

## Brain tumor MRI images identification and classification based on the recurrent convolutional neural network

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### ABSTRACT

Brain tumor detection and analysis are necessary for any indicative system and have testified that exhaustive research and procedural development over time. This work needs to implement an effective automated system to improve the accuracy of tumor detection. Various segmentation algorithms have been developed to achieve and enhance the accuracy of brain tumor classification. Brain image segmentation has been recognized as a complex and challenging area in medical image processing. This paper proposes a novel automated scheme for detection and classification. The proposed method is divided into various categories: MRI image preprocessing, image segmentation, feature extraction, and image classification. The image preprocessing step is performed using an adaptive filter to remove the noise of the MRI image. Image segmentation is performed using the improved K-means clustering (IKMC) algorithm, and the gray level co-occurrence matrix (GLCM) is used for feature extraction to extract features. After extracting features from MRI images, we used a deep learning model to classify the types of images such as gliomas, meningiomas, non-tumors, and pituitary tumors. The classification process was performed using recurrent convolutional neural networks (RCNN). The proposed method provides better results for classifying brain images from a given input dataset. The experiments were conducted on the Kaggle dataset with 394 testing sets and 2870 training set MRI images. The results illustrate that the proposed method achieves a higher performance than previous methods. Finally, the proposed RCNN method is compared with the current classification methods of BP, U-Net, and RCNN. The proposed classifier obtained 95.17% accuracy in classifying brain tumor tissues from MRI images.

### 1. Introduction

Imaging segmentation is used in the medical picture domain to divide the image into two parts. An image representation can be improved by splitting it out, so that it can be used for analysis. This is due to the fact that the image is broken up into a series of distinct sections. Medical diagnosis relies heavily on the scientific segmentation of images. Because medical photos tend to include modest differences, specialised kinds of noise, and missing or unverified barriers, this may be a tough problem to solve. Computerized tomography (CT) and magnetic resonance imaging (MRI) can be used to investigate the brain's internal structure (CT). More importantly, it is more comfortable than using an autonomous computed tomography machine (CT). Because it doesn't use radiation, it has no effect on the human body. The magnetic field and radio waves have a role [1].

Brain tumors are one of the most devastating disorders that impact

the human body today. Tumors are usually identified in various areas of the brain. This can cause a problem with body functioning if there are fewer tumors in the brain that can easily find tumors using any of the image processing technique or by a manual segmentation process. Detecting cancerous tumors in different parts of the body and acting quickly to cure them is difficult. The prevalence of brain tumors has risen dramatically, according to a recent research. It was only later that the symptoms of these tumors became apparent, posing a significant threat to human life. Hearing or speech issues, frequent headaches, memory loss, vision loss and personality changes are all symptoms of a brain illness [2].

Magnetic resonance imaging (MRI) is one of the most often used technologies for detecting brain tumors (MRI). It is a widely used non-intrusive imaging design that delivers a sensitive contrast between tissues. Imaging structures of interest in human brain tumors can be facilitated by the ability of MRI to accommodate tissue that is often

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normalised. Researchers have recently confronted a difficult and hard issue when it comes to manually segmenting brain MRI images [3]. Tumors and their locations in the brain must be classified accurately using a classification system. Medical image segmentation and volume estimation are critical tools in radiation and medicine. The location of a tumor in the brain is helpful in identifying the factors that have an impact on a person's normal functioning.

Various researchers have provided different methods to classify brain tumors. However, their research works rely on machine learning algorithms such as support vector machines (SVMs) and genetic algorithms (GAs) in [G. Rajesh Chandra et al. [4]]. Abnormal brain tumors have been identified using image segmentation in many scenarios. Many algorithms require a patient-specific training dataset to perform specific MRI tumor image experiments. This dataset makes it more demanding for experts. These approaches usually rely on other images, like T1-weighted contrast-enhanced images. One of the unsolved problems is fully automatic extract segmentation, which is accurate image segmentation itself. 2D T2-weighted magnetic resonance images (2D-T2MRI) were proposed in [Capelle et al. [5]] and could be used to determine whether the tumor is present at the location with the accurate detection of the brain tumor for consequent segmentation.

Various mechanisms have been developed for segmentation, automation, and semi-automation because of the problematic brain tumor segmentation and its significance in the medical environment. They provided considerable research on these algorithms [6,7]. Algorithm checking is challenging; most of these approaches were tested on smaller datasets with various parameters to discover a regular medical imaging dataset. Various types of brain tumors given Fig. 1.

In medical image research and retrieval, deep learning-based algorithms have become the norm [8,9]. Pixel-based prediction algorithms for deep learning are current learning methodologies. The CNN is a deep learning-based classification technique for classifying brain cancers. Malignant and benign tumor categorization might benefit from this method. A deep neural network-based 3D-CNN has been used for brain tumor segmentation employing 3D random applicants as a fully connected layer (FCL), which is critical in reducing false positive (FP) rates. A variety of brain tumors are listed here.

This paper proposes a novel, efficient automated classification

method with an improved K-means clustering (IKMC) algorithm for MRI image segmentation.

The main presents of this study are listed as follows.

