

Brain Tumor Segmentation and Classification Using Deep Learning with Hybrid KFCM Clustering and LuNet Classifier

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ABSTRACT

Brain tumor identification and classification play a critical role in early diagnosis and treatment planning. This research presents a hybrid deep learning-based architecture for accurately classifying and segmenting brain tumors from MRI images. The T1-W CEMRI dataset is used as the input data set for the suggested approach. The data set is first preprocessed by turning it into greyscale images with a fixed pixel resolution. Techniques for noise reduction are used to improve image quality and maintain structural details that are essential for diagnosis. Using a Hybrid Kernelized Fuzzy C-Means (KFCM) clustering technique, which efficiently defines tumor borders by utilizing both spatial and intensity information in a kernel-induced space, tumor regions are segmented. This makes segmentation more robust, particularly in areas with poor contrast or noise. A deep convolutional neural network called VGG-16 is used for feature extraction in order to extract high-level spatial characteristics from the segmented brain tumor images. After extraction, a lightweight convolutional neural network architecture called LuNet which has been trained to differentiate between meningioma, glioma, and pituitary tumors is used to classify the retrieved tumor sections. According to experimental data, the suggested model achieves an astonishing 98% classification accuracy, showing its potential for accurate tumor diagnosis. By fusing the advantages of deep learning and conventional clustering, this hybrid framework provides a very effective and precise method for analyzing brain tumors in clinical settings.

Keywords: Tumor Classification, Deep Learning, Hybrid KFCM Clustering, LuNet Classifier, Brain Tumor, VGG-16.

INTRODUCTION

Finding brain tumors is a challenging medical process that necessitates a close examination of MRI data by specialists [1]. The clinical diagnosis of neurologists in the medical field is greatly influenced by image processing. A variety of imaging modalities are employed for tumor categorization, segmentation, and diagnosis. All other modalities are inferior to the use of MRI because of its noninvasiveness and better presentation of interior tumor data. In fact, early diagnosis may improve the likelihood of saving lives [2]. Brain tumors (BTs) are quickly growing around the world. Every year, brain tumors cause hundreds of deaths. Thus, precise identification and categorization are crucial for brain tumor treatment. For BT identification and classification, a variety of research methods based on deep learning (DL) and conventional machine learning (ML) have been introduced [3]. According to their experience, radiologists or clinical professionals must perform a time-consuming and difficult task while attempting to identify, separate, and extract contaminated tumor regions from MRI pictures, despite the fact that these difficulties are significant. Concepts from image processing can visualize the different human organ anatomical structures. It is difficult for simple imaging tools to identify aberrant structures in the human brain [4]. Thus, computerized brain tumor detection is challenging, error-prone, and time-consuming. Because of this, there is a present need for highly accurate automated computer-assisted diagnostics [5]. Brain tumor identification and MR imaging (MRI) segmentation are difficult but essential tasks for many medical analysis applications. Many modern procedures use the four neural imaging modalities T1, T1c, T2, and FLAIR because they each offer unique and crucial information about different tumor regions [6]. Doctors use precise brain tumor segmentation as a foundation for surgery preparation and treatment. When a patient's survival depends on prompt treatment, manual detection using MRI scans is computationally complex, and performance depends on domain

expertise [7]. Separating an image into its various components is known as segmentation. To identify the many items in an image, segmentation is a crucial technique in several main industries, including face tracking, satellite, tracking of objects, remote sensing, and most notably, the medical industry [8]. So, deep learning has radically changed and improved detection, prediction, and diagnosis techniques in many medical fields, such as diseases, brain lesions, cancer of the lung, the intestines, the heart, and the retina [9]. To detect a tumor from brain MRI images, the most advanced deep learning method, a CNN, was used. The drawn-out training procedure still has issues [10].

The primary contribution of the suggested approach is as follows:

- Using the publicly available T1-W CEMRI dataset, a database, the suggested approach was evaluated.
- Developed a strong preprocessing step that enhances tumor visibility and segmentation quality by applying noise reduction, resizing images to a standard resolution (255×255), and converting images to grayscale.
- For precise brain tumor segmentation, an improved Hybrid Kernelized Fuzzy C-Means (KFCM) clustering technique that manages noise and intensity inhomogeneity in MRI images. High-level spatial information are extracted from the segmented brain tumor images using the VGG-16 deep convolutional neural network.
- Created LuNet, which maintains computing efficiency while classifying segmented brain tumors (glioma, meningioma, and pituitary) with excellent accuracy.
- Achieved a 98% classification accuracy, proving that segmentation and deep learning-based classification work well together to diagnose brain tumors.

