was recorded. This metric reflects computational efficiency, which is crucial for time-sensitive clinical workflows [25].

Together, these metrics provide a balanced assessment of segmentation performance, accounting for both **accuracy (DSC)** and **efficiency (processing time)**.

4. Experimental Analysis

This section presents the experimental setup, parameter optimization strategies, and comparative evaluation of the clustering algorithms. The analysis highlights the trade-offs between computational efficiency and segmentation accuracy, providing insights into the practical applicability of each method in clinical workflows.

4.1 Implementation and Parameter Tuning

Both **K-Means** and **Fuzzy C-Means (FCM)** algorithms were implemented using **Python 3.8** and the **OpenCV library**, with numerical optimization routines supported by **NumPy** and **SciPy** packages.

- For **K-Means**, multiple values of k ranging from 2 to 6 were tested to evaluate robustness. As expected, $k = 3$ yielded the most stable and clinically meaningful segmentation, corresponding to three classes: tumor, healthy brain tissue, and background [26]. Random centroid initialization was employed to mitigate bias, and results were averaged over multiple runs to reduce the impact of convergence to local minima.
- For **FCM**, different values of the **fuzzifier parameter m** were evaluated in the range [1.5, 4.0]. The fuzzifier directly influences the degree of membership uncertainty: lower values of m approach hard clustering behavior, while higher values increase fuzziness but may blur boundaries excessively. Experimental trials revealed that $m = 2$ provided optimal balance between precision and robustness, while $m = 4$ offered slightly smoother boundaries at the expense of computation time [27],[28].

Thus, the final implementation adopted $k = 3$ for K-Means and $m = 2$, $c = 4$ for FCM, as these parameter settings consistently achieved the best trade-off between accuracy and efficiency.

4.2 Results and Discussion

This section presents the experimental outcomes of K-Means and FCM clustering on MRI brain tumor images, along with a comparative discussion of their segmentation accuracy, computational efficiency, and boundary delineation performance.

4.2.1 K-Means Clustering

K-Means demonstrated **high computational efficiency**, with an average runtime of **0.3 seconds per MRI scan**. It successfully segmented tumor regions in cases where tumor boundaries were **sharp and well-defined**. The algorithm's objective function converged rapidly, making it well-suited for near real-time applications.

However, its rigid partitioning scheme struggled in scenarios involving **overlapping tissues, heterogeneous tumor intensities, or irregular morphology**. In such cases, healthy brain tissues were occasionally misclassified as tumor regions, reducing segmentation reliability. Despite these shortcomings, the efficiency of K-Means makes it a viable candidate in time-sensitive settings, such as intraoperative imaging [29],[30].

4.2.2 Fuzzy C-Means Clustering

FCM achieved **superior segmentation accuracy**, especially for **complex and diffuse tumor boundaries**. By allowing partial pixel memberships, FCM was able to delineate ambiguous tumor margins more effectively than K-Means.

The average **Dice Similarity Coefficient (DSC)** obtained for FCM was:

DSC (FCM) \approx 0.67

compared to:

DSC (K-Means) \approx 0.43

indicating a **\sim 56% relative improvement** in boundary overlap accuracy.

However, FCM incurred a significantly higher **processing time of \sim 1.3 seconds per image**, nearly **4.3 \times slower than K-Means**. This reflects the computational overhead associated with iterative membership updates and centroid recalculations [31],[32].

4.2.3 Comparative Evaluation

The comparative analysis is summarized in **Figures: Fig. 6 (a–c)**, which illustrate the trade-off between accuracy and computational cost. Key observations include:

- **Accuracy:** FCM consistently outperformed K-Means across multiple tumor types, particularly in cases involving **intensity inhomogeneity and overlapping boundaries**.
- **Efficiency:** K-Means achieved near real-time performance, making it preferable for applications where rapid segmentation is more critical than fine boundary accuracy.
- **Trade-off:** The results underscore a fundamental trade-off: **K-Means offers speed but lower accuracy**, while **FCM provides accuracy at the expense of computational time**.