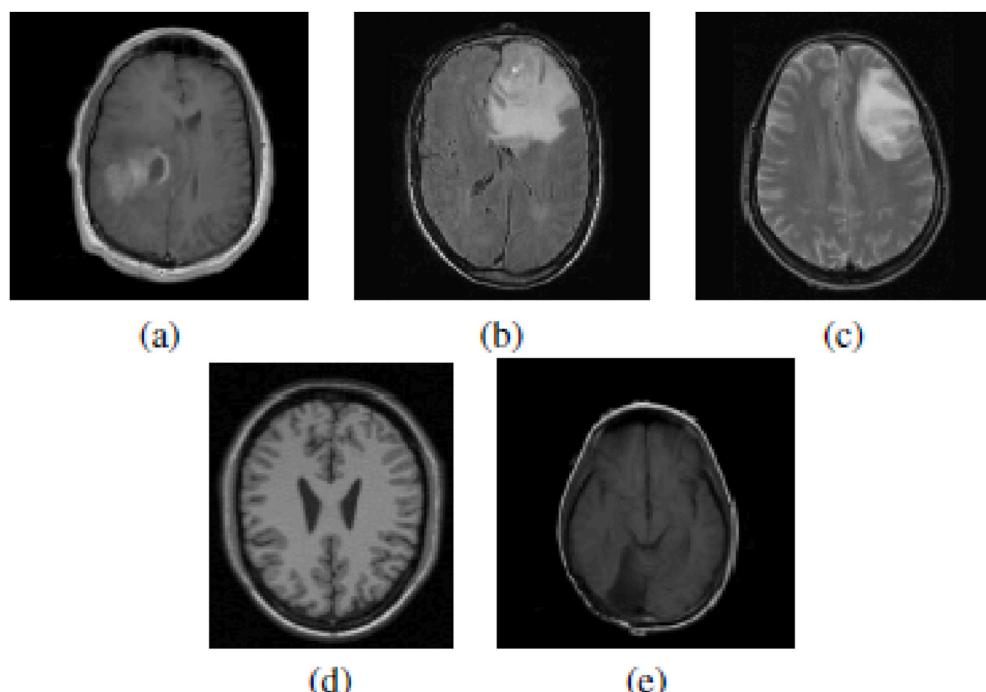
- 1) To determine an automated approach that increases against the present method of discovery and classification of brain tumors.
- 2) Therefore, we use the improved version of the K-means clustering method and adaptive filter segmentation to optimize the pre-processing of MRI images as exposed to the past simple K-means clustering approach for basic segmentation.
- 3) Use recurrent convolutional neural networks to classify brain malignancies, including gliomas, meningiomas, and pituitary tumors.

The remainder of this work is structured as follows: 1. Introduction 2. MRI image detection and categorization are the subject of Section II. Section III deals with the proposed methodology and system architecture with a deep discussion of each part. In addition, the proposed deep learning-based recurrent convolutional neural network is discussed. Section IV discusses the dataset used and the implementation of experiments with accuracy, sensitivity, and specificity parameters. There are findings and discussion in Section V. Section VI, the final section, brings the paper to a conclusion.

## 2. Related works

The different analyses were performed using deep learning techniques to automatically segment and detect brain tumors. This section discusses various current brain tumor detection techniques in the field.

For brain tumor segmentation, Yanming Sun et al. [10] suggested a reliable and computationally efficient Convolutional Neural Network (CNN) approach. Segmentation-CNN, pre-CNN data reduction block, and refinement block make up this model's three main components. The one and only The ASCNN (Application Specific CNN) paradigm is recommended for the extraction of mono-modality and cross-modality feature sets, tumor localization, and pixel classification using CNN. Mode-wise normalization, depthwise convolution, instance normalization, bilinear upsampling, and weighted data addition are some of the features of this algorithm that help improve the quality of data input. For



**Fig. 1.** Various types of brain tumors (a) Astrocytoma, (b) Glioblastoma, (c) Oligodendrogioma, (d) Tissue with healthy, and (e) Unidentified tumor.

convolution layers with high pass filters, Full-ReLU can help reduce the number of kernels while retaining processing quality. Using just 108 kernels and a total of 20,308 trainable parameters, the CNN is built to include seven convolution layers. Rather than exponentially extending across layers, the number of kernels in each layer is chosen just-enough to meet its function in order to improve information density in data channels and minimise unpredictability in network training. In order to verify the system's high-level processing quality and repeatability, extensive experiments were conducted on the BRATS2018 dataset. The average dice scores for augmenting tumor, total tumor, and tumor core are 77.2%, 89.2%, and 76.3%, respectively. 29.07G Flops is a tiny fraction of what is described in the literature for each patient. Installation and medical use of the proposed system would be made easier by its simple construction and guaranteed high processing quality.

Zexun Zhou et al. [11] suggested for entirely autonomous brain tumor segmentation, traditional deep convolutional neural networks have two drawbacks: loss of spatial information owing to recurrent pooling/striding and a lack of multi-scale lesion processing capabilities. For the first problem, we use a single-stride 3D atrous-convolution to replace pooling/striding and provide the groundwork for feature learning. An atrous-convolution feature pyramid is developed and joined to the end of the backbone to answer the second challenge. By including surrounding data, this structure improves the model's ability to distinguish between tumors of varying sizes. Last but not least, a 3D fully connected Conditional Random Field is constructed as a post-processing step to get structural segmentation in both the appearance and spatial consistency of the network output. Comprehensive ablation testing on MRI datasets reveal our method's lossless feature computations and multi-scale information fusion to be able to overcome the concerns listed above. When compared to current methods on publicly accessible benchmarks, our technology gives competitive performance and may be readily adopted into clinical medical applications.

John Schmeelk [12] employed a two-dimensional wavelet transform (2D-WT) to operate with 2D (two dimensional) images. The authors provided an in-depth conversation regarding comparing the two transforms on separated elements. In addition, a comparison between the global properties granted in the Fourier transform (FT) method and wavelet transform was applied to a similar image. The wavelet selected in this research is the Gaussian subfield because, for some reason, it allowed a helpful comparison to the Fourier approach.

Parra et al. [13] implemented an artificial neural network (ANN) algorithm to accomplish the process of MRI brain image segmentation. The multi-spectral features of MR images using multiple models, such as T1-weighted, T2-weighted, and proton density (P.D.) were utilised to segment various brain tissues. The proposed ANN algorithm was used to develop a learning vector quantization (LVQ) network. The McConnell Brain Imaging Center brain database trained and tested the required images. The proposed segmentation algorithms were compared with phantom images to facade every brain tissue and improve the computational efficiency. However, it is sensitive to the local structure of the data.

Papageorgiou et al. [14] developed a fuzzy cognitive map (FCM) method to represent model experts. The FCM ranking model's classification ability was improved by including a computational intelligent training method called the activation Hebbian algorithm. The proposed approach was verified for medical materials, which included 100 cases. The FCM model yielded an accurate diagnostic result of 90.26% (37/41) and 99.22% (55/59) for low-grade and high-grade brain tumors, respectively. The proposed model results provide a slightly higher accuracy compared to current algorithms, such as fuzzy decision trees and decision trees. They were examined using the same type of primary data and achieved success with high accuracy but not supported for high memory.

