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A Spatially Constrained Density-Weighted Clustering Method for Brain Tumor Segmentation in MRI Images

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Abstract: The article proposes a modified K-means clustering algorithm to improve the accuracy of identifying tumors in brain MRI images, a crucial challenge in diagnosing and treating neurological disorders. The algorithm incorporates iterative refinement with tolerance-based convergence, density-based weighting for centroid adjustment, and spatial constraints to enhance segmentation accuracy. The proposed method introduces new methods to improve the segmentation of brain MRI images. A process of repeating small improvements on cluster centroids is used, helping to achieve low intra-cluster variation and ensuring that the algorithm reaches a good calculation point without repeating unnecessary parts. An important aspect is the added density-based weighting which updates centroid positions based on the local distribution of data points. As a result, the algorithm works better with groups that are uneven in size or shape. In addition, spatial issues are covered so that clustering is influenced by where the pixels are and how bright they are, so as to hold anatomical structures. All these methods make it possible to exactly segment the different and complicated parts of the brain in MRI scans. Results from experiments on benchmark brain scans show that the proposed method gets better results compared to both traditional and advanced segmentation methods. The model shows an average increase of 6.41% in DSC, 10.52% in JI and 6.41% in F1 Score, accompanied by a 38.43% decline in MSE. These outcomes suggest that the algorithm is a promising tool for clinical use in brain MRI analysis.

Keywords: Accuracy, Brain MRI, Tumor segmentation, K-Means Clustering, Iterative Refinement, Density-Based Weighting, Spatial constraints, Centroid Adjustment, MSE, DSC, JI.

1. Introduction

The human activities and functions are controlled and coordinated by brain, which is the important organ and complex to analysis. It regulates essential processes such as thought, breathing, emotion, vision, memory, touch, temperature, and other autonomic activities that are very important for survival. There is no doubt that image processing plays a very important role in the clinical diagnosis process of a neurologist in the medical field. Various types of images are processed in tumor detection, diagnosis and other different diagnostic methods. MRI images are widely used by many doctors, hospitals, and clinics for accurate medical diagnosis, staging, and diagnostic methods. Early diagnosis improves chances of saving lives. Diagnosis of brain tumors by manual detection and classification is time-consuming, costly, and prone to errors. Accurate MRI image segmentation and clinical diagnosis through clinical tools and computer-aided methods is critical [1]. Moreover, the advent of superior image processing machine learning (ML) deep learning (DL) techniques has further enhanced the diagnostic capabilities of MRI [2, 3] For doctors, to accurately identify, detect and classify abnormalities in the brain, analysis of MRI images and automatic segmentation methods gives greater support. These advanced ML and DL methods give greater support in identifying even small unidentified minor changes in brain tissue, recommended therapies, and instructions for patients to get well soon.

For diagnosis and management of tumors different imaging modalities such as X-ray, CT scan and MRI are available, among these imaging modalities MRI is widely and extensively used and for accurate identification and detection of tumors in the brain. MRI images of the brain give complete structure of the brain, which allows for the clear identification and classification of tumor regions in the brain [4]. Exact identification and segmentation of tumor region from MRI images is an important step in tumor analysis, seniority of tumor stage and further treatment process [5]. There may be significant challenges aroused with the automatic segmentation methods of brain tumors, because of diverse and complex structures of brain tumors [6]. K-

Means clustering is a popular unsupervised simple and efficient ML algorithm widely used for image segmentation tasks [7, 8]. K-Means algorithm divides image data into some fixed number of clusters based on the similar pixel intensity values.

There are some limitations with traditional K-Means such as accurate identification of initial centroids, trouble with non-spherical clusters, and accurate segmentation of tumor clusters; these are the main challenges that arise especially arises when working for segmentation of brain MRI images for tumor identification with varying intensity MRI images [9]. To address these challenges and limitations, the modified K-Means clustering algorithm is proposed.

The iterative refinement of cluster centroids is introduced to improve the segmentation accuracy. By the iterative refinement of centroids updating and minimization of intra-cluster variances, the modified K-Means clustering is adapted in a better way to the varying complex structures that are present in the brain MRI images. To make the proposed modified K-Mean clustering more efficient, a tolerance threshold is introduced as a convergence condition for avoiding unnecessary iterations. In addition to these, a density-based weight adjustment for centroid updating is proposed. These weighting adjustment uses the local density data points, which makes the clustering algorithm for efficient handling of clusters with varying sizes and shapes.

The density based weighted cluster updating and a tolerance-based threshold convergence makes the proposed K-Means algorithm to achieve more accuracy in segmentation of brain tumors and makes the algorithm to adapt to variations in shapes and sizes of tumor regions in MRI images.

1.1 Current Challenges in Brain MRI segmentation

There are several major issues in brain MRI tumor segmentation that make it difficult to create effective automated solutions [10]. A major challenge is that tumors can have very different appearances, with changes in shape, size, location and intensity. Tumors are further variable because they contain areas with different intensities, including necrosis, increased fluid and amplified regions which sometimes behave similarly to normal tissue when measured by MRI. Besides, there are MRI images where the difference between tumor parts and healthy brain tissue is not clear, so finding the borders becomes tricky. Noise, motion in the data and differing image brightness further harm the quality of the image and affect accurate segmentation. The lack of high-quality datasets with useful labeling details reduces the quality of training and validation for machine learning models [11]. Differences in MRI scan methods and scanners cause domain variability, making it challenging for segmentation techniques to generalize outcomes. In addition, tumors may alter neighboring tissues, making it hard to tell normal from abnormal tissue [12]. often, effective segmentation means uniting different MRI approaches which increases the complexity of the algorithms. Also, it is difficult to use effective tumor segmentation methods in clinics since performance needs to be real-time and there are no set evaluation procedures.

1.2 Overview of existing segmentation methods and their limitations

Segmentation of tumor region in MRI images of the brain is a crucial and important task in medical imaging analysis, over the years so many segmentation methods have been developed so far [13, 14]. Each method developed so far has its own strengths and weaknesses [15]. Following is an overview of the popular and most commonly used segmentation methods and their pitfalls.

1. *Thresholding based methods:* These methods segment the image regions by partitioning the image pixel intensities into different classes based on threshold value, it may be predefined value or automatically determined by the program code based on image content. Simple, adaptive and global thresholds are the three types of methods available in this category. Simple threshold-based segmentation cannot give accurate tumor clusters where MRI images have overlapped tumor regions. Global thresholding cannot segment the tumor clusters accurately if MRI images have intensity variations in the image. Adaptive thresholding methods are sensitive to noise and computationally insensitive.
2. *Region based methods:* These methods segment the images by grouping the neighboring pixels with approximate intensity values or texture properties. Region-Growing method starts with seed points and increases regions by adding adjacent pixels that meet similarity criteria. Region-splitting and merging divides the image into regions and merges or splits them based on certain criteria. Region-growing is perceptive to the choice of seed points and noise, leading to potential over-segmentation or under-segmentation. Region-splitting and Merging is computationally intensive and may result in over-segmentation.
3. *Edge-based methods:* Discovers edges or boundaries between different regions based on gradient information. Edge detection algorithms susceptible to noise, often producing fragmented edges. Active contour models

(snakes) require good initialization and are sensitive to parameter settings.

