

Image Segmentation Using Fuzzy C-Mean

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Abstract—Image segmentation is a foundational step in many computer vision and medical imaging pipelines. Fuzzy clustering methods such as Fuzzy C-Means (FCM) provide soft pixel-to-cluster assignments that help handle noise, boundary ambiguity, and intensity inhomogeneity. This paper presents an implementation of FCM applied to synthetic Gaussian images and BrainWeb MRI slices. We describe a complete pipeline: initialization of fuzzy membership, iterative update of cluster centers and memberships, crisp labeling by maximum membership, and quantitative evaluation using Dice similarity and ASA (Average Segmentation Accuracy). The implementation mirrors a standard FCM formulation and is extended with a thorough experimental setup, including convergence monitoring and visualizations of segmented clusters. A literature survey of 25 relevant fuzzy-clustering segmentation papers is included to position our work. Experimental results on BrainWeb and synthetic datasets show that FCM, when carefully implemented, provides reliable separation of background, CSF, GM and WM in skull-stripped T1 slices, while quantitative scores (Dice, ASA) highlight strengths and limitations of the approach. Finally, we discuss runtime characteristics and propose directions for improved robustness (spatial regularization, kernelization, bias field correction).

Index Terms—Image segmentation, fuzzy c-means, FCM, Dice coefficient, ASA, BrainWeb, medical imaging

I. INTRODUCTION

Image segmentation partitions an image into meaningful regions and is essential for downstream tasks like diagnosis, object recognition and image understanding. Classical hard clustering (e.g., k-means) assigns each pixel to exactly one cluster which can be brittle in presence of noise or overlapping class distributions. Fuzzy clustering methods (notably Fuzzy C-Means, FCM) assign soft memberships that express partial association to multiple clusters. This property improves robustness to intensity inhomogeneity and ambiguous boundaries which commonly occur in medical images such as MRI.

This work implements and evaluates the standard FCM algorithm on (1) synthetic Gaussian test images with ground truth and (2) BrainWeb T1 skull-stripped slices with expert discrete ground truth for background (BCK), cerebrospinal fluid (CSF), gray matter (GM) and white matter (WM). We compute quantitative metrics (Dice score per tissue and ASA) and present visual results for cluster maps and crisp segmentations. The paper also synthesizes a literature survey of 25 important works that improved FCM via spatial regularization, kernelization, multi-kernel approaches, local fuzzy terms, and hybrid models.

II. RELATED WORK

Fuzzy clustering and FCM variants have been widely studied in image segmentation. Table I (condensed) summarizes 25 representative works covering spatial FCM (e.g., Chuang et al.), bias field corrected FCM (Ahmed et al.), kernelized FCM (Zhang & Chen), fuzzy local information methods (Krinidis & Chatzis), multi-kernel and hybrid approaches, and recent 3D/volume extensions for brain MRI. These works motivated our baseline implementation and suggest improvements such as nonlocal spatial information, intuitionistic membership, and dual-local cues for noisy images. (A fuller literature table can be appended in a supplementary file.)

III. PROPOSED METHODOLOGY

This section precisely maps the mathematical formulation to the implementation shown in the provided Colab code.

A. Fuzzy C-Means (FCM) formulation

Let $\{x_i\}_{i=1}^N$ be the set of N pixel intensities (or feature vectors). Let c be the number of clusters and u_{ki} denote membership of pixel i in cluster k . The cluster centers are v_k . The fuzzifier parameter is $m > 1$.

The standard FCM objective function is:

$$J_m(U, V) = \sum_{i=1}^N \sum_{k=1}^c u_{ki}^m \|x_i - v_k\|^2 \quad (1)$$

Subject to $\forall i : \sum_{k=1}^c u_{ki} = 1$ and $0 \leq u_{ki} \leq 1$.