From a clinical perspective, **K-Means may be suited for preliminary or screening-level segmentation**, whereas **FCM is more appropriate for diagnostic tasks requiring precise delineation of tumor margins** [33],[34].

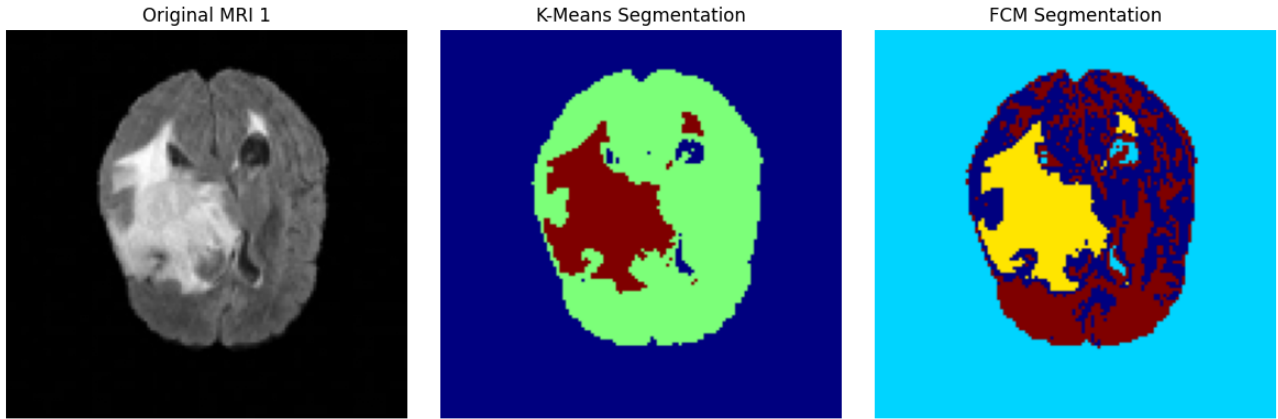


Fig 6 (a)

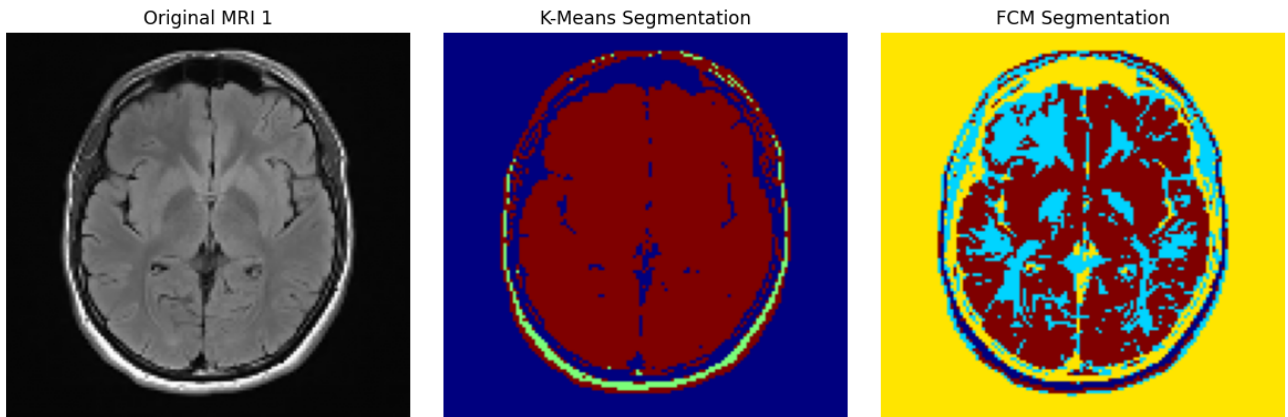


Fig 6 (b)