The following will be the format for the following sections: The literature review for our suggested strategy and other pertinent details are covered in Section 2. Section 3 provides an explanation of the suggested methodology, Section 4 describes the experiment and data analysis, and Section 5 summarizes the study's findings and future directions.

2. RELATED WORKS

Muhammad Irfan Sharif et al. [11] have proposed, a feature selection approach based on active deep learning is advised for the segmentation and identification of brain tumors. Muhammad Attique Khan et al. [12] have suggested, a brain tumor categorization and segmentation utilizing improved saliency segmentation and the best choice of characteristics technique. Sarhad Maqsood et al. [13] have recommended, a deep neural networks and multiclass SVM are used for multimodal brain tumor identification. Yong Zhanget al. [14] have described, a data augmentation methods and deep neural network computing (DNN) are used to separate 2-dimensional brain tumors in MR images.

Gökay Karayegen et al. [15] have suggested, a using 3-dimensional Brain Tumor a segmented (BraTS) image data sets, which comprise four various types of images (T1, T1C, T2, and Flip), the semantically segmented approach uses a convolutional neural network to segment brain tumors on its own. Mayur Bhargab Bora et al. [16] have reported, a deep MRI image-based division of brain tumors using hybrid convolutional neural networks. Jae Young Choi et al. [17] have proposed, a methods for statistically analyzing brain MRIs using deep learning-based segmentation to diagnose AD. Raghvendra Kumar et al. [18] have reported, a CNN-based model and deep neural networks are utilized to identify if the MRI indicates "tumor detected" or "tumor not detected."

Kumaragurubaran T et al. [19] have proposed, a extract characteristics from brain MRI scans, PCA is used in conjunction with CNN and Support Vector Machines (SVM). SeungBin Cho et al. [20] have recommended, a brain tumor segmentation study will benefit from the use of BU-Net, a 2D image segmentation technique. Yasar Mehmood et al. [21] have proposed, aclassify of brain tumors into three groups glioma, meningioma, and pituitary tumors—a transfer learning-based fine-tuning technique is used with EfficientNets. Lal Hussain et al. [22] have proposed, an automated Ultra-Light Brain Tumour Detection (UL-BTD) system is based on the new Ultra-Light Deep Learner Architecture (UL-DLA) for deep features and highly distinctive textural data that is obtained by the Gray Level Co-occurring Matrix (GLCM).

Tijiang Zhang et al. [23] have proposed, a two rapid and effective deep CNN based techniques for identifying brain tumors use magnetic resonance imaging data to efficiently detect and categorize different types of brain tumors. Xin Lin et al. [24] have recommended, a semantic segmentation of 3-dimensional brain tumors is a sequence-to-sequence prediction job that uses a new three-dimensional medical image segmentation method that combines an encoder–decoder structure, a transformer, and a neural network.

3. PROPOSED SYSTEM

Using MRI images, the recently developed classification based brain tumor diagnosis model goes through the following stages. To segment and classify brain tumors, the suggested approach makes use of dataset images.

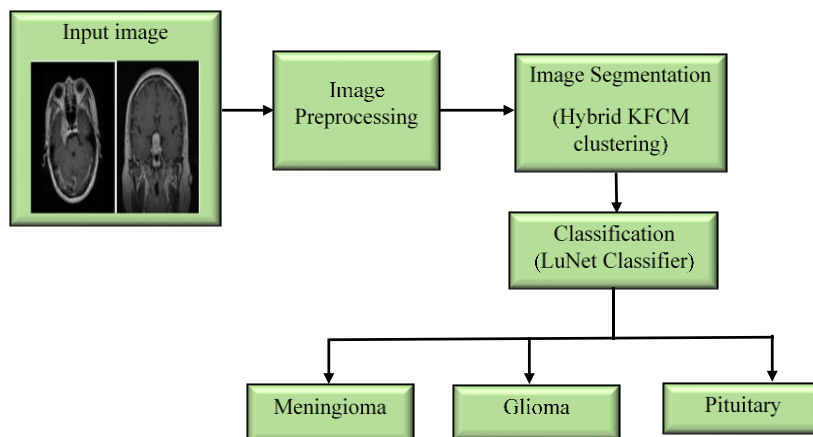


Figure 1: Categorizing brain tumors with the suggested framework.

Preprocessing entails performing noise reduction to improve image quality and transforming the MRI images into grayscale with a resolution. Tumor regions are precisely segmented using a Hybrid Kernelized Fuzzy C-Means (KFCM) clustering technique, which captures both spatial and intensity data. Feature extraction is performed using VGG-16, a deep convolutional neural network, to obtain high-level spatial features from the segmented brain tumor images for accurate classification. LuNet, which is intended to differentiate between gliomas, meningiomas, and pituitary tumors, is then used to classify the segmented tumor. The phases in the suggested method for classifying and segmenting brain tumors are shown in Figure 1, including image gathering, preprocessing, segmentation, and algorithm selection.