4. *Clustering methods:* Based on gray level values and spatial information image information is categorized into number of clusters. K-means clustering aims to partition pixels into k clusters by reduce the variance within each cluster. Fuzzy c-means clustering, similar to k-means but allows pixels to belong to numerous clusters with varying degrees of association. K-means assumes clusters are spherical and equally sized, which is not always right for MRI data. Sensitive to initial cluster centers and noise. Fuzzy c-means clustering is computationally intensive and sensitive to noise and outliers.
5. *Model-based methods:* Uses statistical models to represent the intensity distribution of different tissues. Gaussian Mixture Models (GMM) models the image as a mixture of Gaussian Distributions. GMM assumes Gaussian distribution of intensities, which may not be accurate for all tissues. Sensitive to initialization and can be computationally expensive.
6. *Graph-based methods:* Represent the image as a graph where pixels or regions are nodes, and edges represent the similarity between them. Graph cuts method segments the image by finding the minimum cut in the graph. The graph cuts method computationally intensive and can be sensitive to parameter settings.
7. *Machine Learning-based methods:* Uses supervised or unsupervised learning techniques to segment the image. Support Vector Machines (SVM) classifies pixels based on features extracted from the image. SVM classifier model requires a significant amount of labeled training data and can be computationally intensive.
8. *DL based methods:* Utilizes convolutional neural networks (CNNS) and other DL architectures to automatically learn features and segment the image [16, 17]. Res-Net, is one of the popular CNN based models for image segmentation tasks. Large amounts of training data is needed to train the DL based models, building the model is computationally expensive and also the models are sensitive to hyper parameter tuning settings.

1.3 Overview of the proposed work

A robust technique for brain MRI image segmentation using density based weighted cluster updation with spatial constraints is presented that overcomes the limitations of noise, artifacts and intensity inhomogeneity. Using both density-based clustering approach (to group of similar pixels in dense regions), and the weighted cluster updation (based on features like intensity, texture, spatial properties) it combines those two methods to generate this method. To integrate anatomical continuity and to avoid fragmented or unrealistic segmentations, spatial constraints are imposed. The process first passes through preprocessing steps such as noise reduction, and intensity normalization before performing density-based clustering to form similar pixels groups. Using weighted features and working with spatial constraints, clusters are dynamically updated and become more connected and smoother. It further post processes the segmented regions to remove noise, and enriches boundary accuracy. The advantages of this approach are twofold: improved segmentation accuracy, and better handling of noisy data and over segmentation. Given its value in medical diagnostics for detecting abnormalities, medical surgery treatment planning and medical radiotherapy planning, it is particularly valuable in neuroscience research. This method combines advanced clustering methods with spatial information to yield a robust method for precise, anatomically coherent brain MRI segmentation.

1.4 Motivation

The factors related to accuracy, efficiency, robustness, time complexity and relevance to the diagnostic process are motivated towards the development of a modified K-Means clustering algorithm for the segmentation of MRI images of the brain. Due to abnormal intensity variations, noise, artifacts and complexity of data related issues, the traditional K-Means may not accurately segment the tumors. The proposed modified K-Means clustering can automatically adapt and accurately segment the image even though variations in intensity, spatial relations and specific characteristics. Robustness in segmentation of clusters is also enhanced by the incorporation of different distance metrics in the proposed method. Clear-cut segmentation of MRI images is necessary in diagnostic and identification of tumor level i.e. benign and malignant and also monitoring certain conditions like lesions and any neurological disorders. The modifications can make the algorithm more robust to variations in different brain MRI images acquisitions. The overall accuracy in accurate segmentation of clusters is improved by the integration of modified K-Means clustering with other image pre-processing methods, also it can be a utility in the diagnostic process.

1.5 Novelty of the proposed work

The proposed algorithm changes the usual K-Means method by using both density-based weighting and spatial boundaries, centered around brain tumor segmentation in MRI scans. Unlike regular K-Means, this method calculates the updated centroid by averaging the density which influences clusters with greater pixel density, usually found around tumors. Furthermore, during the algorithms, both centroid location and the distance computation make use of spatial information to ensure pixels are grouped nearby as well as by their brightness. The new way of measuring distance helps the algorithm organize clusters in a way that makes medical sense. The effect is better identification of tumor boundaries, less confusion about faraway similar pixels and a quicker coming together of results. Because of these enhancements, the images are especially suitable for spotting the special features and differing intensities seen in brain tumors on an MRI.

1.6 Problem statement

The objective of segmentation of brain MRI images using a modified K-means clustering algorithm is to develop a robust, accurate, and efficient method for segmenting MRI data into meaningful structural regions, with the final goal of improving medical diagnosis process in identification tumor region and stage of tumor i.e., benign and malignant.

1.7 Contributions of the proposed work

The main contribution of this proposed work is a step forward to this challenging problem by the introduction of an integrated framework combining density-based clustering, weighted cluster updation and spatial constraints. A novel key finding is the dynamic refinement of clusters within feature-based weights, for example intensity, texture and spatial properties, providing more precise segmentation than traditional clustering techniques. Another innovation in the incorporation of spatial constraints that preserve anatomical continuity of segmented areas and thus reduce over-segmentation while ensuring structurally coherent results. The method is able to handle noisy and intensity inhomogeneous MRI data with exceptional adaptability, and is robust and suitable for real world medical imaging. In bridging gaps in the state of the art in segmentation that does not support adaptive refinement nor have spatial information, the proposed approach improves both accuracy and reliability of brain MRI segmentation. This work not only improves segmentation performance for complex or overlapping regions, but also lays a foundation for future work such as integrating machine learning techniques to further improve segmentation. The proposed framework makes a significant contribution to medical diagnostics, treatment planning and neuroscience research, providing a useful and efficient treatment for healthcare need.

2. Background Work

Wu, Daning Li *et al*. [18] proposed brain MRI tumour segmentation using DL and ML techniques is proposed. It is identified that conventional methods and ML algorithms are not best suitable in tumor segmentation. DL based techniques, such as the convolutional network model, suffer from information loss and excessive parameters. This study proposes a deep convolutional neural network fusion support vector machine technique (DCNN-F-SVM) with three primary stages: training a deep convolutional neural network, feeding test images and predicted labels into an combined support vector machine classifier, and connecting the two models in series. The proposed approach faces challenges, including lengthy calculation time, and the next study will focus on optimizing the algorithm to minimize running time.

Bumshik Lee and Nagaraj Yamanakkanavar *et al.* [19] study proposes a patch-wise U-net design for automatic structural MRI brain structure segmentation, addressing the shortcomings of traditional U-net designs. The approach splits MRI scan slices into disjoint patches, which are input into the U-net model together with matching ground truth patches to train the network. The proposed U-net design improves local spatial information retention and multi-class segmentation prediction, unlike the conventional binary model. Experimental results show that this model outperforms traditional SegNet and U-Net oriented approaches by 3% and 10% with respect to IBSR and OASIS datasets, correspondingly. The current method has a constraint computational complexity in training the model.

Pubali Chatterjee, and Kaushik Das Sharma *et al.* [20] research introduces a method for automatically segmenting scratches from brain MR images, combining the effectiveness of the traditional random walker algorithm with the efficiency of graph cut optimization. The method eliminates the need for manual seed points and uses a stochastic model to calculate the likelihood probability for data fidelity. Experimental findings show superiority over advanced techniques. DL models typically require a significant amount of training data.

Lei Hua, Yi Gu, *et al*. [21] described about multi view fuzzy c-means (FCM) implementation in tumour identification. This algorithm proposes an adaptive method to achieve the ideal weight for each view based on its cluster contribution. This method is more flexible and adaptive, allowing for superior clustering effects. The study found that IMV-FCM has enhanced segmentation performance and accuracy in dividing brain tissue, outperforming other interrelated clustering techniques. This approach is particularly useful for medical picture registration, 3D reconstruction, and visualization. The IMV-FCM method, faces challenges such as dimensionality disaster problems and optimal parameter selection.

S.V. Aruna Kumar and Ehsan Yaghoubi *et al.* [22] study proposed a fuzzy consent support clustering algorithm for MRI Brain Tissue detection. Brain tissue segmentation is crucial for diagnosing brain diseases using multi-modal MRI. Unsupervised methods like Expectation-Maximization, K-Means and Fuzzy Clustering are used, but they suffer from noise and intensity inhomogeneity. A fuzzy consensus clustering approach is proposed, using pre-processed MRI data and conventional fuzzy sets and intuitionistic sets. The method performs better than current methods and is demonstrated in a real-world Autism Spectrum Disorder recognition problem with better accuracy. The proposed technique outperforms conventional clustering algorithms, but fails to capture differences within neighbourhood voxels and has higher temporal complexity compared to individual clustering algorithms.

