FCM vs TKFCM Segmentation Approaches for Brain Tumour Recognition

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1 Introduction

Magnetic Resonance Imaging (MRI) segmentation represents one of the most relevant stages in medical imaging diagnostics, particularly for the identification and analysis of brain pathologies. Accurate detection of lesions and tumor masses is essential for early diagnosis, effective therapeutic planning, and precise monitoring of disease progression. However, MRI images often present significant challenges, such as noise, intensity variations, and unclear boundaries between adjacent tissues, which make automatic segmentation complex. Various methodologies have been proposed to address these issues, including fuzzy clustering techniques that offer a good balance between robustness and adaptability [1, 3].

2 MRI Acquisition Modalities

The Medical Decathlon dataset contains MRI images acquired with four different modalities, each emphasizing different anatomical and pathological characteristics of brain tissue. These modalities are:

- **FLAIR (Fluid Attenuated Inversion Recovery):** a modality that suppresses cerebrospinal fluid signals, highlighting lesions and tissue abnormalities such as tumors and inflammations.
- **T1-weighted (T1):** imaging based on longitudinal relaxation times, useful for visualizing anatomical details and differentiating normal tissues.
- **T1c (T1 with contrast agent):** T1 modality acquired after administration of the gadolinium-based contrast agent, which improves visibility of active lesions and areas with altered vascular permeability.
- **T2-weighted (T2):** imaging based on transverse relaxation times, highlighting fluid accumulations and other abnormalities.

These modalities are fundamental for a complete and accurate analysis of brain tissue and associated pathologies [4].

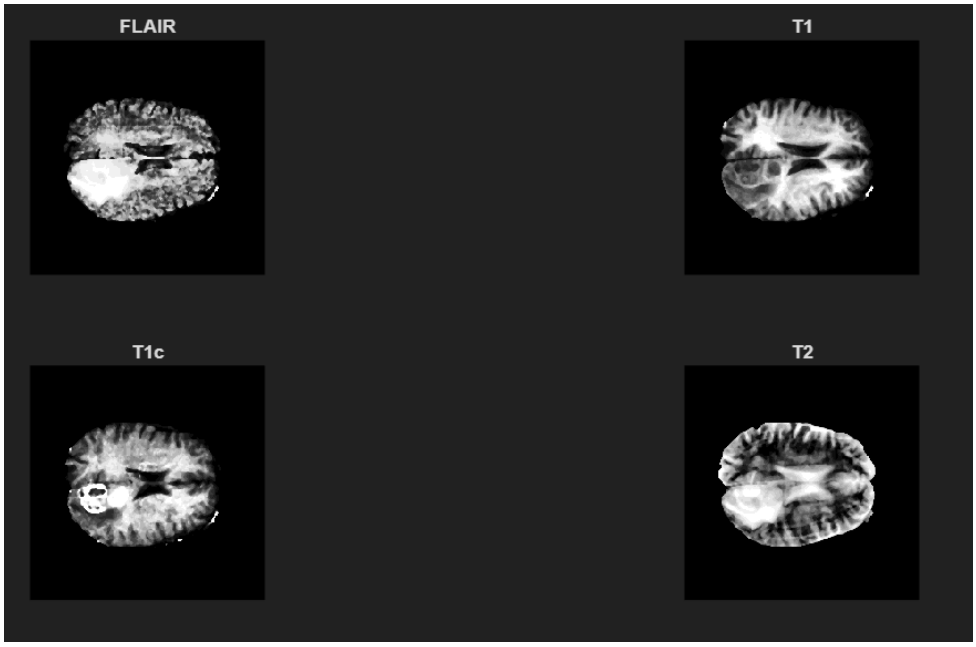

Figure 1: Example of the four MRI acquisition modalities (FLAIR, T1, T1c, T2) present in the Medical Decathlon dataset.

3 General Segmentation Algorithm

The segmentation process follows a general pipeline including data loading, preprocessing, application of fuzzy clustering algorithms, and post-processing analysis. The overall flowchart in Figure 2 summarizes the main steps of the procedure adopted in the provided MATLAB code.