3.1 Image preprocessing

Enhancing the qualities of the particular required image and removing unwanted distortion are the goals of the preprocessing stage, which gets ready for further processing. An image enhancement preprocessing approach is used to improve an image that isn't quite perfect. The following actions ought to be taken in the pretreatment phase: To increase the effect, combine the sharpened image with the original. When the MRI scan image is saved in the system, it is transformed into a 255×255 greyscale image. These photos have been subjected to noise reduction, which has reduced their quality. The high-pass filter produces high-resolution, noise-free images for sharpening. One preprocessing technique is data expansion, which involves tilting and vertically rotating the image to transform the visual source from the brain into a uniform three-dimensional image. Therefore, the proposed hybrid architecture benefits from data expansion in order to achieve high assessment accuracy and precision.

3.2 Segmentation using Hybrid KFCM clustering technique

For automatic brain tumor segmentation, this hybrid clustering method integrates clustering using K-means with the FCM system. By combining FCM and K-means clustering, this method significantly reduced the amount of time needed to calculate picture segmentation. Created a novel method using a morphological pyramid and FCM clustering for multi-resolution MRI image segmentation. The initial method for controlling the spatial context between the pixels was Wavelet Multi Resolution (WMR). The generated multi-resolution images are then fused with the original image using a morphological pyramid to make the processed image as crisp as possible and to minimize noise. Finally, the FCM was used to segment the images. One of the main reasons for incorrect segmentation in FCM processing is noise in the image. The FCM issue is resolved by using the KFCM. This study employs the hybrid KFCM to segment the tumor regions from MRI data. Based on the hyper tangent function, this hybrid KFCM algorithm uses the heterogeneity of the neighborhood's grayscales to construct a new kind of distance metric, Eqn. (1).

$$M(a_k, b_i) = 1 + \tan m \left(\frac{-\|a_k, b_i\|^2}{\sigma^2} \right) \quad (1)$$

A limited collection of N data points that are part of the cluster b_i is denoted by the symbol a_k . Where σ is the user-supplied parameter, C is the cluster. Eq. (2) specifies the relevant goal function.

$$R_h = \sum_{k=1}^N \sum_{i=1}^c q_{ki}^h \|\varphi(a_k) - \varphi(b_i)\|^2 \quad (2)$$

With regard to cluster i , q_{ki}^h is the fuzzy connection of the k th data number, and h indicates that the weighting exponent $1 \leq h$. Map function is φ . Using the Gaussian kernel function, non-linear picture mapping onto linear high Dimensional Feature Space (DFS) is achieved here. According to hybrid KFCM, $\|\varphi(a_k) - \varphi(b_i)\|^2 = 2(1 - P(a_k, b_i))$, and a new version objective function utilizing the aforementioned equation is represented in eqn 3:

$$R_h = 2 \sum_{k=1}^N \sum_{i=1}^c q_{ki}^h (1 - P(a_k, b_i)) \quad (3)$$

Using Equations (4) and (5), the membership function (q_{ki}) and uploading centroid (b_i) are completed here:

$$q_{ki} = \frac{\frac{1}{1-P(a_k, b_i)}^{\left(\frac{1}{h-1}\right)}}{\sum_{j=1}^c \left(\frac{1}{1-P(a_k, b_j)}\right)^{\left(\frac{1}{h-1}\right)}} \quad (4)$$

$$b_i = \frac{\sum_{k=1}^N (q_{ki}^h P(a_k, b_i) (1 + \tan m(\frac{-\|a_k, b_i\|^2}{\sigma^2})) a_k)}{\sum_{k=1}^N (q_{ki}^h P(a_k, b_i) (1 + \tan m(\frac{-\|a_k, b_i\|^2}{\sigma^2}))} \quad (5)$$

Lastly, segmented clusters can be selected for optimal clustering using Otsu's threshold technique.

3.3 Feature Extraction using VGG-16 Network

Thirteen distinct categories are created by the VGG16. A deeper design and better performance are now features of many CNN models. Deeper networks, on the other hand, require millions of parameters and a substantial amount of data, making training them difficult. For models to be more accurate and broadly applicable, a large, properly labeled dataset must be included. For healthcare issues, no sizable tagged datasets are available. In order to solve this problem, transfer learning approaches are used, in which the model is trained first on a large raw image dataset, like ImageNet, and then modified to suit the specific problem [25].