JingjingGaoet al. [15] proposed skull stripping MR brain images with a three-stage sequence method. The proposed method was implemented based on morphological processing (MRP), edge detection, and

anisotropic diffusion filtering (ADF). The MR images were modified to smooth noisy regions using an ADF filter, and anatomical boundaries were located using an edge detector. Finally, the selection of pixels equivalent to the brain tissue from the central brain image was performed using morphological processing. The experimental results show that the proposed method can create a segmented brain precisely. However, there was complexity at the time of the edge detection.

El-Sayed et al. [16] presented Decision assistance systems based on normal and abnormal classifications in the medical field. The categorization of MRI images was done in a hybrid framework. As part of the suggested hybrid architecture, there are three distinct stages. As part of this process, features are extracted from MRI scans using a discrete wavelet transform (DWT). In the second step, principal component analysis (PCA) was used to decrease MR image characteristics. In the last step, two classifiers were used to categorise normal and abnormal MR pictures. There were two types of classifiers: a K-Nearest Neighbor (K-NN) algorithm and an artificial neural network (ANN) (FP-ANN). One hundred percent sensitivity and ninety percent specificity were both reached by the FP-ANN classifier and the k-NN classifier, respectively, in experiments conducted to test the suggested approach. The ANN technique has the poorest sensitivity and specificity rates of all of the methods. However, the output findings may be partial and have a misleading tolerance after the ANN training process is complete.

Othman et al. [17] proposed a probabilistic neural network (PNN) with data processing techniques and image processing to design an automated brain tumor classification. For the MR brain image classification and tumor discovery, various convolutional methods have been provided by humans. Operator-assisted classification mechanisms are not practical for a massive amount of information. The MR image had noise, leading to dangerous classifications with accuracy. Neural networks, fuzzy logic, and artificial intelligence techniques have shown significant advantages in this field. The suggested PNN classifier was operated on the decision-making process in two stages: the first stage was feature extraction using principal component analysis(PCA) and the second stage was classification using PNN. The performance of the proposed PNN classifier was calculated using both training and classification accuracies. The PNN was given fast and accurate classification and was a promising tool for classifying tumors. However, this requires more memory space to store the model.

PushpaRathi et al. [18] suggested an approach based on linear discriminant analysis for classifying brain activity automatically (LDA). A picture's visual content can be extracted using a method known as feature extraction. Pattern classification methods, such as those used to offer the raw image in its reduced form, have also been utilised to speed up the decision-making process. Most scientists have attempted to categorise MRI brain pictures by developing a classifier that is both robust and accurate. It was the primary goal of this investigation to identify and then extract certain characteristics from an MR brain picture. They used texture, shape, and intensity-based criteria to classify brain tumors into gray matter (GM), white matter (W), normal, and pathological positions of the tumor. To prepare the dataset for analysis, PCA and LDA were employed. In the end, a support vector machine classifier was utilised to compare nonlinear and linear techniques. Many characteristics were eliminated by employing techniques such as principal component analysis (PCA) and local discriminant analysis (LDA). Classes that are well-separated, on the other hand, are unstable.

Islam et al. [19] proposed a stochastic model using brain MRI image texture characterization. The efficiency of the proposed model was described in both feature extraction of independent-patient brain tumors and brain tumor segmentation in MRI. For the MRI feature extraction method, the multi-resolution fractal model (MRFM), which is known as multi-fractional Brownian motion, was used to depict the texture of brain tumors (MBM). The mBm model was provided with an accurate mathematical derivation and an effective algorithm to extract multiple fractal features spatially. Following multi-fractal feature-based segmentation of the brain, tumor techniques have been proposed. To

calculate the brain tumor segmentation performance and efficiency was compared with Gabor (Gb) feature extraction method like multi-scale feature extraction. Furthermore, an extended machine learning-based AdaBoost algorithm was proposed to patient-independent tumor segmentation. Experiments were performed using the BRATS2012 dataset. Performance evaluation showed that segmentation outcomes were more compatible and, on average, exceeded these approaches for patients. However, this is a more complicated stochastic process.

Mikael Agn et al. [20] presented a fully automated generative (FAG) technique for the segmentation of brain tumors using multi-model MRI images. The generative model is regularly used for healthy brain tissues where tissues are represented by Gaussian mixture models (GMM) joined with a spatial tissue earlier further elongated basic model using tumor prior, which uses machine learning-based modified Boltzmann convolutional to alter tumor contour. They performed experiments on the 2013 and 2015 BRATS datasets, which indicated that the model performance was comparable to the present state of the art area. However, it is easily extendable to any number of input differences and is not attached to any particular imaging protocol. However, the GMM has one limitation: there is no uncertainty measure.

TriptiSinghal et al. [21] proposed a system for automatically detecting and segmenting brain tumors. Preprocessing and segmentation of the image are the first two steps in the method's development. To begin, MRI images were preprocessed and given into the system as input, and then an image segmentation procedure was applied. For example, fuzzy C-means clustering (FCM), K-means clustering (KMC), and area increase for brain tumor identification from MRI images were discussed throughout the performance evaluation. The performance analysis of these methods was determined based on the error percentage relative to the ground reality. Their performance assessment was performed with the Rajiv Gandhi Cancer Institute & Research Center, Delhi, India (RGCI&RC) real-time dataset and achieved high-precision results. However, k-means is one limitation, such as its lack of flexibility in a cluster shape.

Sonavane et al. [22] proposed a novel method for brain tumor classification using a neural network and a segmentation algorithm classifier that included morphologically developed skull striping designating image preprocessing. The proposed work was in three stages: in the first stage, image smoothing with edge detection by located image boundaries, and for noise removal, anisotropic diffusion filtering was used. In the second stage, the feature extraction of brain MRI images was performed using wavelet transform and mixing MRI image features. In the third stage, the machine learning-based AdaBoosting algorithm was used to classify MRI images. This classifier was classified as malignant or benign. Their experiments were performed using 155 MRI images, and the results showed 99% accuracy.

Narmada et al. [23] recommended a deep learning-based sophisticated CNN for the classification of brain tumor images. A CNN was used to improve brain tumors' detection and diagnosis accuracy and precision. A few complicated CNN representations have been proposed to expedite brain tumor prediction and classification into five different MRI brain image classes. Median plane and coronal images were used to train and test the proposed classification model. The proposed model performed an average F1-measure of 99.46%, and the accuracy of the recommended model was 99.68%, which was higher than the accuracy of the previous methods. However, it takes a lot of time to train cases if the PC does not have a good GPU.