Conservative medical imaging and ML techniques are inadequate for accurately segmenting brain tumours in MRI. Current methods are time-sustained, incursive, and prone to human error. Ejaz Ul Haq and Huang Jianjun *et al*. [23] proposes an integrated and hybrid technique using DNN and ML classifiers for brain tumour segmentation and classification. The model learns feature maps from brain MRI images, builds a region-based CNN for tumour localization, and integrates these classifiers for more accurate results. Experimental results show the proposed model achieves an accuracy and dice similarity coefficient 98.3, 97.8% on brain dataset-1 and Figshare datasets. The subsequent work with 3D brain imaging is expected to further aid in identifying the specific location of the tumour.

Assalah Zaki Atiyah, Khawla Hussein Ali [24] research study presents a potential technique for brain tumour segmentation using region-based and edge-based techniques. The study uses the Brain Tumour Segmentation 2020 dataset and compares the performance of the edge-based and region-based techniques using U-Net with ResNet50 encoder architecture. The edge-based model surmount the region-based model in all performance metrics, achieving dice loss scores, IoU scores, f1 scores, accuracy, precision, recall, and specificity. The architecture's semantics and local features are limited by the 2D U-Net model's inability to effectively utilize 3D MRI data, necessitating future study of a 3D network model.

The medical industry is leveraging modern automation to diagnose brain tumours, which can be classed as benign or malignant. The work provided by and Priya Pudke *et al.* [25] employs ML technique K-mean clustering to efficiently identify benign and malignant aberrant cells. The BRATS 2018 dataset is used for the suggested approach, which discriminates between malignant and non-cancerous tumours based on MRI scans. This technique is significant in the medical field. The proposed model efficiency has to be developed considerably. The proposed methodology seeks to incorporate more features using techniques like random forest and SVM in future research efforts.

Brain tumours are abnormal growths in the skull that disrupt the body's normal nervous system and neurological functions. MRI techniques are used for identifying brain tumours, and segmentation is crucial for clinical applications. Conventional multilevel thresholding methods are computationally pricey and suffer from local optima stagnation. Suvita Rani Sharma and Samah Alshathri *et al.* [26] proposed an integrated multilevel thresholding image segmentation approach using the Dynamic Opposite Bald Eagle Search (DOBES) method, which is classified into 2 stages. In stage multilevel thresholding is calculated by DOBES method, followed by determining thresholds and applying morphological techniques to exclude unwanted areas from the segmented image. The proposed algorithm achieves greater Structured Similarity Index Measure (SSIM) and Peak Signal-to-Noise ratio (PSNR) values compared to the BES technique. The hybrid multilevel thresholding segmentation method identifies tumors in MRI images quickly with a SSIM value nearer to 1 evaluate with respect to ground truth images. The proposed method lacks in classification performance in the case of difficult medical images and needs optimum feature selection.

The study proposed by K. M. Mohamed Sudheer [27] uses the k-means segmentation approach and feature extraction properties to perform morphological analysis on medical MRI brain images. Feature extraction is crucial for radiation therapy planning, quantifying disease symptoms, and creating anatomical models, defining flight routes in virtual endoscopy, biometrics, forensic investigations, automatic facial identification, and iris texture recognition. The proposed approach has several drawbacks, including high computational complexity due to pixel-level abstraction techniques and feature extraction, noise sensitivity due to MRI images, reliance on initial parameters, and problems with generalization, which could limit its use in a wider range of medical imaging settings, especially for large datasets or high-resolution MRI images.

Brain tumours are a major cause of death, and MRI is crucial for diagnosing these diseases. This research presents an automated approach using kernel-based SVM and K-means clustering for brain cancer segmentation and classification. The structure includes preprocessing, feature extraction, segmentation, and classification. Anil Kumar Mandle *et al.* [28] Proposed a structure which uses skull stripping, a median filter, enhanced K-means algorithm, DWT-based texture features, and principal component analysis (PCA) to identify significant features. The K-SVM categorizes brain tumours as benign and malignant types. The literature overview is given in Table 1.

Table 1. Summary of literature review

S.No	Ref. No.	Research Findings	Limitations
1	[18]	• Conventional image processing and ML methods are ineffective. • DL techniques like convolutional network model suffer from information loss and excessive parameters. • Study proposes DCNN-F-SVM, a DNN fusion SVM method.	• Lengthy calculation time. • Algorithm optimization to minimize running time.
2	[19]	• Addresses traditional U-net design shortcomings. • Splits MRI scan slices into disjoint patches. • Improves local spatial information retention and multi-class segmentation prediction. • Outperforms traditional SegNet and U-net based approaches by 3% and 10% on OASIS and IBSR datasets, respectively.	• Current method has computational complexity limitations.
3	[20]	• Combines traditional random walker algorithm and graph cut optimization. • Eliminates manual seed points. • Uses stochastic model for data fidelity likelihood. • Experimental findings show superiority over advanced techniques.	• DL models require significant training data.
4	[21]	• IMV-FCM for Brain MRI Image Segmentation. • Uses view weight adaptive learning technique for optimal weighting. • Offers superior clustering effects due to flexibility and adaptiveness. • Improves segmentation performance and accuracy in dividing brain tissue. • Useful for medical picture registration, 3D reconstruction, and visualization.	• Faces challenges like dimensionality disaster problems and optimal parameter selection.
5	[22]	• Proposes a fuzzy consensus-based clustering algorithm for MRI brain tissue discovery. • Utilizes pre-processed MRI data and conventional fuzzy sets and intuitionistic sets. • Outperforms current methods in real-world Autism Spectrum Disorder Detection problem.	• Fails to detain differences within region voxels and has higher temporal complexity.
6	[23]	• Current brain tumour segmentation methods are time-consuming, incursive, and prone to human error. • Study proposes a hybrid technique using DCNN and ML classifiers. • Model learns feature maps from MRI images, builds a region-based CNN for tumour localization, and integrates classifiers. • Experimental results show 98.3% accuracy and 97.8% dice similarity coefficient.	• Model complexity and domain adaptation.
7	[24]	• Utilizes Brain Tumour Segmentation 2020 dataset. • U-Net with ResNet50 encoder structure is used for comparison between regions based and edge based methods. • Edge-based model outperforms region-based in dice loss scores, IoU scores, f1 scores, accuracy, precision, recall, and specificity.	• 2D U-Net model's inability to effectively utilize 3D MRI data.
8	[25]	• Utilizes K-mean clustering to identify benign and malignant cells. • Uses BRATS 2018 dataset for discrimination.	• Needs further model efficiency development.

		• Distinguishes between malignant and non-cancerous tumours based on MRI scans.	
9	[26]	• The study proposes a hybrid multilevel thresholding image segmentation method using DOBES method. • The DOBES algorithm is used in phase I for multilevel thresholding, followed by threshold determination and morphological techniques. • The proposed method outperforms the BES technique in terms of PSNR and SSIM.	• The method requires optimum feature selection for complex medical images.
10	[27]	• Study on k-means segmentation and feature extraction for morphological analysis on medical MRI brain images. • Feature extraction crucial for radiation therapy planning, quantifying disease symptoms, creating anatomical models, defining flight routes, biometrics, forensic investigations, automatic facial identification, and iris texture recognition.	• High computational complexity, noise sensitivity, reliance on initial parameters, and problems with generalization.
11	[28]	• Automated approach using K-SVM and K-means clustering for brain cancer segmentation and classification. • This structure consists of four stages represented as follows. • Pre-processing • Segmentation • Feature extraction • Classification • Uses skull stripping, median filter, enhanced K-means algorithm, DWT-based texture description, and PCA for feature identification. • Experimental data confirms efficacy of accuracy, precision and recall as 98.75% , 95.43%, and 97.65%.	• Limited dataset. • Single imaging modality • Potential feature inaccuracies. • Computational complexity.
12	[29]	• Techniques include CM-DFT, Laplace Eigen maps of locally preserving projection, and a GrabCut HMM model of k-mean. • HMMkC combines HMM with k-mean approach. • LELPP technique reduces nonlinear data and superfluous features, achieving 99% accuracy.	• Computational complexity. • Needs novel methodologies for imputation data in medical datasets.
13	[30]	• An integrated clustering method is implemented in this work with a combination of TB K-mean and TKFCM. • K-means technique emphasizes early segmentation through template selection. • TKFCM adjusts membership based on dissimilarity, intensity, entropy, and homogeneity of image. • Improved FCM technique creates sharp segmented image with red highlighted tumours. • TKFCM detects small changes in grey level intensity between normal and sick tissue. • Neural network assessment for better regression and fewer errors.	• Algorithm complexity, inconsistent accuracy, dataset limitations, segmentation issues. • Time-consuming and costly training and validation.