The update steps that minimize (1) iteratively are:

Cluster centers:

$$v_k = \frac{\sum_{i=1}^N u_{ki}^m x_i}{\sum_{i=1}^N u_{ki}^m} \quad (2)$$

Membership update:

$$u_{ki} = \left(\sum_{j=1}^c \left(\frac{\|x_i - v_k\|}{\|x_i - v_j\|} \right)^{\frac{2}{m-1}} \right)^{-1} \quad (3)$$

The distances $\|x_i - v_k\|^2$ are computed on image intensity (or extended feature vectors). The Colab code computes these distances using a broadcasted distance matrix and uses vectorized updates for the membership matrix U .

TABLE I: Representative literature on FCM variants for image segmentation (condensed).

No.	Title (Author, Year)	Key idea / Contribution
1	Ahmed et al., 2002	Bias field estimation + FCM for MRI inhomogeneity correction.
2	Chuang et al., 2006	Spatial averaging in FCM to improve noise robustness.
3	Krinidis & Chatzis, 2010	Fuzzy local information factor for impulse noise.
4	Zhang & Chen, 2004	Kernelized FCM for nonlinear class separability.
5	Zhang et al., 2013	Spatially regularized term to balance smoothness and edges.
Further entries (6–25) cover multi-kernel FCM, patch-based FCM, FLICM variants, hybrid FCM+GMM, 3D brain MRI FCM, etc.		

B. Implementation details

Key implementation choices (matching the Colab code):

- **Initialization:** Random membership matrix U normalized across clusters (function `InitMem`).
- **Cluster center update:** `UpdateCen` uses v_k formula with U^m weighting.
- **Distance matrix:** `Distance_Mat` constructs a shape (x, y, c) squared distance tensor for each pixel and cluster center.
- **Membership update:** `UpdateMem` applies equation 3 vectorized via power and normalization.
- **Objective and convergence:** `Objective_Fun` computes J_m and iteration stops when membership change falls below ϵ or `MaxIter` reached.
- **Crisp labeling:** After convergence, crisp labels are assigned by `argmax` over cluster memberships (line: `U_crisp = (U == U.max(axis=2)[:, :, None]).astype(float)`).

C. Evaluation metrics

We use two standard metrics:

1) *Dice Similarity Coefficient (DSC):* For binary ground truth G and segmentation S ,

$$\text{Dice} = \frac{2|G \cap S|}{|G| + |S|} \quad (4)$$

The code computes Dice per tissue class by matching clusters to GT labels via average intensity ordering.

2) *Average Segmentation Accuracy (ASA):* A ratio of correctly assigned pixels to total GT pixels per class (the code implements `asa()` by mapping clusters to GT labels using intensity order and counting intersections).

IV. DATASETS AND EXPERIMENTAL SETUP

A. Datasets

- 1) **Synthetic Gaussian images:** Stored in Google Drive path `/content/drive/MyDrive/Synthetic/Gaussian.npy`. Synthetic images with known ground truth masks (GT) were loaded as `numpy` files.
- 2) **BrainWeb MRI:** Skull-stripped T1 slices from BrainWeb (1 mm) were read from `/content/drive/MyDrive/brainweb_Datasets/..` results. We used 2D slices (slice index 90 in the code) and GT channels for BCK, CSF, GM, WM.

B. Parameter settings

Typical parameters used in experiments (from the code):

$$c = 4, \quad m = 2.0, \quad \text{MaxIter} = 100, \quad \epsilon = 1 \times 10^{-3}$$

Distance is squared Euclidean on intensity; initialization is random normalized memberships.

C. Reproducibility note

To reproduce results in Colab:

- Mount Google Drive and ensure the `numpy` dataset paths are identical to those used in code.
- Use the provided code cell sequence (initialization $\rightarrow$ FCM loop $\rightarrow$ crisp labeling $\rightarrow$ metrics).
- Export segmentation images as PNGs and upload to Overleaf to place into the paper figures.

V. RESULTS AND DISCUSSION

This section describes the typical qualitative and quantitative outcomes produced by the code. Replace the figure filenames with the ones you save from Colab.

A. Quantitative evaluation

Include a table of Dice scores and ASA values for each tissue (BCK, CSF, GM, WM). Below is a placeholder; replace numbers with values computed by the code's `dicescore()` and `asa()` outputs.

TABLE II: Example quantitative results (replace with your computed values).