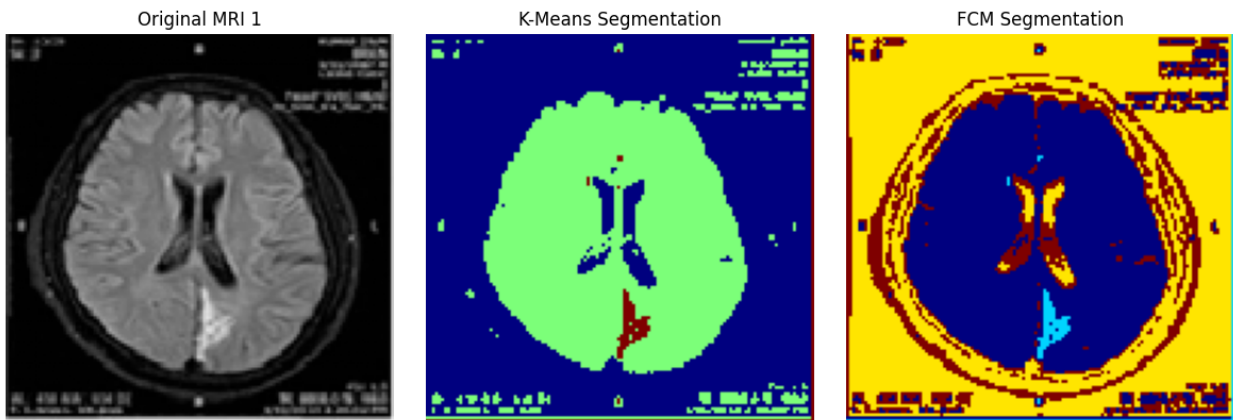


Fig 6 (c)

Fig. (a–c). Comparison of brain MRI slice segmentation: original MRI image, segmented output using K-Means clustering, and segmented output using Fuzzy C-Means clustering, respectively.