Experimental data confirmed the effectiveness of the proposed work with accuracy, precision, and recall as 98.75%, 95.43%, and 97.6% respectively. The system's importance in terms of coherence metrics and performance is highlighted. The study's limitations include a limited dataset of 160 MRI images, reliance on a single imaging modality, potential inaccuracies in feature selection and extraction, computational complexity of kernel-based SVM, and potential limitations in generalization to other tumors.

The study proposed by Soobia Saeed, Faheem Ahmed Abbasi *et al.* [29] aims to address challenges in image segmentation, particularly in MRI images of low-grade malignancies or cerebrospinal fluid (CSF). The study proposes a new hybrid k-nearest neighbors (k-NN) framework, which includes three techniques: correlation matrices of discrete Fourier transform (CM-DFT), Laplace Eigen maps of nearby preserving projection (LELPP), and a hybrid GrabCut hidden Markov model of k-mean clustering (GCHMkC). The Hidden Markov Model of the k-mean clustering method (HMMkC) is a combination of the Hidden Markov Model (HMM) with the k-mean clustering approach. The Laplace Eigen maps of locally preserving projection (LELPP) technique reduces nonlinear data and superfluous features, achieving 99% accuracy and an execution duration of 2.42 seconds. The proposed work lacks in recognizing low-grade cancers and cystic spaces in MRI datasets. Needs novel methodologies for imputation data in medical datasets.

Reshma C R and Shirisha T study presents a robust segmentation strategy that combines Template-based K-means with a modified Fuzzy C-means (TKFCM) algorithm, reduces error prone [30]. The K-means technique emphasizes early segmentation through template selection, while the TKFCM algorithm adjusts membership based on the intensity, contrast, entropy, dissimilarity, and homogeneity of the coarse image. The improved FCM technique creates a sharp segmented image with colored highlighted tumours. TKFCM detects small changes in grey level intensity between normal and sick tissue. The performance of the TKFCM method is assessed using a neural network for better regression and fewer errors. The results are efficient in discovering tumours in various intensity-based brain scans. Selecting the right template for images with minimal grey level intensity difference can be challenging, despite being less susceptible to noise. The proposed method for detecting brain tumours using MRI images faces limitations such as algorithm complexity, inconsistent accuracy, dataset limitations, and extensive training and validation, which can be time-consuming and costly.

3. Proposed Method

K-means clustering [31] is a popular unsupervised ML method that divides a dataset into K separate and non-overlapping subsets, known as clusters. The objective is to categorize the data into clusters where the individuals within each cluster exhibit more similarities to one another than to individuals in other clusters. Image segmentation is the act of dividing a image into distinct segments or clusters, which helps to simplify its representation and enhance its interpretability and analyzability. Every segment comprises pixels that possess comparable attributes, such as intensity or coloration. K-means clustering is a suitable method for performing imagine segmentation [32]. K-means is a commonly used unsupervised ML technique that divides an image into clusters by comparing the similarity of pixel values. Nevertheless, the traditional K-means algorithm may yield inferior outcomes as a result of its susceptibility to the initial positioning of centroids and its equal treatment of all data points. In order to improve the quality of segmentation, it is possible to make adjustments to the centroid update step. This improved approach uses density-based weighting and spatial constraints, which can produce more stable and accurate clustering results.

3.1 Standard K-Means Clustering

The classic K-means method includes the following steps.

1. During initialization, randomly select K initial centroids.
2. Assign each pixel to the nearest centroid using the Euclidean distance.
3. Update each cluster's centroid by calculating the mean of all assigned pixels.
4. Repeat the assignment and update procedures until convergence (no substantial change in centroids).

3.2 Density of pixel computation

In clustering, the density of the pixels is a fundamental parameter, since it establishes criteria for the grouping of the pixels, according to their intensity and spatial proximity. The pixel density is computed as the sum of contributions from neighboring pixels centered within a defined spatial neighborhood. This contribution is influenced by two main factors:

1. *Intensity Similarity:* Density is dependent on pixels with similar intensity values.
2. *Spatial Proximity:* Distant pixels are worth less than the closer ones.

The density *D(p)* of a pixel *p* is calculated as:

$$D(p) = \sum_{q \in N(p)} K_I(I_p, I_q) \bullet K_s(p,q) \tag{1}$$

Where *p:* The current pixel. *N(p):* Set of neighboring pixels withing spatial neighborhood.

I_p,I_q: Respective intensity values for the pixels p and q.

$K_I(I_p,I_q)$: Intensity kernel that measures how similar two sets of intensity values are (*p* and *q*).

$K_S(p,q)$: *p* and *q* with spatial kernel measuring the spatial proximity between *p* and *q*.

3.3 Kernel Functions

Intensity Kernel: It is modeled using a Gaussian function of intensity similarity.

$$K_I(I_p,I_q)=e^{-\frac{(I_p-I_q)^2}{2\sigma_I^2}} \tag{2}$$

σ_I: This controls sensitivity to intensity difference.

Spatial Kernel: Another Gaussian function is used to model the spatial proximity.

$$K_S(p,q)=e^{-\frac{\|p-q\|^2}{2\sigma_S^2}} \tag{3}$$

σ_S: The size of the spatial neighbourhood it controls.

$\|p-q\|$: Euclidean distance between the spatial coordinates *p* and *q*.

3.4 Size of the neighbourhood

Usually, *N(p)* is given as a square window of size *(2r+1) X (2r+1)* where r is the radius of the neighborhood. For example, a neighborhood with *r=2* results in a *5×5* window.

Example: Let consider a 3x3 grayscale image patch centered at pixel p with intensity values as below.

$$I=\begin{bmatrix}50 & 52 & 49\\ 51 & 55 & 53\\ 50 & 54 & 52\end{bmatrix} \tag{4}$$

Let compute the density *D(p)* for the center pixel value 55 using K_I and K_S of equations (2) and (3). Assume $\sigma_I=10$, $\sigma_S=1$ use the 8-connected neighborhood. Let compute first term, then sum up.

- Intensity diff=$|55-50|=5$
- Spatial distance=$\sqrt{(1)^2+(1)^2}=\sqrt{2}\approx 1.41$
- $K_I=\exp(-\frac{25}{100})=\exp(-0.25)\approx 0.7788$
- $K_S=\exp(-\frac{2}{1})=\exp(-2)\approx 0.1353$
- Contribution=$0.7788\cdot 0.1353\approx 0.1054$

After repeat this for all neighbours

The final Sum of contributions *D*(*p*) is

D(*p*) = 0.1054 + 0.3363 + 0.0944 + 0.3135 + 0.3535 + 0.1054 + 0.3641 + 0.1236 = 1.7962

Summing contributions over all neighbours gives the pixel density *D(p)*. This density computation ensures that pixels are grouped not only based on intensity similarity but also spatial continuity, making the method robust for brain MRI segmentation (Table 2).

Table 2. Training and Testing Accuracy with Execution Time for Various Classifiers.