Tang et al. [24] introduced a new framework for the identification of tumors in brain MRI images using multi-atlas segmentation (MAS). To create a fresh brain picture for segmentation, the MAS framework was utilised to register and merge design information from several normal atlases. We used a low-rank technique based on the average of two different sets of brain atlas data to better represent how the new tumor-related brain MRI picture actually looks. The MAS framework was broken down into two parts. Spatial restrictions were imposed in the initial phase to increase appearance while preserving typical brain

regions. Natural brain atlases were able to be shown in the recovered picture without the need for tumor controls after the second stage. The final segmentation of the tumor brain picture was achieved by repeatedly rerunning both steps. In addition, the atlases used for label evaluation must be correlated to the quantity of labels produced.

PalashGhosal et al. [25] suggested a deep neural network-based squeeze and excitation ResNet-101 for automatic brain tumor classification. This MR image classification is classified into glioma, pituitary tumor, and meningioma. The use of zero-centering intensity normalization for smooth energy adaptation over the tissues was further explored as a preprocessing stage, which was confirmed to be very efficient along with data creation. Experimental findings also showed that the proposed method could offer significant performance improvement in terms of overall precision, specificity, and sensitivity, surpassing the other two new aggressive methods of classification of brain tumors. It may also be suitable in various ways, such as the classification of liver wounds and the classification of breast tumors. The feature extraction of the proposed model improved the CNN-based architecture to 3D data produced by MRI results and covered a vast number of classes. However, CNN is significantly more delayed because of an action such as a max pool.

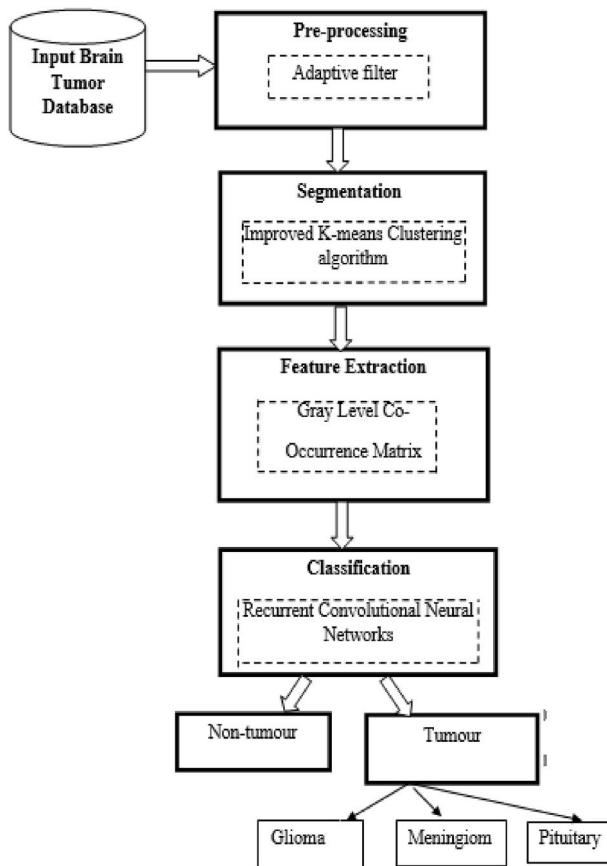
Reddy et al. [26] identified brain tumors as significant in assessing tumors and selecting cases according to their grades. Various imaging techniques have been used to detect brain tumors. However, MRI is widely used because of its excellent image quality and the fact that it does not rely on any cosmic radioactivity. Deep learning (DL) is a machine vision of research (automated techniques) that has shown outstanding predictive efficiency, especially in segmentation and classification problems. A deep learning-based convolutional neural network was developed to detect different brain tumors using two publicly accessible sources or the advantage of databases. Tumors are recognized in the former (glioma, pituitary, and meningioma tumors). Of all three classes, another distinguished class (grade II, grade III, and grade IV).

According to the results of the study, there are a variety of approaches to segmentation, including a region of interest (RoI), feature extraction methods, as well as methods for training and testing utilising just classifiers trained for classification. Few features could be recovered due to the inability to perform effective segmentation and linked feature extraction, resulting in low tumor detection and classification accuracy. Also inefficient were the classifiers used to learn the features themselves.

With the analysis of current methods in brain tumor segmentation and classification, there are various limitations in their development, such as some of the works sensitive to the local structure of the data, memory limitations, complexity, false tolerance, unstable, complicated stochastic processes, no uncertainty measure, lack of flexibility, and training time.

### 3. Proposed methodology

To overcome the limitations of previous works, this paper proposes a new deep learning-based classification technique with the name of recurrent convolutional neural networks (RCNN). The proposed work mainly focuses on classifying brain tumors to decrease the human death rate and improve human lifetime. The proposed work aims to classify brain tumors with low complexity and high accuracy rates compared with previous developments. The proposed methodology consists of four stages, as described below. The first stage is preprocessing using an adaptive filtering algorithm, and the second stage is the clustering algorithm for segmentation. The third process is feature extraction, performed using a gray-level co-occurrence matrix (GLCM). The fourth stage of the work is classification using RCNN. A detailed description of each step is provided below Fig. 2.



**Fig. 2.** Proposed methodology overview.

### 3.1. Proposed architecture

The architecture of the proposed methodology is provided with four categories: preprocessing, segmentation, feature extraction, and classification. A detailed description of each step is provided below.

#### A. Image Preprocessing

To decrease the noise and undesired perversions in images, even before they are supplied into the segmentation tools, we process the images in this step right down to their deepest levels and filter them according to competing factors. We can filter the image according to its median or apply an adaptive filter approach to produce more precise image divisions.

