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MRI-BRAIN TUMOR CLASSIFICATION USING K-MEANS CLUSTERING AND ENHANCED FEATURE SELECTION

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Abstract

Brain tumors are among the most lethal and complex neurological disorders, often requiring precise diagnosis for effective treatment. Magnetic Resonance Imaging (MRI) plays a crucial role in detecting and classifying brain tumors due to its high-resolution imaging and contrast capabilities. However, accurate classification remains challenging due to overlapping tissue intensities, noise, and irrelevant features. Existing classification techniques often suffer from low precision due to redundant or non-discriminative features, especially when working with unsupervised clustering methods like K-Means. These shortcomings can result in misclassification, delayed treatment, and poor prognosis. This work proposes an improved method for MRI brain tumor classification by integrating K-Means clustering with an enhanced feature selection mechanism. Initially, preprocessing techniques such as grayscale conversion and histogram equalization are applied. K-Means clustering is used to segment the tumor region, followed by extraction of statistical and texture-based features (e.g., mean, entropy, contrast, GLCM). An enhanced feature selection approach based on Mutual Information and Principal Component Analysis (PCA) is used to reduce dimensionality and retain only the most relevant features. A classifier such as Support Vector Machine (SVM) is finally used for tumor type prediction. The proposed method was evaluated on a standard MRI brain tumor dataset. Experimental results showed improved classification accuracy (95.3%), precision (94.6%), sensitivity (95.1%), and F1-score (94.8%) compared to existing techniques such as basic K-Means and PCA-SVM.

Keywords:

MRI, Brain Tumor, K-Means Clustering, Feature Selection, Classification

1. INTRODUCTION

Magnetic Resonance Imaging (MRI) has revolutionized the diagnosis of neurological disorders, offering non-invasive, high-resolution imaging critical for identifying brain tumors at early stages [1–3]. Brain tumors, whether benign or malignant, alter normal brain structures and require accurate detection for appropriate therapeutic intervention. Among all neuroimaging techniques, MRI stands out due to its ability to differentiate soft tissues and capture subtle anomalies, making it highly suitable for brain tumor classification.

Despite technological advances, several challenges persist in automated tumor classification. First, MRI images often suffer from noise, intensity non-uniformity, and varying resolutions that complicate segmentation [4]. Second, the presence of overlapping intensity regions between tumor and normal tissue leads to misclassification [5]. Third, the lack of high-quality, annotated datasets often hampers supervised learning techniques, especially deep learning models that require large volumes of labeled data for accurate training [6].

These issues highlight the problem definition: designing a robust, accurate, and computationally efficient method for brain tumor classification using MRI that can handle noise, reduce dimensionality, and overcome class imbalance [7–9]. The aim is to improve tumor detection accuracy without excessively relying on manual labeling or computationally intensive models.

1.1 OBJECTIVES

- To develop an unsupervised segmentation framework using K-Means clustering to localize tumor regions in MRI scans.
- To enhance classification accuracy by applying a two-stage feature selection process involving Mutual Information and Principal Component Analysis (PCA).

Novelty

Unlike existing methods that rely solely on supervised learning or deep learning models, this approach combines K-Means clustering-based segmentation with enhanced feature selection, enabling high accuracy even with limited labeled data. The integration of Mutual Information and PCA ensures that only the most informative and non-redundant features are retained, significantly boosting performance while minimizing overfitting.

1.2 CONTRIBUTIONS

- A hybrid approach combining unsupervised and supervised techniques to classify MRI brain tumors with high precision.
- A two-stage feature selection mechanism that combines filter (Mutual Information) and projection (PCA) methods to eliminate irrelevant or noisy features.
- An experimental comparison with state-of-the-art techniques using standard metrics such as accuracy, precision, recall, and F1-score.
- Demonstrated improved performance on limited data, making the method suitable for real-time clinical applications or settings where labeled data is scarce.

2. RELATED WORKS

Several methods have been proposed over the years to improve brain tumor classification using MRI images, ranging from conventional machine learning to modern deep learning frameworks. Early studies employed thresholding and region growing techniques for segmentation, but these methods were highly sensitive to noise and lacked robustness [7]. Subsequently, clustering algorithms like K-Means and Fuzzy C-Means were introduced to segment tumor regions without prior labeling, offering better resilience to noise and image variability [8].

In [9], the authors used Support Vector Machines (SVM) after manually extracting texture and shape-based features. While

effective in small datasets, this approach was limited by its dependency on feature engineering. To address feature selection challenges, [10] proposed using Principal Component Analysis (PCA) to reduce dimensionality before classification, significantly improving speed and performance. However, PCA alone may miss out on non-linear feature interactions, which are crucial for accurate tumor classification.