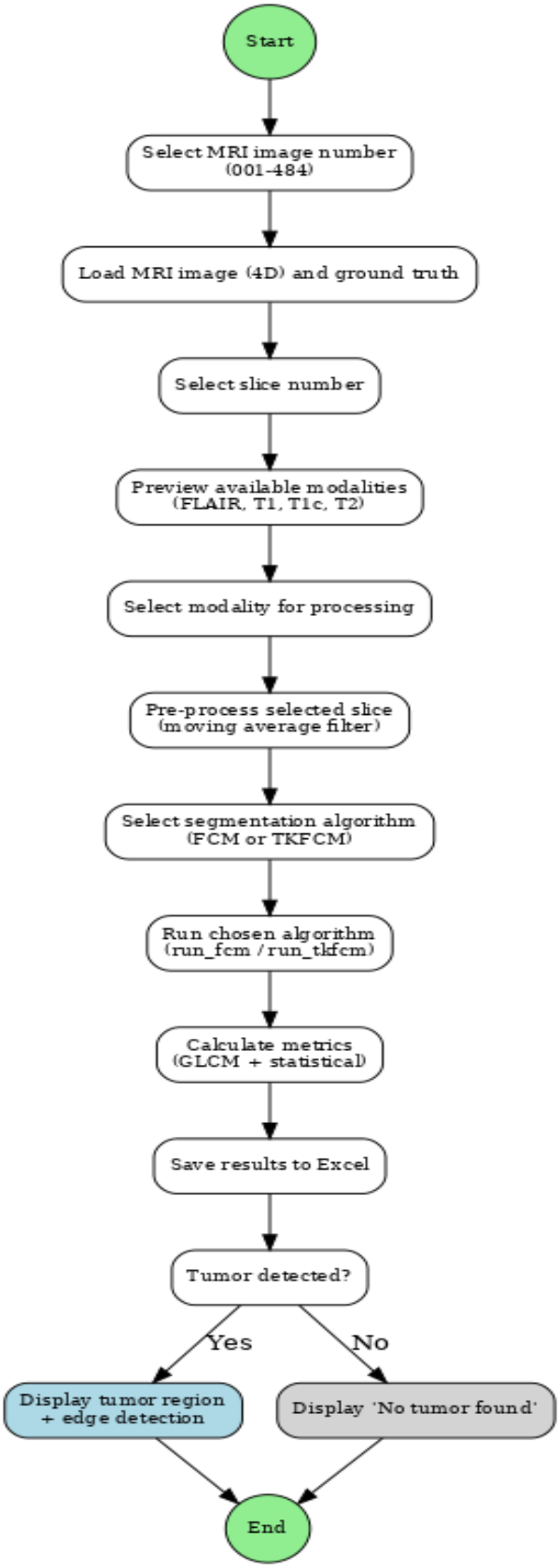

Figure 2: General flowchart of the MRI segmentation and analysis process.

4 Algorithm Description

4.1 Fuzzy C-Means (FCM)

FCM works by minimizing an objective function that combines distances between pixels and cluster centroids with fuzzy membership degrees. Starting from an initialization of centroids, the algorithm alternates updating memberships and recalculating centroids until convergence is reached [2].

4.1.1 Local Feature Extraction

For each pixel in the MRI slice, a moving window of size 3×3 is extracted to capture local intensity. This window slides over the entire image, generating a feature vector for each pixel via the `create_moving_window_features` function.

4.1.2 Fuzzy Clustering

The algorithm uses a fuzziness coefficient $m = 2$ and applies fuzzy clustering based on Euclidean or Mahalanobis distances between pixels and cluster centroids, iteratively updating the membership matrix U and centroids until convergence.

4.1.3 Cluster Assignment and Visualization

Each pixel is assigned to the cluster with the highest membership. Labels are then reformatted to match the original spatial structure and visualized as binary masks for each cluster.