##### a) Adaptive filter

In the image preprocessing technique, noise elimination is the primary intention to improve the damaged image features by eliminating noise [27]. Adaptive filtering is a particular case where denoising is performed based on the noise data existing in an image regionally. Let us understand the reduced image is defined by  $\hat{I}(x,y)$ , the variance across the entire noise image is represented by  $\sigma_y^2$ , the mean of local is given by  $\hat{\mu}_L$  around a window pixel, and the variance local in a window is provided as  $\hat{\sigma}_y^2$  then a possible way of the de-noising image is presented as below:

$$\hat{I}(x,y) - \frac{\sigma_y^2}{\hat{\sigma}_y^2} (\hat{I}(x,y) - \hat{\mu}_L) \quad (1)$$

If the noise variance over the image is close to zero

$$\sigma_y^2 = 0 \Rightarrow \hat{I} = \hat{I}(x,y) \quad (2)$$

If the global noise variance is small, and the local variation is more significant than the worldwide difference, then the ratio is equal to one, that is,

$$\hat{\sigma}_y^2 \gg \sigma_y^2, \text{ then } \hat{I} = \hat{I}(x,y) \quad (3)$$

A high local variance describes the appearance of an edge in the examined image window. When the local and global variations are similar, the equation becomes:

$$\hat{I} = \hat{\mu}_L \approx \hat{\sigma}_y^2 \approx \sigma_y^2 \quad (4)$$

It is a standard application in a healthy region—the mean value of the window throughout a pixel the output is simply provided above similarities. If no anomalies are performed, an edge is transferred to the result. This is an essential function of an adaptive filter. The filter uses the window size as the input and manages the balance based on the input image. The subsequent results were used to investigate noise elimination in brain tumor images using an adaptive filter shown Fig. 3. The purpose was to investigate the impact of adaptive noise removal on the edges.

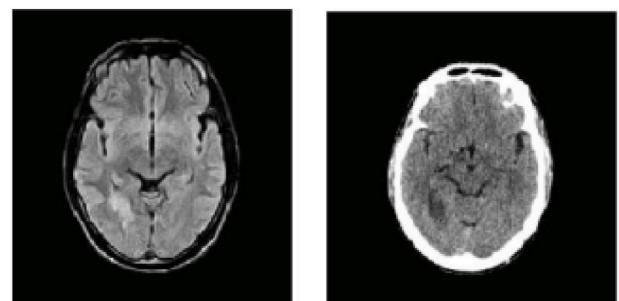
#### B. Segmentation

The process of image segmentation is essential because a vast number of images are produced through the scan. It is incredible for medical authorities to separate these images consistently [28] manually. Several segmentation techniques have been developed for image segmentation. However, the election of segmentation techniques depends on the type of features to be processed and extracted. The K-means clustering algorithm plays a vital role in image segmentation, leading to the division of a given image into various non-overlapping areas. Image segmentation describes the image within sets of pixels that are valuable and convenient for research. K-means clustering is usually applied to improve the edges or objects in an image, and the resulting fragments collectively include a complete picture. The k-means algorithm tasks on one of the two primary features of image energy are similarity and discontinuity.

It plays a vital role in medical diagnosis and can be beneficial in pre-surgical preparation and computer-aided operations. Hence, various segmentation techniques are possible which can be used widely, such as threshold-based segmentation, region-based (region growing, splitting, and merging methods), histogram-based methods, edge-based, and clustering techniques.

#### 3.2. K-means clustering

It is an unsupervised clustering method in which data relating to one collection cannot belong to any other group. This method is easy to connect with other clustering methods. In the proposed segmentation



**Fig. 3.** Adaptive filter.

process, improved k-means clustering is used for brain tumor segmentation. This process clusters the N pixels of an image into k clusters, where  $k < n$  and k is a positive integer. Clustered data were also offered in a separate cluster of data. Furthermore, the fuzzy and c-means approach cannot group the same data currently in another cluster, so we avoid fuzzy c-means and c-means clustering algorithms shown [Table 1](#).

Alternatively, we employed an improved k-means clustering method. It provides good results in segmentation techniques and is very helpful in feature extraction using GLCM.

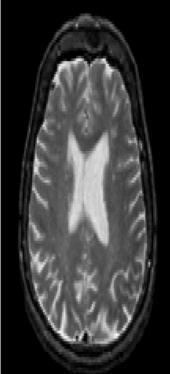
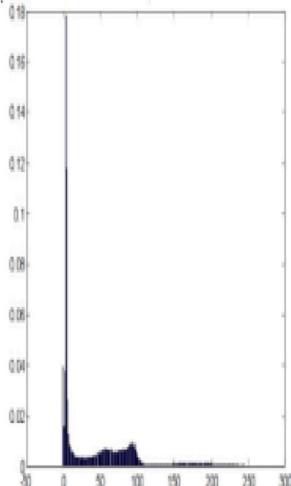
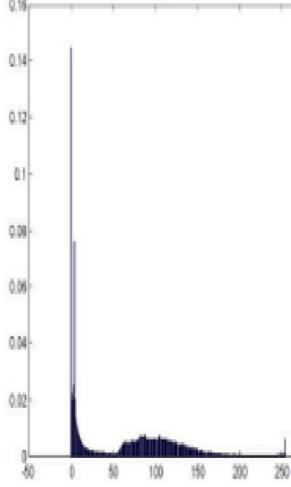
In the proposed approach, 398 MRI brain images of the testing set were examined, carrying 392 normal and 6 with tumor(abnormal).

The improved K-means clustering algorithm involves some steps to obtain the tumor region in the brain image.

Steps for Improved K-means clustering Algorithm:

**Table 1**

Results obtained from proposed Improve K-means.

MRI Image	Radiologist decision	Proposed work decision	Normalized Histogram	Calculation of $\beta$
<b>MRI of Normal Brain</b> 	Tumor not detected	Tumor not detected		3.0365
<b>MRI of Abnormal Brain</b> 	Tumor Detected	Tumor Detected		11.2069