Recent works have leveraged deep learning, particularly Convolutional Neural Networks (CNNs), to automatically learn features from raw MRI data. In [11], the authors trained a CNN on a large annotated dataset, achieving high accuracy. However, deep learning models require extensive computational resources and are often prone to overfitting when data is scarce. Moreover, the training process is time-intensive, limiting their use in real-time applications.

Hybrid approaches have emerged to strike a balance between performance and computational efficiency. For example, [12] integrated K-Means clustering with Random Forest classification, showing improved segmentation accuracy but suffered from high false positive rates. Meanwhile, [13] proposed a multi-phase hybrid model combining wavelet decomposition, feature selection, and SVM, achieving high precision but at the cost of high complexity and execution time.

While these approaches have advanced the state of brain tumor classification, they often suffer from one or more limitations: high computational load, overfitting, low precision, or the need for extensive labeled data [14-15]. The current work builds on these studies by proposing a lightweight yet accurate method that uses K-Means for unsupervised segmentation followed by enhanced feature selection using Mutual Information and PCA. This combination ensures that the classifier focuses only on the most relevant data, achieving high accuracy without the computational burden of deep learning models.

3. PROPOSED METHOD

The proposed method combines image segmentation using K-Means clustering with an enhanced feature selection mechanism for more accurate brain tumor classification. First, the input MRI images undergo preprocessing to improve quality by removing noise and enhancing contrast. The K-Means algorithm then segments the tumor regions from non-tumorous tissues. From these segmented regions, features are extracted, including texture (using GLCM), shape, and intensity-based descriptors. To optimize the feature set, Mutual Information is first used to rank the most relevant features, followed by PCA to reduce dimensionality. These selected features are passed into a classifier such as SVM to predict the type of brain tumor (e.g., glioma, meningioma, pituitary tumor). This hybrid approach ensures efficient clustering, discriminative feature selection, and accurate classification.

3.1 STEP-BY-STEP PROCESS:

1) **Preprocessing:**
   a) Resize MRI images
   b) Convert to grayscale
   c) Apply histogram equalization
2) **Segmentation using K-Means:**
   a) Initialize K (number of clusters)
   b) Assign each pixel to the nearest cluster
   c) Recalculate centroids and iterate until convergence
3) **Feature Extraction:**
   a) Extract features like entropy, mean, energy, contrast, and correlation
   b) Use GLCM for texture features
4) **Enhanced Feature Selection:**
   a) Apply Mutual Information to rank features
   b) Use PCA to reduce dimensionality and retain significant features
5) **Classification:**
   a) Use SVM to classify the tumor based on selected features
6) **Evaluation:**
   a) Compute metrics: accuracy, precision, sensitivity, and F1-score

3.2 PREPROCESSING STAGE

The preprocessing stage is crucial for enhancing the quality of MRI images before segmentation and classification. This step ensures uniformity in image size, removes noise, and improves contrast to make tumor regions more distinguishable.

3.2.1 Key Preprocessing Steps:

1. **Image Resizing**: All MRI images are resized to a standard dimension (e.g., 256×256 pixels) to ensure uniform processing.
2. **Grayscale Conversion:** MRI scans in RGB or color format are converted into grayscale, reducing computational complexity and focusing on intensity values which are critical for medical interpretation.
3. **Histogram Equalization:** This technique improves image contrast by spreading out the most frequent intensity values, which enhances the visibility of edges and boundaries (e.g., tumor boundaries).

Table.1. Preprocessing Summary

Image ID	Original Size	Resized Size	Color Mode	Histogram Equalization Applied
IMG_001	512×512	256×256	RGB	Yes
IMG_002	300×300	256×256	Grayscale	Yes
IMG_003	400×400	256×256	RGB	Yes

Histogram equalization is applied uniformly to all images to normalize intensity distribution.

3.3 SEGMENTATION USING K-MEANS CLUSTERING

K-Means is an unsupervised learning algorithm used for image segmentation, where it clusters image pixels based on their intensity values. In MRI brain tumor classification, K-Means helps isolate tumor regions from normal brain tissue.

Step 1: Initialize K (Number of Clusters): Set the number of clusters, typically $K = 3$ (representing tumor, background, and other brain tissue).

Step 2: Assign Pixels to Clusters: Each pixel's intensity value is compared against the centroid of each cluster, and it's assigned to the nearest one using Euclidean distance.

Step 3: Update Centroids: New centroids are calculated by averaging the intensity values of all pixels in each cluster. Steps 2 and 3 are repeated until the centroids stabilize.

Step 4: Generate Segmented Image: The segmented image highlights the tumor region as a separate cluster for further feature extraction.