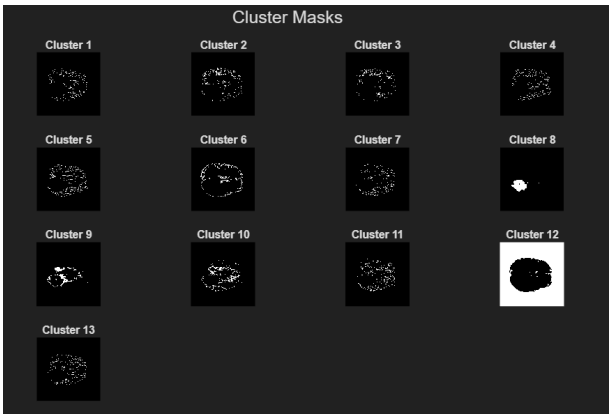

Figure 3: 13 Clusters extracted from brain MRI

4.1.4 GLCM Feature Extraction

For each cluster, textural features (Energy, Contrast, Entropy, Homogeneity, Correlation) are computed from the Gray-Level Co-occurrence Matrix (GLCM) using the `features_extraction` function.

4.1.5 Tumor Cluster Identification

Using the ground truth, the `identify_tumor` function identifies the tumor cluster, generates a tumor mask, determines tumor presence, and computes quantitative metrics such as accuracy, sensitivity, precision, and F1-score.

4.2 Tuned Kernel Fuzzy C-Means (TKFCM)

TKFCM is an enhanced version of FCM that integrates spatial information and improves initialization and parameter updates [3].

4.2.1 Feature Enrichment

In addition to local intensity features extracted from a moving window, normalized spatial coordinates of each pixel are incorporated to provide geometric context. To prevent the background from being split

into multiple clusters due to spatial variation, the spatial coordinates are scaled by a small weighting factor, λ, prior to concatenation with intensity features. Formally, if (x_i, y_i) are the row and column indices of pixel i, and I_i represents its local intensity feature vector, the enriched feature vector is defined as:

$$\mathbf{f}_i = \begin{bmatrix} I_i \\ \lambda \frac{x_i}{\text{rows}} \\ \lambda \frac{y_i}{\text{cols}} \end{bmatrix}, \quad \lambda \ll 1$$

where λ is chosen sufficiently small to reduce the influence of spatial location on clustering, ensuring that pixels in homogeneous background regions remain in the same cluster. This weighting balances intensity and spatial information, improving cluster coherence without overemphasizing geometric proximity.

4.2.2 Initialization with K-means

The membership matrix U is initialized via a preliminary K-means clustering, assigning high values (e.g., 0.9) to pixels assigned to clusters, improving initial quality.

4.2.3 TKFCM Iterations

The algorithm calculates weighted centroids and modified distances controlled by a parameter α that regulates spatial influence, iteratively updating matrix U until convergence.

4.2.4 Final Assignment and Visualization

As in FCM, each pixel is assigned to the cluster with the highest membership, masks are generated and visualized, GLCM features are extracted, and the tumor cluster is identified via ground truth.