## Steps for Improved K-means clustering Algorithm:

**Step1:** Take MRI scan of brain as an image

**Step2:** Convert it into the greyscale image

if it is not

**Step3:** Then we apply noise removal on

a greyscale image

**Step4:** Sharp the image

**Step5:** Pass the resulting image through

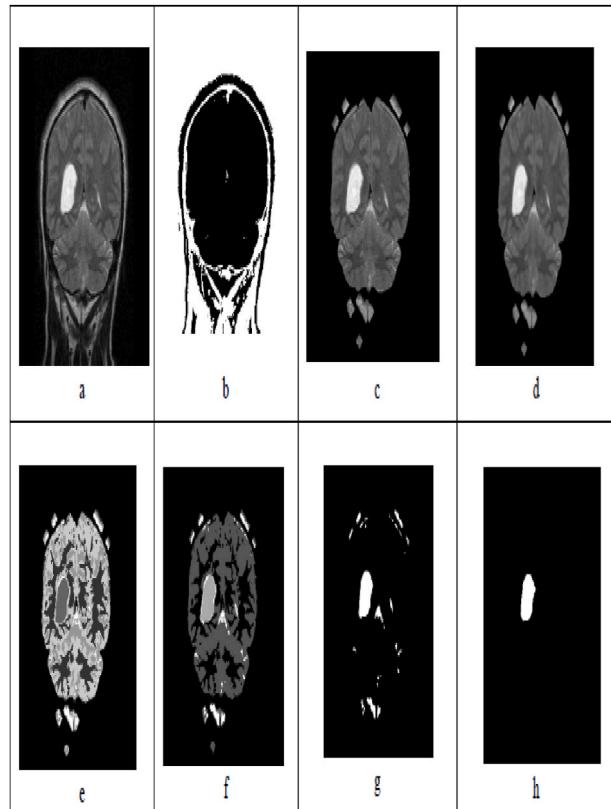
Adaptive filter to enhance the quality

of an image

**Step6:** Compute K – means segmentation

**Step7:** Compute thresholding segmentation

**Step8:** Finally output will be a tumor region



**Fig. 4.** (a) Original MRI image (b) Binary image (c) Image after the morphological operation (d) Final image after improvement (e) K-means cluster 1 provided (f) K-means cluster 2 (g) K-means cluster 3, and (h) Tumor after segmentation.

In Fig. 4, the results are shown for the improved K-means clustering method using the original filter.

As shown in Fig. 4, the segmentation process is taken as an improved version of the K-means clustering (IKMC) algorithm. This includes various stages, as shown in the figure. After performing IKMC, a final segmented tumor appeared. The proposed segmentation process takes less time and is computationally less difficult.

### C. Feature Extraction

Feature extraction is used to decrease the number of expected resources to describe a massive amount of data. To feature extraction of images, a large number of strength grades of the image are provided as input for feature extraction. The output may be higher-level data, such as variance, shape, mean, and color. For image applications, the gray-level co-occurrence matrix (GLCM) method is one of the leading methods [29]. In object classification, various feature extraction techniques are used, such as GLCM and K-nearest neighbor (KNN) (Bharanidharan et al. [30]). The GLCM is the most commonly used MR image feature extraction technique because of its high accuracy; it is also broadly used in texture feature analysis. Textural analysis could help to increase the determination of tumors and identification of tumor grade.

#### 3.3. GLCM feature extraction

GLCM benefits from determining the features from the various GLCMs that are input to the function. The GLCMs are saved in  $ai \times j \times nmatrix$  where n is the determined number of GLCMs, normally because of the various adjustments and displacements used in the algorithm shown Fig. 5. The statistical feature formulas that will be helpful are given below:

**Energy:** This includes the summation of the squared element values of the GLCM method. The amount of energy ranged between 0 and 1, and regular image energy values were 1.

$$Energy = \sum_{i,j} p(i,j)^2 \quad (5)$$

**Homogeneity:** This is a determination of the closeness of elements distributed in the GLCM to find the values of GLCM. Homogeneity values ranged from 0 to 1.

$$Homogeneity = \sum_{i,j} \frac{p(i,j)}{1 + |i - j|} \quad (6)$$

**Contrast:** This is a measure of the contrast intensity and is a parameter that describes the strong difference between its pixel and its nearest pixel over the entire image. For a constant image, the contrast

GLCM							
1	2	3	4	5	6	7	8
1	1	2	0	0	1	0	0
2	0	0	1	0	1	0	0
3	0	0	0	0	1	0	0
4	0	0	0	0	1	0	0
5	1	0	0	0	0	1	2
6	0	0	0	0	0	0	1
7	2	0	0	0	0	0	0
8	0	0	0	0	1	0	0

**Fig. 5.** Generation of GLCM feature extraction.

was 0. The contrast property is also known as the variance.

$$\text{Contrast} = \sum_{i,j} |j|^2 p(i,j) \quad (7)$$

**Dissimilarity:** This is a measure of the variance between pixels and their neighbors. The constant image intensity value has infinite dissimilarity. It has values between 0 and 1.

$$\text{Dissimilarity} = \sum_{i,j=1}^N P_{i,j} |i - j| \quad (8)$$

#### D. Classification using RCNN

The classification process was used to categorise every image based on the image features. Classification is an essential technique used to determine normal extensively and tumor brain images. Classification is a data mining function that allows items in a gathering to target classes or levels. The classification aims to perfectly predict the destination class for every event in the data. The current image classification method can be increased to learn MR brain image measures by merely following the CNN layer with the advanced RCNN layer and restoring the fully connected layer with the RNN layer.

The primary aim of this work was to employ RCNN for brain tumor classification actively. While CNN [31] outcomes in this domain have not significantly improved over the last two years, RNNs can implement CNNs through the more positive association of contextual data. Although CNNs currently overperform RCNNs in medical image classification, they have the energy to improve.

The primary part of the recurrent convolutional neural network (RCNN) is the recurrent convolutional layer (RCL). The elements of the RCL units develop over the discrete-time step. For a unit located at  $(l, m)$  on the  $n^{th}$  feature map in an RCL, its net input  $z_{lmn}(t)$  at time step  $t$  is given by

$$w_n^f \left( w_n^f \right)^T u^{(l,m)}(t) + w_n^r \left( w_n^r \right)^T x^{(l,m)}(t-1) + b_n \quad (9)$$

As shown in equation (9).

$u^{(l,m)}$  denote the feedforward and  $x^{(l,m)}(t-1)$  indicates recurrent input, which are vectorized spots centered at  $(l, m)$  of the feature maps in the current layer.  $w_n^f$  denotes the weights of the feedforward,  $w_n^r$  indicates the recurrent weights, and  $b_n$  denotes the bias. As shown in equation (1), the first phrase is used in the standard CNN, and the second phrase is affected by recurrent connections. The state of this unit is a function of its net input, denoted by equation (10):

$$x_{lmn}(t) = g(f(z_{lmn}(t))) \quad (10)$$

Where,

$f$  Indicates the corrected linear activation function and is shown in equation (11), and  $g$  is the local response normalization (LRN) task given below in equation (12).

$$f(z_{lmn}(t)) = \max(N_{lmn}(t), 0) \quad (11)$$

$$g(f_{lmn}(t)) = \frac{f_{lmn}(t)}{f_{lmn'}(f_{lmn'})(f_{lmn'})^2} \quad (12)$$

where the total number of feature maps is denoted by  $K$  in the current layer. As shown in Equation (12), the sum runs on feature maps  $N$  at the same location of  $(l, m)$  (Actually  $N < K$ ), and  $\alpha$  and  $\beta$  are the constants controlling the normalization. LRN affects lateral restraint in the cortex, where various features face large replies. LRN was used in our design to restrict the states from disproving.