Table.2. K-Means Segmentation Clustering Output

Cluster ID	Pixel Intensity Range	Cluster Label	Description
1	0: 80	Background	Skull, dark regions
2	81: 160	Brain Tissue	Gray matter
3	161: 255	Tumor Region	High-intensity tumor area

The pixel intensity values are grouped based on grayscale intensity, which helps separate bright tumor regions from darker brain tissues.

- **Cluster 1 (black):** Outer skull and background
- **Cluster 2 (gray):** Normal brain tissue
- **Cluster 3 (white):** Potential tumor area with high intensity

This segmentation greatly simplifies the subsequent steps of feature extraction and classification by focusing only on the relevant region (tumor).

4. RESULTS AND DISCUSSION

- **Simulation Tool**: MATLAB R2022b
- **Hardware Used**: Intel Core i7 10th Gen, 16GB RAM, 512GB SSD and NVIDIA GTX 1650 GPU (4GB VRAM)
- **Dataset:** Brain MRI dataset (Kaggle: 3-class labeled dataset: glioma, meningioma, pituitary)
- Training and Validation Split: 80:20

The proposed K-Means + Enhanced Feature Selection method was compared with: Basic K-Means with Manual Feature Selection: Lacked automated selection, resulting in lower accuracy (89.4%) and PCA-SVM without Clustering: Bypassed segmentation, resulting in misclassification in complex regions (accuracy: 91.2%)

Table.3. Experimental Parameters

Parameter	Value
Image Resolution	256 × 256 pixels
Number of Clusters (K)	3
Feature Extraction Technique	GLCM, statistical descriptors
Feature Selection	Mutual Information + PCA
Classifier	Support Vector Machine (SVM)
Kernel Function (SVM)	Radial Basis Function (RBF)
Train-Test Split	80% training, 20% testing

4.1 PERFORMANCE METRICS

- **Accuracy:** Measures the proportion of correctly classified tumor types among the total samples. It is a primary indicator of overall effectiveness.
- **Precision:** Reflects how many of the predicted positive results (tumor cases) are actually positive. High precision indicates fewer false positives.
- **Sensitivity (Recall):** Measures the model's ability to correctly identify actual positive cases (true tumors). High recall means fewer false negatives.
- **F1-Score:** Harmonic mean of precision and recall. It provides a balance between the two, especially useful in datasets with class imbalance.

Table.4. Accuracy Comparison

Method	Accuracy (%)
Basic K-Means + Manual Features	89.4
PCA + SVM (No Clustering)	91.2
Proposed K-Means + Enhanced FS	95.3

Table.5. Precision Comparison

Method	Precision (%)
Basic K-Means + Manual Features	87.5
PCA + SVM (No Clustering)	90.1
Proposed K-Means + Enhanced FS	94.6

Table.6. Recall (Sensitivity) Comparison

Method	Recall (%)
Basic K-Means + Manual Features	88.9
PCA + SVM (No Clustering)	90.7
Proposed K-Means + Enhanced FS	95.1

Table.7. F1-Score Comparison

Method	F1-Score (%)
Basic K-Means + Manual Features	88.2
PCA + SVM (No Clustering)	90.4
Proposed K-Means + Enhanced FS	94.8

The proposed method outperforms existing approaches across all key performance metrics using an 80/20 train-test split. Compared to basic K-Means and PCA-based classifiers, the integration of enhanced feature selection significantly boosts accuracy (95.3%) and F1-score (94.8%), indicating better overall classification. Precision (94.6%) and recall (95.1%) values show that the method reduces false positives and negatives effectively. The improved results are attributed to the effective segmentation using K-Means and the optimal feature reduction using Mutual Information and PCA, which eliminate irrelevant features and focus the classifier on discriminative tumor traits.

5. CONCLUSION

Accurate classification of brain tumors is essential for timely diagnosis and treatment planning. The proposed approach, which combines K-Means clustering with enhanced feature selection, addresses common challenges in MRI-based brain tumor analysis, such as overlapping intensities, irrelevant features, and misclassification. Through systematic preprocessing, unsupervised segmentation, and intelligent feature reduction using Mutual Information followed by PCA, the system effectively isolates the tumor region and extracts highly discriminative features. When evaluated against existing methods using a standard 80/20 train-test strategy, the proposed model consistently achieved higher scores in accuracy, precision, recall, and F1-score. These improvements are particularly significant in clinical applications, where even a small increase in diagnostic accuracy can lead to better outcomes for patients. The enhanced performance shows the benefit of combining clustering with supervised classification techniques and optimizing the feature space. This hybrid strategy is robust, scalable, and adaptable to various types of brain tumors and imaging modalities. The reduced dimensionality also lowers computational complexity, making the method suitable for real-time or embedded diagnostic systems. Future work may extend this approach with deep learning for automatic feature learning or include multi-modal imaging data for improved diagnosis.

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