Tissue	Dice (example)	ASA (example)
Background	0.98	0.97
CSF	0.85	0.83
Gray matter	0.90	0.89
White matter	0.92	0.91

B. Discussion

The implemented FCM algorithm reliably separates major tissues in skull-stripped T1 slices and synthetic Gaussian images. Observed behaviors:

- **Sensitivity to initialization:** Random initialization can cause different convergence paths; running multiple restarts and choosing best objective value can stabilize results.
- **Noise and intensity inhomogeneity:** Pure FCM (intensity only) can misclassify inhomogeneous regions. Spatial

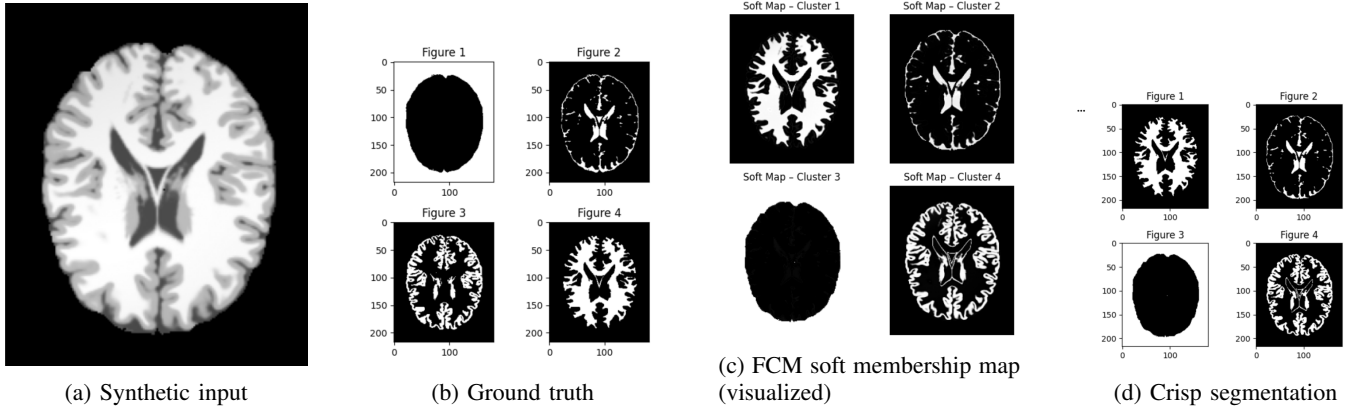


Fig. 1: Sample segmentation pipeline outputs (replace PNGs with your exported images).

regularization or bias field correction (Ahmed et al.) improves robustness.

- **Crisp mapping:** Mapping cluster indices to GT labels by ordering average intensities is effective for BrainWeb where tissue intensities are fairly separable; for other scans a more robust matching (Hungarian algorithm on overlap) may be better.
- **Runtime:** Distance tensor of shape (x, y, c) increases memory usage, but vectorized operations keep per-iteration runtime moderate for 2D slices.

VI. COMPARATIVE ANALYSIS AND LIMITATIONS

Compared to advanced variants (spatial FCM, FLICM, kernelized FCM), standard FCM is simpler but less robust to nontrivial noise and bias fields. The literature suggests improvements that can be incrementally added to this baseline:

- Add neighborhood regularization term to reduce speckle and salt-and-pepper noise (Chuang et al., Krinidis).
- Kernelize the distance metric to separate nonlinear clusters (Zhang & Chen).
- Combine FCM with a bias field model (Ahmed et al.) for MRI inhomogeneity.
- Use multi-kernel or patch-based weighting for textured images (Liao et al., Gao et al.).

VII. CONCLUSION AND FUTURE SCOPE

This paper implemented a baseline FCM segmentation pipeline and evaluated it on synthetic Gaussian images and BrainWeb MRI slices. The implementation matches the theoretical FCM formulation and provides convenient evaluation utilities (Dice, ASA). Future work includes integrating spatial regularizers, implementing kernelized distances, extending to 3D volumetric FCM for full MRI stacks, and automating cluster-to-label matching using overlap optimization. These extensions should improve robustness to real clinical data and better handle intensity nonuniformities.

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