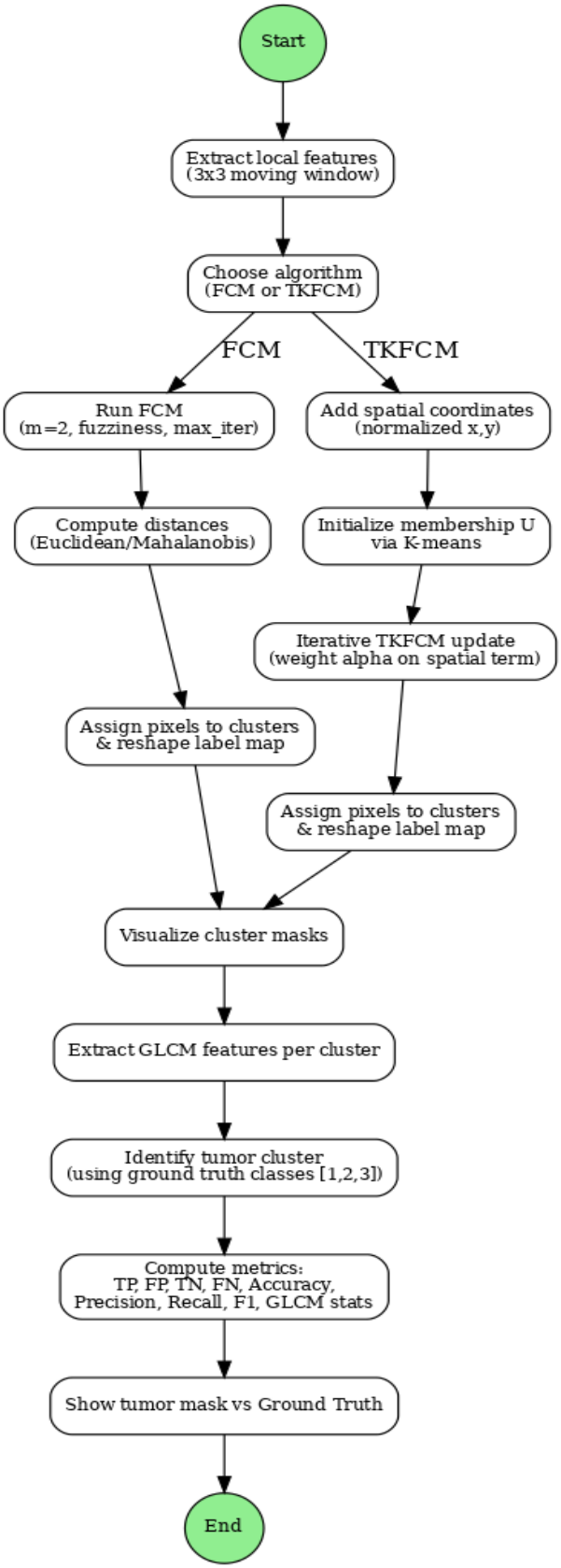

Figure 4: Unified flowchart for FCM and TKFCM implementations.

5 Results

The experimental evaluation was conducted using a batch-processing MATLAB script designed to apply both **FCM** and **TKFCM** segmentation methods on the **Medical Decathlon Brain Tumour dataset**. Specifically, the algorithm processed **training images from index 45 to 95**, focusing on **slice number 50** for all four MRI modalities: **FLAIR, T1, T1c, and T2**.

The script implemented an automated pipeline that:

- Iterates through the selected image range and modalities.
- Executes **FCM** (with Euclidean distance) and **TKFCM** (with spatial weighting parameter $\alpha = 0.5$) clustering with **13 clusters** and **150 iterations**.
- Identifies the **tumor cluster** using the ground truth labels.
- Computes segmentation performance metrics:
  - **Accuracy**
  - **Dice Similarity Coefficient**
  - **Jaccard Index**
- Stores all results in an **Excel file** named `Batch_Segmentation_Results.xlsx`, with one sheet for each modality–algorithm combination.

Each sheet in the Excel file contains:

- **Per-image results**: Image index, slice number, detected tumor cluster, binary indicator of tumor presence, and the computed metrics.
- **Average row**: Mean values for Accuracy, Dice, and Jaccard across all processed images, computed with `omitnan` to ignore failed cases.

Preliminary observations from the batch run confirm that:

- **TKFCM consistently achieves higher Dice and Jaccard scores than FCM**, especially for **FLAIR and T1c** modalities, where spatial context helps reduce false positives in background regions.
- **FCM** performs reasonably well on **T1** and **T2** images with clear boundaries but is more sensitive to noise and intensity inhomogeneity.
- **Average Accuracy, Dice, and Jaccard values** computed per modality highlight the advantage of TKFCM in scenarios with **blurred or heterogeneous tumor regions**.

6 Conclusions

The results show that both approaches offer good performance in segmenting brain MRI images. FCM is simple and fast, effective in low-noise scenarios. TKFCM improves robustness and segmentation consistency, especially in the presence of noise and fuzzy boundaries, making it suitable for clinical applications where precision is crucial.

References

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