Equations (9) and (10) define the RCL active behavior. Describing this layer for  $T$  time-step outcomes in a feed-forward (F.F.) subnetwork

of depth  $T + 1$ . As shown in Fig. 6, recurrent input emerges over iterations, and the feed-forward input continues to be equal in all iterations.

As shown on the left side of Fig. 6, an RCL displays a time step for  $T = 3$  s, pointing to a feedforward subnetwork with the most significant depth of 4 and a minor depth of 1. At  $t = 0$ , only the feedforward calculation requires a place. On the right side of the figure, the RCNN applied here includes one convolutional layer, four RCLs, three max-pooling layers, and one softmax layer. In addition, RCNN combines a stack of RCL layers of max-pooling with optionally interleaved layers. The longest direction passes through all frequent open links (hence length =  $T + 1$ ), at the same time as the shortest path passes through the more practical F.F. connection (hence length = 1).

## 4. Experiments

### A. Dataset

In this study, the proposed methodology experiments were conducted on the Kaggle dataset. This dataset was divided into two categories: training and testing. Every training and testing set included four types of images: glioma tumor, meningioma tumor, pituitary tumor and no-tumor. The testing set consisted of 394 images and a training set with 2870 various images and data preprocessing actions, similar to brain stripping, have been presented to increase the data description. The performance evaluation process is presented in four classes: glioma tumor, meningioma tumor, no-tumor, and pituitary tumor. Fig. 7 show examples of the types of tumors in different places.

The dataset reference link is given below.

Data set source:

<https://www.kaggle.com/sartajbhuvaji/brain-tumor-classification-mri>.

### B. Implementation process

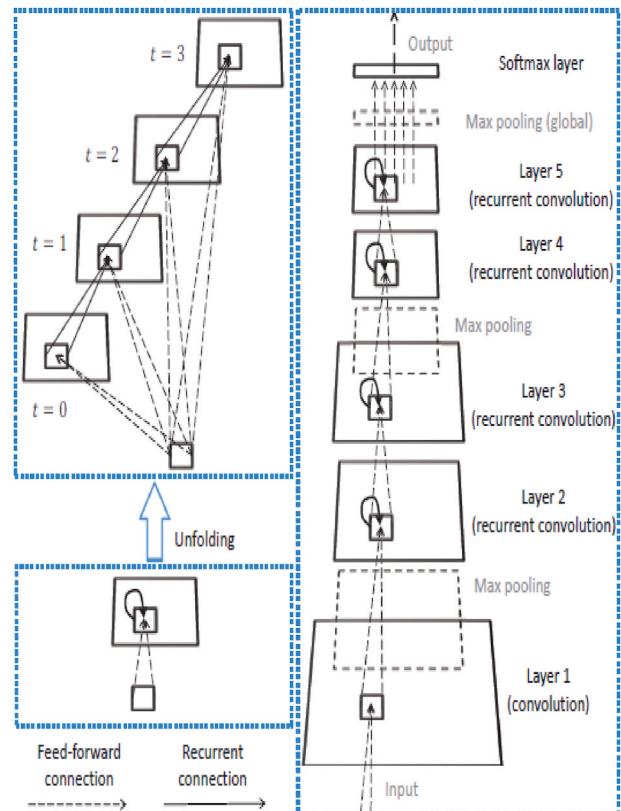
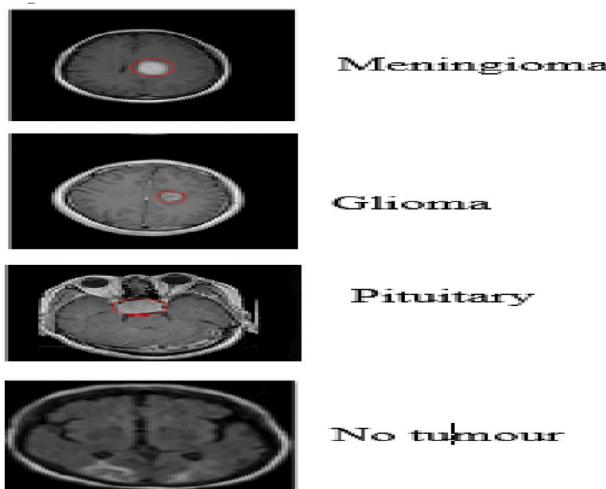


Fig. 6. Architecture for proposed RCNN



**Fig. 7.** Types of tumors in various places.

The proposed method was executed in the machine learning-based Keras library in Python. Python is a high-level programming tool applied to implement neural networks, and it can run over TensorFlow. This helps in both CPU and GPU processing. Hyper-parameters are attuned by applying a network search and the parameters on which the plan worked best on the chosen test data. Parameters such as the testing rate and energy were different when testing. Energy was initially set to 0.5, slowly improved to 0.9, the learning rate was initially set to 0.003 and then slowly reduced to  $0.3 \times 10^{-5}$ .

### C. Evaluation Parameters

The experimental results were estimated using three main measures: accuracy, sensitivity, and specificity. These measurements were calculated using Truepositive, True Negative, False Positive, and False Negative values. The evaluation measures are explained in the following equations.

**Sensitivity:** Brain tumor sensitivity is defined using the ratio of the number of true positives and false negatives. This correlation can be expressed as:

$$S_t = \frac{\text{True positive}}{\text{True positive} + \text{False negative}} \quad (13)$$

**Specificity:** The specificity of brain tumor detection can be evaluated using the ratio of the number of true negatives to various false positives and true negatives. It can be represented as

$$S_p = \frac{\text{True negative}}{\text{True negative} + \text{False positive}} \quad (14)$$

**Accuracy:** The brain tumor detection accuracy can be determined using the ratio of the exact values present in the population. The following equation describes the accuracy:

$$A = \frac{\text{True positive} + \text{True negative}}{\text{True positive} + \text{False positive} + \text{False negative} + \text{True negative}} \quad (15)$$

### 5. Results and discussions

This section analyzes and calculates the proposed method using the Kaggle dataset. The classification was divided into training and testing sets, and the testing set consisted of 394 MR images and a training set with 2870 various MR images from 233 patients. The dataset also includes synthetic data with low variance in the energy values of a similar class that is relatively easy to classify. Hence, only accurate patient data

were used to estimate the proposed model. The evaluation metrics are defined for four tumor regions: a) glioma tumor, b) meningioma tumor, c) no-tumor d) pituitary tumor. In **Table 2** shows, Experimental results with a sample image.