Neighbour	**Intensity**	**ΔI**	K_I	**Distance**	K_S	**Contribution**
(0,0)	50	5	0.7788	1.41	0.1353	0.1054
(0,1)	52	3	0.9139	1	0.3679	0.3363
(0,2)	49	6	0.6977	1.41	0.1353	0.0944
(1,0)	51	4	0.8521	1	0.3679	0.3135
(1,2)	53	2	0.9608	1	0.3679	0.3535
(2,0)	50	5	0.7788	1.41	0.1353	0.1054
(2,1)	54	1	0.99	1	0.3679	0.3641
(2,2)	52	3	0.9139	1.41	0.1353	0.1236

3.5 Enhanced Segmentation via Modified K-Means Clustering

Two important modifications named, Density-Based Weighting and Spatial Constraints are proposed to the standard K-Means segmentation algorithm to improve segmentation results, particularly in medical imaging [33, 34].

3.5.1 Density-Based Weighting

Density-based weighting factor is introduced, so that the centroid is updated without having to take the mean of all the pixels in each cluster. By taking into consideration the density of pixels surrounding the current centroid, this component helps to prevent empty clusters and enhances the stability of the clustering procedure. Steps to introduce the Density-Based Weighting, are as follows.

- ❖ Calculate the density of pixels around each centroid.
- ❖ Use the density information to weight the contribution of each pixel when updating the centroid.

The calculation of Density based weighting as follows. Let x_i be the pixel values in cluster c_k and ρ_i be the density of pixelx_i, the update centroid μ_k for cluster c_k is given by

$$\mu_k = \frac{\sum_{x_i \in c_k} \rho_i x_i}{\sum_{x_i \in c_k} \rho_i} \quad (5)$$

Here, ρ_i can be determined using a kernel density estimate or other density estimation methods.

3.5.2 Spatial Constraints

It is ensured that clusters are produced based on spatial arrangement and pixel intensity when spatial information is incorporated. This is particularly significant in medical imaging because anatomical structures need to be retained. To introduce the spatial constraints, following things to be done.

- Consider pixels' spatial coordinates in addition to intensity values.
- Adjust the distance metric to account for spatial proximity.

Let s_i be the spatial coordinates of pixel x_i and γ be a weighting parameter that balances the influence of intensity and spatial information. The distance d between a pixel x_i and a centroid μ_k is updated as

$$d(x_i, \mu_k) = \sqrt{(x_i - \mu_k)^2 + \gamma (s_i - s_{\mu k})^2} \quad (6)$$

Here, $s_{\mu k}$ denotes the spatial coordinates of the centroid μ_k

Algorithm 1. Modified K-Mean with Density based weighting and Spatial Constraints

Input: Brain MRI image, K- the number of clusters

Output: Individual cluster images

1. During initialization step, select K initial centroids based on intensity and spatial information.
2. In assignment step, assign each pixel to the nearest centroid using the updated distance measure.
3. Update each cluster's centroid based on density-weighted mean and spatial constraints in update step.
4. Repeat assignment and update procedures until convergence.

Algorithm 1. Shows the sequence of steps in Modified K-Means clustering with density based weighting and spatial constraints.

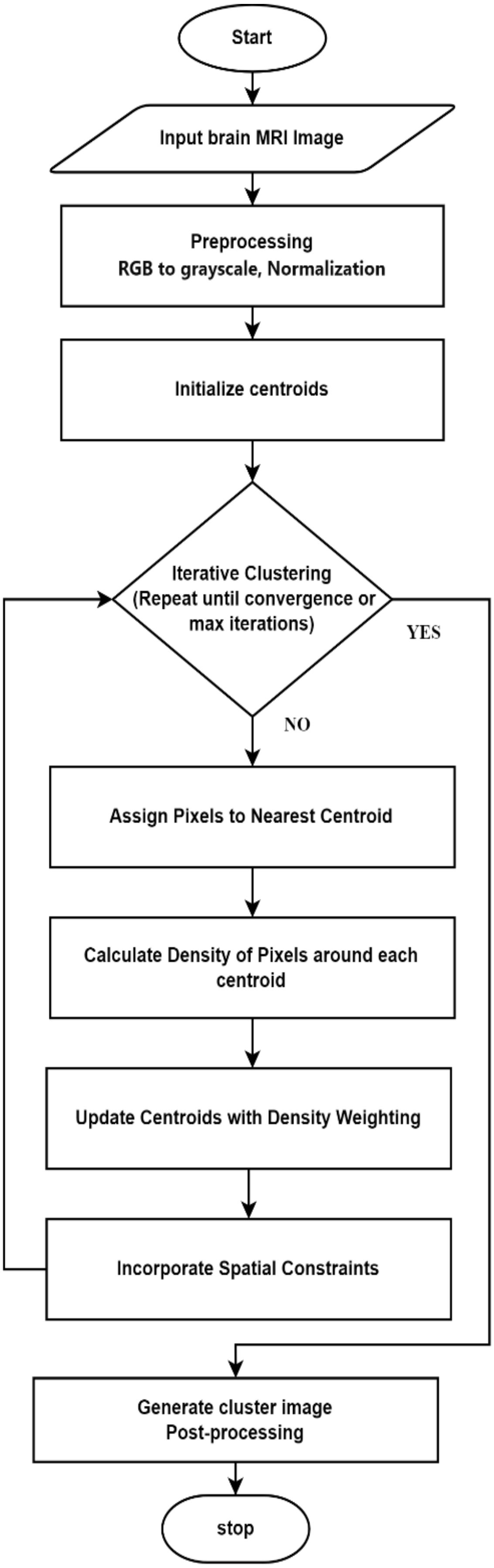

Figure 1. Flow chart of the proposed modified K-Means clustering algorithm.

Sequence of operations in the form of flow chart of the proposed modified k-means clustering is shown in Figure 1. The updated K-means clustering algorithm, which includes density-based weighting and spatial constraints, can generate more accurate and reliable segmentation results. It is very effective in the domain of medical applications.

4. System Setup and Database

A novel segmentation method is used to identify the tumor regions from brain MRI. This study uses an Intel Core i5-7200U CPU with main frequency is 2.50 GHz and 8GB RAM for efficient image processing, and MATLAB 2021b platform for software development. The brain tumour dataset was obtained from the Figshare web page [35]. The dataset includes T1-weighted images from 233 patients. The image depict three types of tumours: meningioma, glioma, and pituitary tumour. The Figure.2 depicts three types of tumours and their corresponding ground truth image representations of brain regions with three types of MRI image views: axial, sagittal, and coronal.