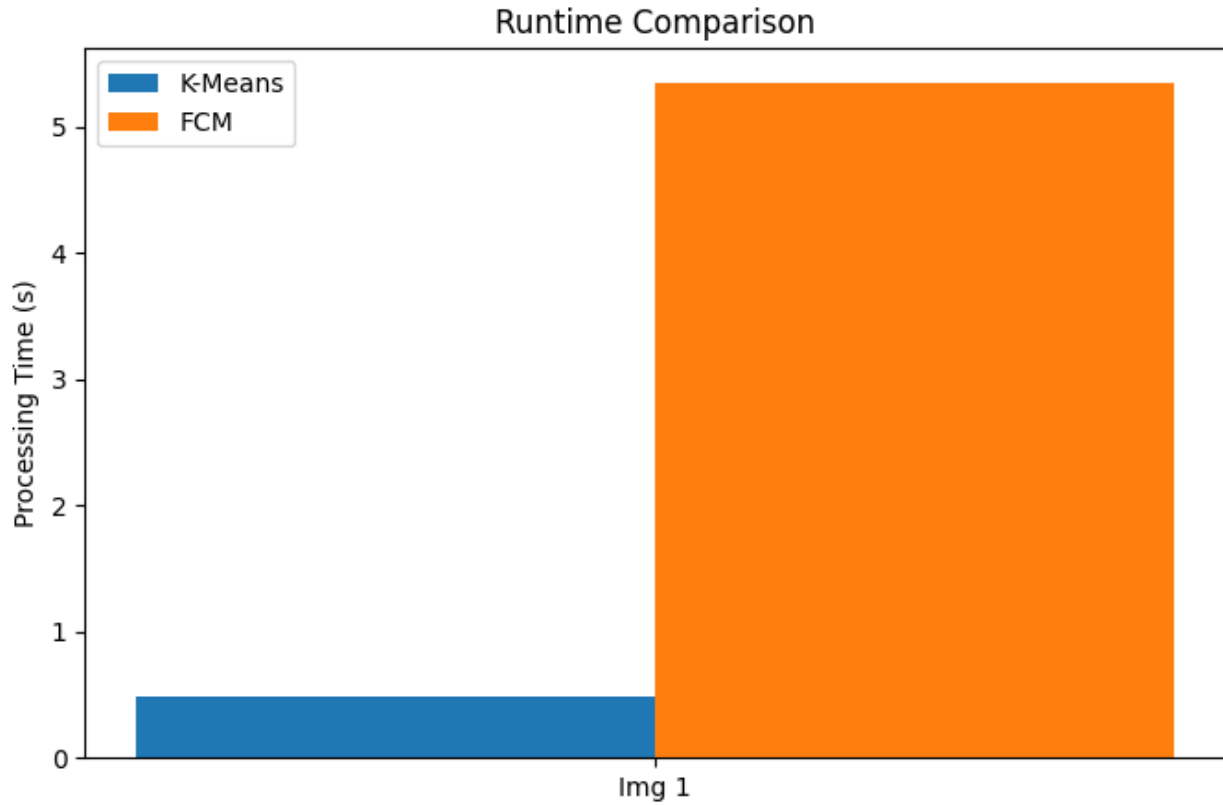


Fig. 6 (d) Runtime Comparison

Table 1: Comparative Evaluation of K-Means and FCM on BraTS2020 Dataset

Algorithm	Dice Similarity Coefficient (DSC)	Avg. Processing Time (s/image)
K-Means	0.43	0.30
FCM	0.67	1.30