A comparison of various classifiers is presented in **Table 3** to estimate the effectiveness of the proposed model. **Table 3** provides a comparison between multiple algorithms in terms of accuracy, sensitivity, and specificity. The proposed RCNN classifier is compared with the BP, U-Net, and RCNN algorithms.

As shown in **Fig. 8**, the X-axis indicates the classification techniques and the Y-axis indicates the accuracy (%) for various techniques. The graph shows a comparison between various algorithms of the BP, U-Net, and RCNN classification techniques. The proposed RCNN achieved a higher accuracy of 95.17% compared to previous classification techniques.

**Fig. 9** shows the sensitivity of the various classification techniques. The X-axis shows the classification techniques, and the Y-axis shows the

**Table 2**

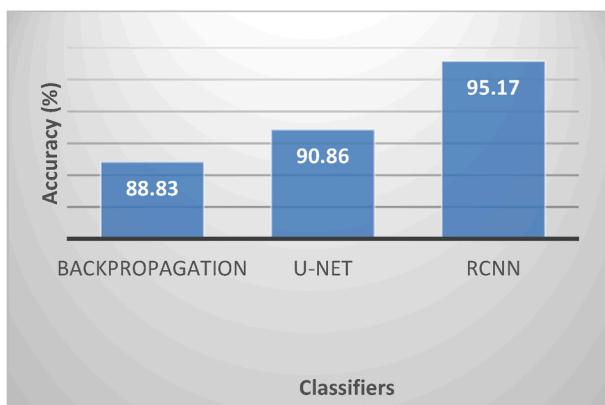
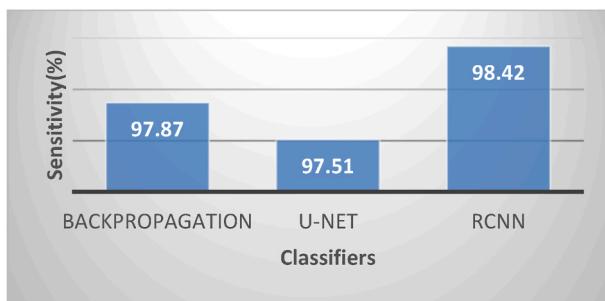
Shows some experimental work on various types of images and that the proposed classifier classified various types of brain tumors such as glioma, normal, meningioma, pituitary.

Input Image	Segmented Image	Type of tumor	Tumor effected area ( $\text{mm}^2$ )	Number of Defect cells
		glioma	28.6525	11771
	Given input image is the normal image so we cannot segment the image	Normal	0	0
		Meningioma	18.455	4887
		pituitary	22.1256	5242

**Table 3**

Comparison of the accuracy of various classifiers.

Number of test images 394 (normal = 105, abnormal = 289)			
Evaluation parameter	Back Propagation	U-Net	Proposed RCNN
True Negative	120	123	125
False Positive	39	30	15
True positive	230	235	250
False negative	5	6	4
Specificity (%)	75.47	80.39	89.28
Sensitivity (%)	97.87	97.51	98.42
Accuracy (%)	88.83	90.86	95.17

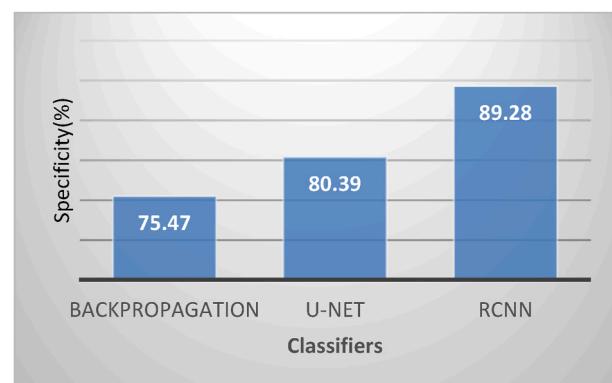
**Fig. 8.** Accuracy for various classifiers (%).**Fig. 9.** Sensitivity for various classification techniques.

sensitivity for multiple classifications. The comparison shows that the proposed RCNN classification techniques provide a higher sensitivity rate of 98.42% compared with previous BP, U-Net, and RCNN.

Fig. 10 indicates the specificity for different classification techniques. The X-axis shows the various classification techniques, and Y-axis indicates the specificity for different classifications. The comparison shows that the proposed RCNN classification method gave a more sensitivity rate of 89.28% than the existing profiling techniques of BP, U-Net, and RCNN.

## 6. Conclusion

The categorization of a brain tumor is critical to determining the best course of action. For the first time, researchers have developed an automated method for recognising and categorising brain cancers using MRI scans. The suggested study was separated into four categories: preprocessing, segmentation, MR image feature extraction, and final image classification. The brain tumor pictures were segmented using improved K-means clustering techniques in the segmentation step. Employing a convolutional neural network (CNN) that has been trained using deep learning (RCNN). A performance evaluation of the proposed

**Fig. 10.** Specificity for various classification techniques.

technique was carried out on the Kaggle dataset using the Keras package in Python using 394 test photos and 2870 training images. Back-propagation (BP), U-Net, and RCNN, which are all neural network-based classification methods, were all compared to the proposed RCNN methodology. MRI brain pictures may now be used to detect malignancies using a method that outperforms prior algorithms, according to the results of the research. Using MR images, the suggested approach accurately classified normal and pathological tissues with a precision of 95.17%. To summarise, we've found that the proposed strategy works well for sorting out the various forms of brain tumors.

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## Informed Consent

The author 's declare is no Informed Consent.

## Author's contribution

The author 's declare no contribution.

## Declaration of competing interest

The authors declare no conflict of interest in preparing this article.

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