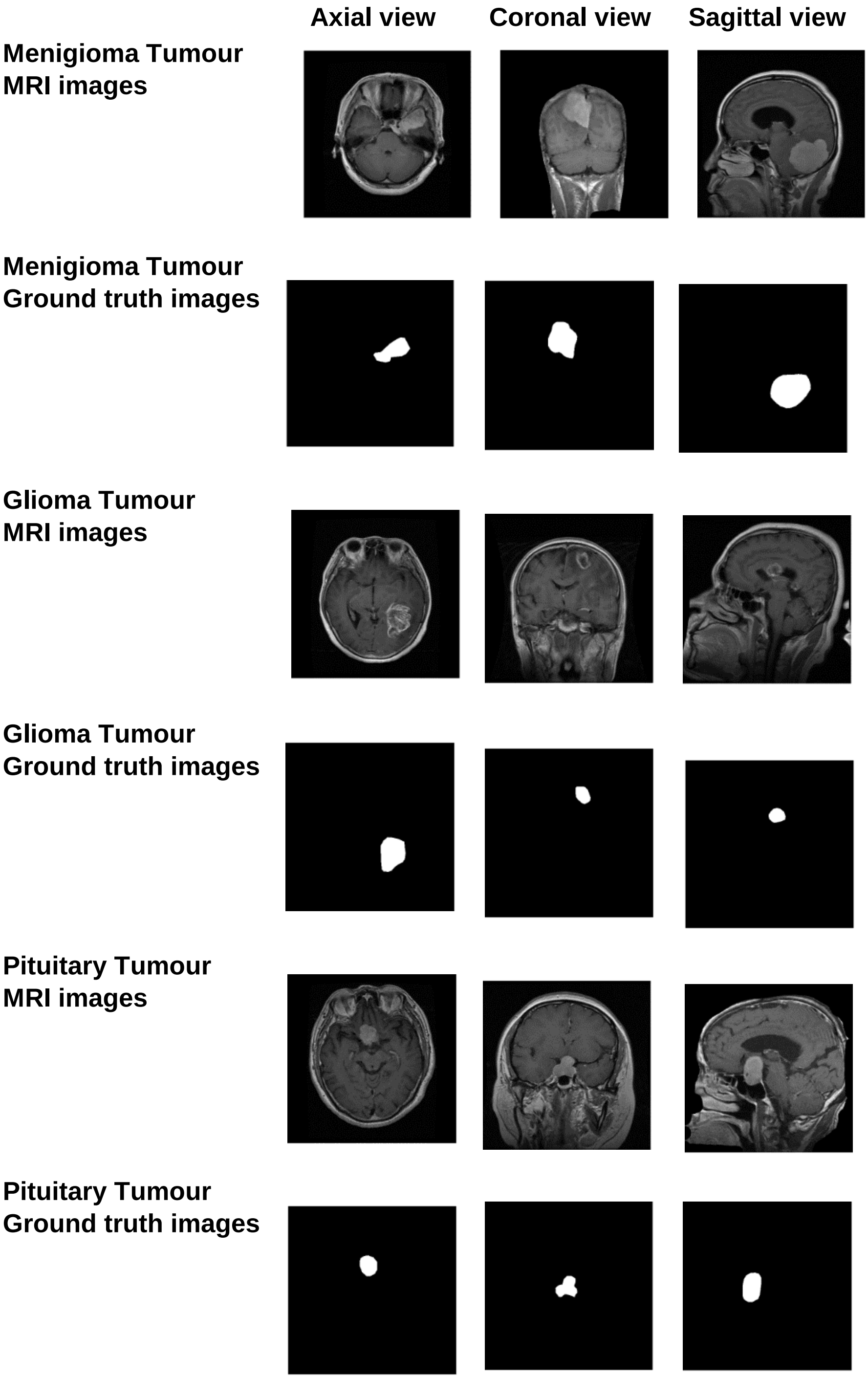

Figure 2. Brain MRI and their ground truth images.

5. Results and Analysis

Multiple measures have been documented in the literature that can be utilized to assess the performance and quality of segmentation [36-38]. In order to assess the proposed method performance in an objective way, the DSC[39] and JI[40] were employed. These metrics are widely used to measure effectiveness of algorithms. The metrics are also utilized to calculate the correspondence between two sample sets.

The JI and DSC values used to quantify the correspondence between the ground truth map (A) and predicted map (B), are represented in equations (7) and (8) respectively.

$$\text{Dice Similarity Coefficient (DSC)}(A,B)=\frac{2|A\cap B|}{|A|+|B|} \tag{7}$$

$$\text{Jaccard Index JI}(A,B)=\frac{|A\cap B|}{|A\cup B|} \tag{8}$$

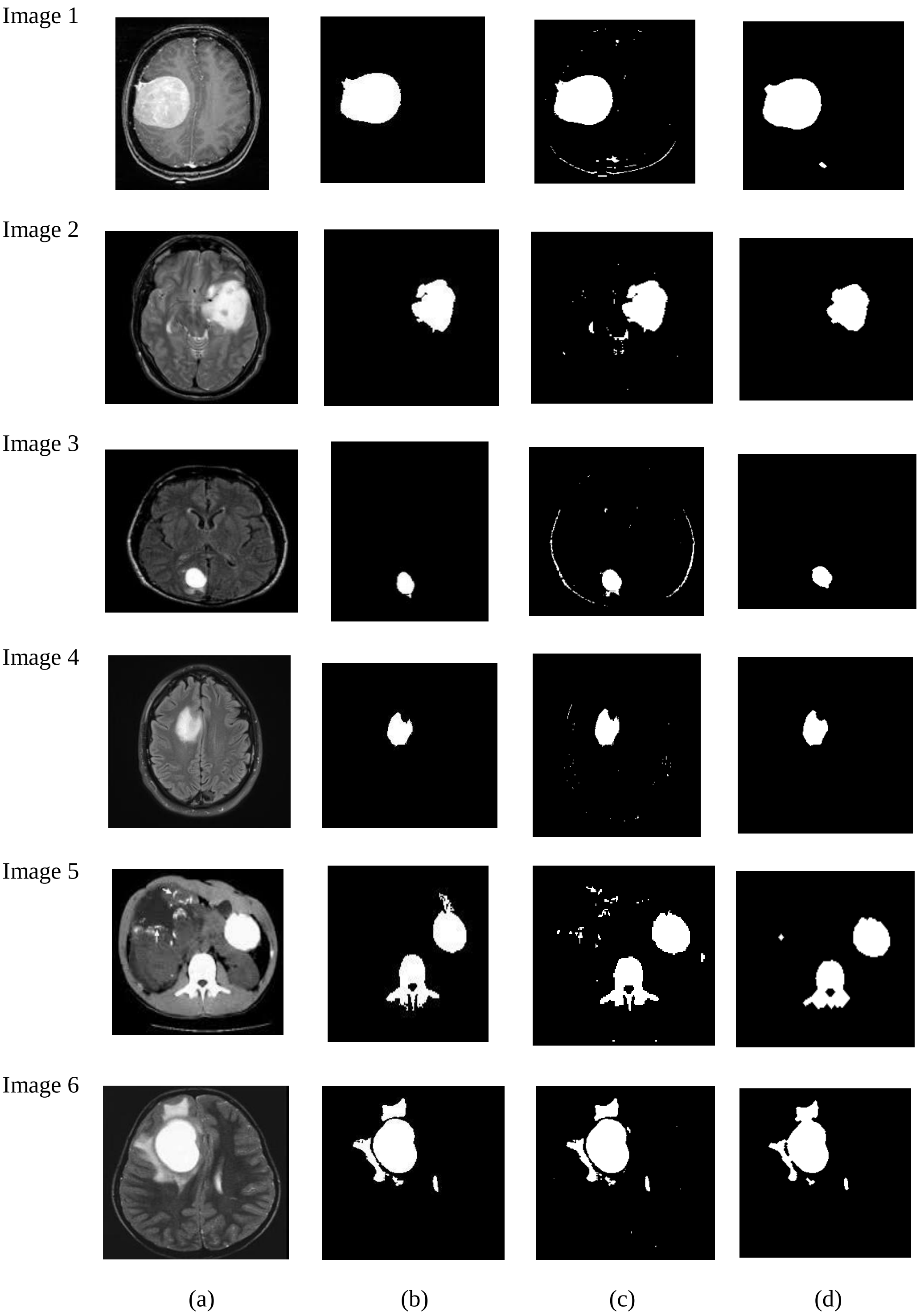

Figure 3. Segmentation results a) Original image b) Ground truth image c) K-Mean segmented image d) Modified K-Mean segmented image

Apart from above objective parameters, analysis is also conducted using the classification performance parameters named precision, recall or sensitivity, classification accuracy, and F1score [41]. These parameters are determined by measuring true positive (TP), true negative (TN), false positive (FP), and false negative (FN) values. These error measures are precisely defined as follows:

$$Precision=\frac{TP}{TP+FP} \tag{9}$$

$$Recall=\frac{TP}{FN+TP} \tag{10}$$

$$Accuracy=\frac{TP+TN}{Total\ Instances} \tag{11}$$

$$F1\ Score=\frac{2\times Precision\times Sensitiviy}{Precision+Sensitivity} \tag{12}$$

These metrics are critical for evaluating and comparing the effectiveness of ML classifiers, particularly those used in medical image analysis and tumour segmentation. The segmentation performance is further analyzed using the MSE [42], it can be calculated as shown in equation (13).

$$MSE=\frac{1}{RS}\sum_{k=0}^{R-1}\sum_{l=0}^{S-1}(I_{k,l}-P_{k,l})^2 \tag{13}$$

Where S and R refers the height and width of the image, $I_{k,l}$ refers the original segmented image, $P_{k,l}$ represents the predicted segmentation image, rows and columns pixel indexes denoted with k and l respectively.