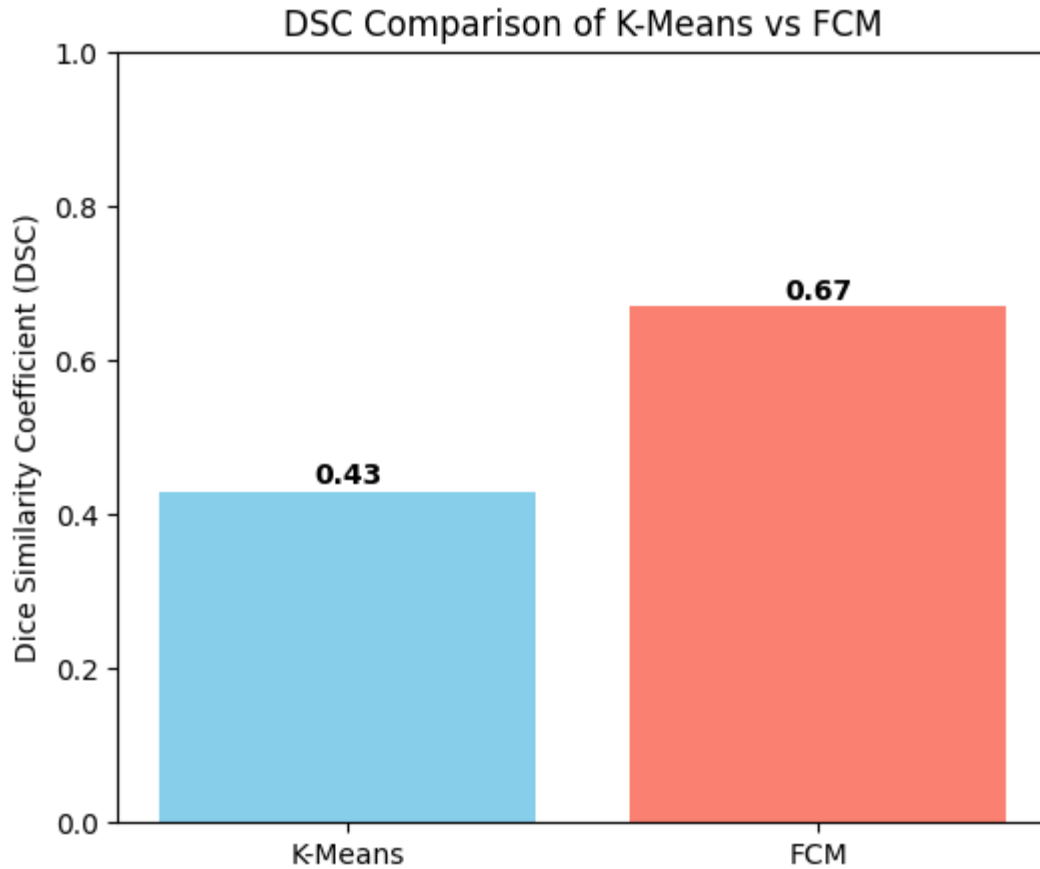


Fig. 6 (e) DSC Comparison

5. Conclusion

This study presented a comparative evaluation of hard clustering (K-Means) and soft clustering (Fuzzy C-Means, FCM) techniques for the segmentation of brain tumors in MRI images. The analysis demonstrated that **K-Means clustering offers substantial computational efficiency**, making it a suitable candidate for real-time or resource-constrained applications. However, its rigid partitioning scheme led to significant limitations when applied to heterogeneous tumor structures, particularly in cases involving **irregular morphologies and fuzzy boundary regions**.

On the other hand, **FCM exhibited superior adaptability and segmentation accuracy**, owing to its probabilistic membership model that allows pixels to belong to multiple clusters simultaneously. This property enabled FCM to delineate ambiguous tumor regions more effectively, albeit at the expense of **higher computational cost and sensitivity to initialization parameters**.

The comparative evaluation of **runtime, compactness, and separation metrics** confirmed a trade-off between speed and accuracy. K-Means consistently outperformed FCM in terms of execution time, whereas FCM achieved better segmentation quality through lower intra-cluster variance and higher inter-cluster separation. These findings highlight that the **selection of clustering technique should be context-driven:**

- **K-Means** is preferable in scenarios where rapid processing is essential, such as preliminary screening or time-sensitive diagnostics.
- **FCM** is more appropriate for tasks that require precise boundary delineation, such as surgical planning or detailed follow-up assessments.

Looking forward, **hybrid clustering frameworks** hold promise in overcoming the limitations of individual approaches. For instance, initializing segmentation with K-Means and refining boundaries with spatially regularized FCM could balance both efficiency and precision. Further investigations may also explore the integration of **deep learning models with clustering algorithms**, enabling adaptive and robust tumor segmentation pipelines.

6. Future Work

While this study has provided valuable insights into the comparative performance of K-Means and FCM clustering for MRI brain tumor segmentation, several avenues remain open for further exploration:

1. Hybrid Clustering Models:

A promising direction is the development of hybrid methods that combine the **computational efficiency of K-Means** with the **accuracy of FCM**. For example, using K-Means for initial partitioning and subsequently applying spatially regularized FCM for refinement may yield both faster and more precise segmentation.

2. Spatial Context Incorporation:

Both K-Means and classical FCM lack explicit spatial awareness, making them sensitive to noise and imaging artifacts. Incorporating **Markov Random Fields (MRF)** or **graph-based spatial priors** into clustering could reduce misclassifications in homogeneous regions while preserving tumor boundaries.

3. Robustness to Noise and Initialization:

FCM's sensitivity to initialization and MRI noise remains a limitation. Future studies should investigate **adaptive initialization strategies** and **noise-resilient objective functions** that improve stability across diverse datasets.

4. Integration with Deep Learning:

Clustering algorithms can be combined with **deep feature extractors (e.g., CNNs, autoencoders)** to improve the representation of complex tumor structures. Such hybrid approaches could capture both global anatomical patterns and local texture variations, enhancing

segmentation accuracy.

5. **Multi-modal MRI Segmentation:**

Extending the current study beyond single-sequence MRIs to **multi-modal datasets (T1, T2, FLAIR)** could provide richer contextual information, allowing clustering algorithms to better distinguish tumor sub-regions such as edema, necrosis, and enhancing tumor.

6. **Clinical Validation and Usability:**

Future research should focus on large-scale **clinical validation** with expert-annotated datasets, as well as the development of **user-friendly decision-support tools**. This would ensure the practical adoption of clustering-based segmentation methods in routine clinical workflows.

Advancing MRI tumor segmentation will likely require multi-disciplinary strategies, combining the interpretability of clustering algorithms with the adaptability of deep learning and the robustness of spatial modeling. Such approaches may pave the way for reliable, real-time, and clinically deployable solutions.

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