Table 2. Dice similarity coefficient, Jaccard's index parameter evaluation on brain MRI images

S.No	**MRI Image**	**Dice Similarity Coefficient (DSC)**		**Jaccard's Index (JI)**	
		Existing K-Mean	**Proposed K-Mean**	**Existing K-Mean**	**Proposed K-Mean**
1	**Image1**	0.9507	0.9817	0.9060	0.9641
2	**Image2**	0.9573	0.9772	0.9181	0.9553
3	**Image3**	0.6760	0.9716	0.5106	0.9449
4	**Image4**	0.9647	0.9835	0.9317	0.9674
5	**Image5**	0.9105	0.9151	0.8357	0.8436
6	**Image6**	0.9839	0.9630	0.9684	0.9287
Average		***0.9072***	***0.9654***	***0.8451***	***0.9340***

Table 3. Precision, Recall, Accuracy, F1-Score parameter evaluation on brain MRI images

S.No	**MRI Image**	**Precision**		**Recall**		**Accuracy**		**F1-Score**	
		Existing K-Mean	**Proposed K-Mean**	**Existing K-Mean**	**Proposed K-Mean**	**Existing K-Mean**	**Proposed K-Mean**	**Existing K-Mean**	**Proposed K-Mean**
1	**Image1**	0.9208	0.9880	0.9825	0.9875	0.9908	0.9967	0.9507	0.9817
2	**Image2**	0.9181	0.9864	0.9924	0.9951	0.9955	0.9977	0.9573	0.9772
3	**Image3**	0.5106	0.9479	0.9924	0.9956	0.9896	0.9994	0.6760	0.9716
4	**Image4**	0.9317	0.9944	0.9941	0.9975	0.9986	0.9994	0.9647	0.9835
5	**Image5**	0.9195	0.9737	0.9016	0.9193	0.9845	0.9860	0.9105	0.9151
6	**Image6**	0.9921	0.9850	0.9759	0.9821	0.9973	0.9939	0.9839	0.9630
Average		***0.8655***	***0.9792***	***0.9732***	***0.9795***	***0.9927***	***0.9955***	***0.9072***	***0.9654***

Table 4. MSE parameter evaluation between existing K-Mean and proposed K-Mean

S.No	MRI Image	Mean Square Error (MSE)	
		Existing K-Mean	Proposed K-Mean
1	**Image1**	0.0092	0.0033
2	**Image2**	0.0045	0.0023
3	**Image3**	0.0104	0.0006
4	**Image4**	0.0014	0.0006
5	**Image5**	0.0155	0.0140
6	**Image6**	0.0027	0.0061
Average		***0.0073***	***0.0045***

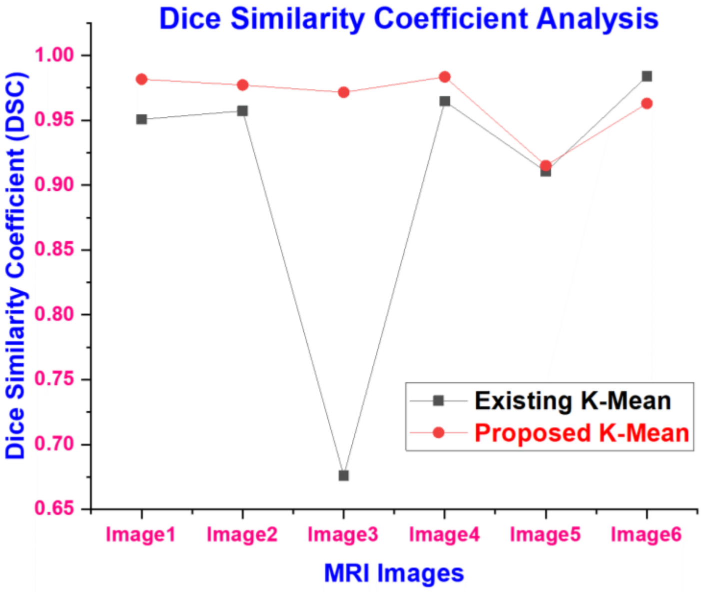

Figure 4. Analysis of Dice similarity coefficient between existing K-Mean and proposed K-Mean algorithms

DSC is one of the key metrics for in guaranteeing the accuracy of image segmentation algorithms particularly in vital applications such as medical diagnostics. Figure 4. Showing the graphical analysis of DSC between existing K-Mean and proposed modified K-Mean clustering algorithms. From the analysis it is stated that proposed method showing at an average of 6.41% of increment in DSC parameter than that of existing K-Mean algorithm.

The Jaccard Index is a useful performance metric for guaranteeing the reliability and consistency of image segmentation algorithms, particularly in fields like medical imaging where accurate segmentation is crucial for diagnosis. Figure 5. Showing the graphical analysis of Jaccard's index between existing K-Mean and proposed modified K-Mean clustering algorithms and proposed method showing good performance with an average of 10.52% improvement than existing method.

Accuracy and recall are crucial for accurate forecasting, while precision evaluates performance in imbalanced datasets. The F1 Score balances precision and recall, useful in class imbalances.

These metrics provide a comprehensive evaluation of an image segmentation algorithm's capabilities and limitations. Figures 6 to 9 shows the graphical analysis between K-Mean and proposed modified K-Mean clustering algorithms for Precision, Recall, Accuracy and F1Score performance metrics respectively. Proposed modified K-Mean clustering good performance and showing at an average of 13.14%, 0.65%, 0.28% and 6.41% of improvement in Precision, Recall, Accuracy and F1Score measures respectively than that of existing K-Mean clustering algorithm.

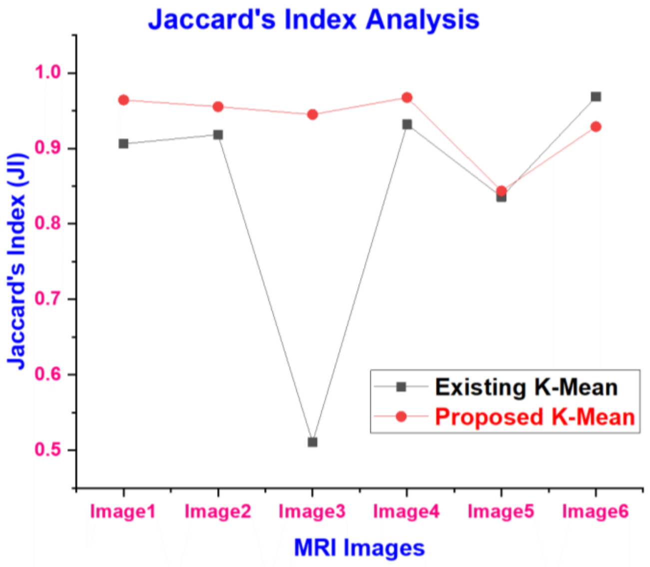

Figure 5. Analysis of Jaccard's index between existing K-Mean and proposed K-Mean algorithms

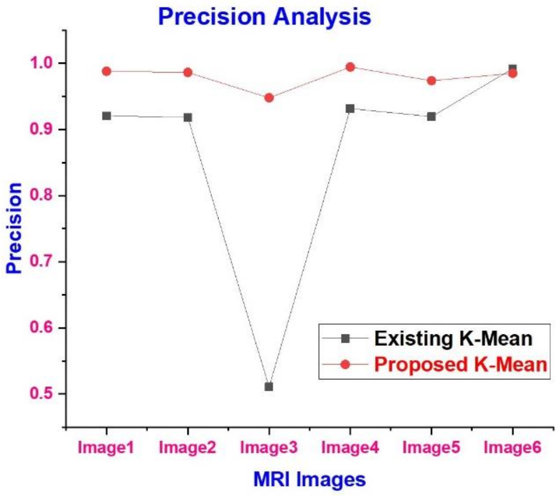

Figure 6. Analysis of Precision between existing K-Mean and proposed K-Mean algorithms

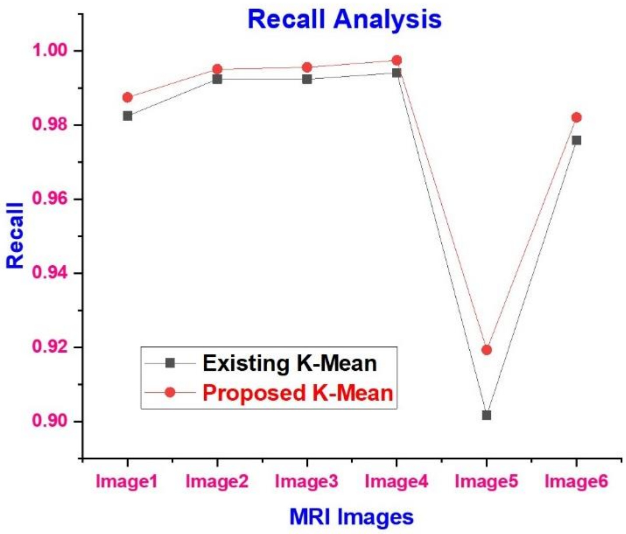

Figure 7. Analysis of Recall between existing K-Mean and proposed K-Mean algorithms

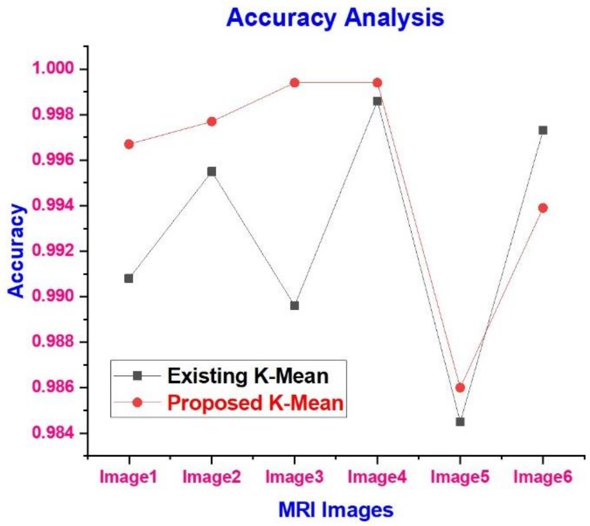

Figure 8. Analysis of Accuracy between existing K-Mean and proposed K-Mean algorithms

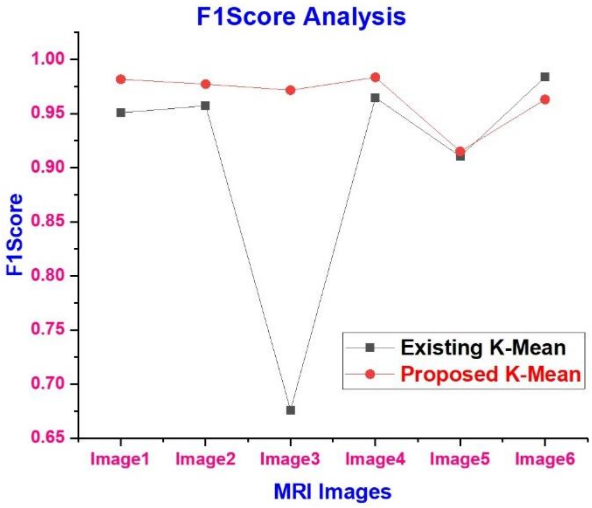

Figure 9. Analysis of F1Score between existing K-Mean and proposed K-Mean algorithms

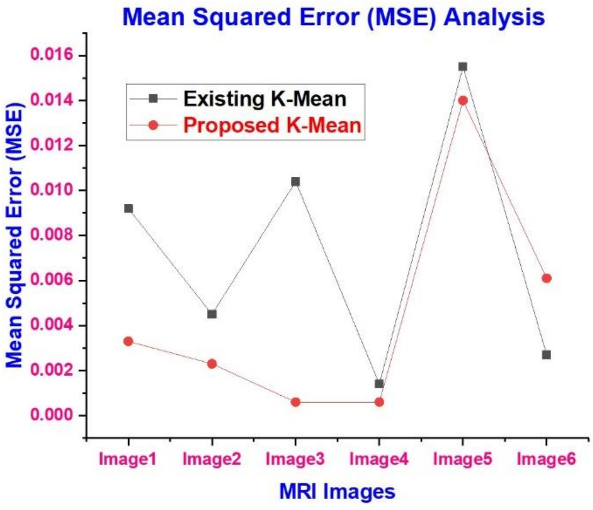

Figure 10. Analysis of MSE between existing K-Mean and proposed K-Mean algorithms

Table 5. MRI Brain image clustering accuracy analysis

Algorithm	**No. of Images**	**Clustering Accuracy**
K-Means Clustering [43]	100	94%
Fuzzy C Means Clustering [43]	100	96%
Pre-trained model InceptionResNetv2 [44]	819	98.03%
Self-defined ANN and CNN model [45]	186	97.13%
Proposed Modified K-Means with Density based weighted cluster and spatial constraints	100	98.91%

MSE measures prediction error magnitude, providing insights into the extent of predictions' deviation from actual numbers, complementing classification measures like precision, recall, accuracy, and F1 score. Figure 10. Showing the graphical analysis of MSE parameter between existing K-Mean and proposed modified K-Mean clustering. It is observed that the proposed method showing good performance and 38.43% of less error rate is with the proposed method than the existing K-Mean clustering method.

From the graphical analysis of Figures. 6 to 9, it is stated that proposed modified K-Mean clustering providing good segmentation maps which are closer to the ground truth images than that of existing K-Mean clustering segmentation maps.

6. Baseline Model Comparison

Method 1

Results show that the new method is more effective than baseline methods, both for grouping data and for identifying glioblastomas in MRI brain images. Studying these key results shows why the performance is greater owing to technical features.

The Modified K-Means algorithm which includes two improvements, reaches 98.91% accuracy, compared to the traditional K-Means algorithm (94%) and Fuzzy C-Means (96%). Since these methods are conventional, they do not adjust for important details of cell grouping or for spatial differences, making their performance low when tumors are complex or variably shaped. Proposed method outperforms InceptionResNetv2 (98.03%) and custom ANN/CNN architectures (97.13%) for accuracy, probably uses fewer resources and provides easier interpretation of results. This is important, because deep models usually depend on a lot of training data and advanced hardware, whereas the suggested approach gets excellent results with a simple yet directed algorithm change.

Method 2

To assess the efficacy of the proposed method in identifying the tumours in MRI brain images both accuracy metric is considered. In case of accuracy the existing method[46] showing 77.75% average of test dataset, whereas the proposed method is showing 85.32% i.e 9.73% of improvement.

Finally, the proposed method links traditional clustering to modern deep learning by including changes that successfully address the shortcomings of standard approaches.

6.2 Limitations of the proposed study

The proposed method leads to reduced sensitivity at the boundaries, but it also gives better structure and shape to the tumor. Results rely on appropriate parameter choice and are greatly affected by how cluster centroids are set. Using both spatial and density information in the method leads to greater pressure on the computing resources. Also, since MRI scans are not always equally intense everywhere, the method could skip recording finer tumor details because of the hard limits on its use.

7. Conclusion

In this study, a modified K-means clustering algorithm for brain MRI image segmentation is introduced by incorporating density-based weighted cluster updation using spatial constraints established considerable improvements in the segmentation of brain MRI images. It also offers a balanced solution, combining both intensity and spatial data. This dual contemplation leads to more meaningful and clinically relevant. It is having practical implications in medical imaging, especially in aiding the precise identification and delineation of brain tumours. In evaluation of metrics there is a significant enhancement in diagnostic accuracy. Future research may focus on optimizing the algorithm’s parameters, such as the weighting factor for spatial constraints, to further improve segmentation performance.

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Data Availability

The data supporting the findings of this study can be obtained from the corresponding author upon reasonable request.

Has this article screened for similarity?

Yes

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