Features are extracted using a VGG-16 system that has been previously trained with ImageNet. The LSTM uses these characteristics as its input signal. VGG-Net consists of 16 convolutional layers and 3x3 filter, with one layer of convolution pace and three fully connected (FC) layers. The VGG-16 network is composed of many stacked tiny kernels with filters to enhance its depth and extract more intricate features at a lower cost. In this study, the extractor of features VGG-16 is compared to AlexNet and ResNet.

3.4 Classification using Enhanced LuNet

VGG-16 features are pre-trained and fed into the LuNet network. The degradation issue can be resolved by LuNet by releasing memory. The more complex CNN variation LuNet has three gates: arrival, exit, and forgetting. There are 100 nodes in each of the neural network's two hidden layers. Long-term dependencies are progressively found by LuNet with the aid of these gates. This suggested that LuNet for MRI image-based brain tumor identification is easy, quick, and effective. The development of the extremely successful CNN framework known as LuNet for categorization of medical pictures is the aim of this project. The proposed design, which has been altered in numerous ways, combines LuNet and UNet.

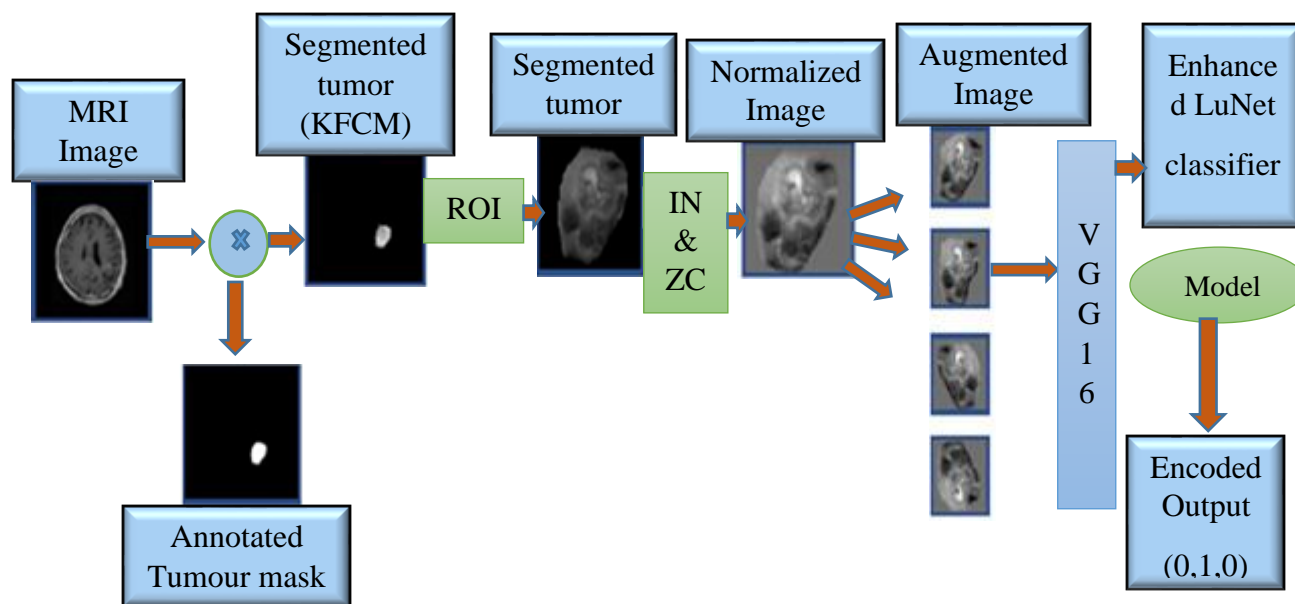


Figure 2: Summary of the Suggested Work

The new CNN design is called LuNet, which has fewer layers and is less complicated than Le-Net and U-Net. Its overall architecture includes both upsampling and downsampling. In addition to a Maxpooling process, the downsampling segment consists of just two layers. The input image has dimensions of $224 \times 224 \times 3$. A max-pooling layer with a 3×3 filter size of 32 and two ConvNets comprise the first layer of the LuNet. An overview of the suggested classification method for brain tumors is shown in Figure 2. Two 64-digit ConvNets and a layer of pooling with a 3×3 filter size comprise the LuNet second layer network. The second half uses a two-layer approach to enhance sampling. Sampling is done using two convNets and a transposition layer. To find picture data, the sampling step combines sampled data with the high-resolution functions from the previous section.

The goal of a constant ConvNet with transposed layers is to learn an extremely precise output. Two convolutional layers and a transposition layer make up the LuNet's upsampling part. The two ConvNets have the same size of 3×3 64 numbers, whereas the first inversion layer has a filter size of 2×2 and 64 digits in two stages. A 2×2 filter, two ConvNets of the same number, and 32 digits for two steps make up the second transposition layer. When the sample layer is applied, the output data will therefore have the same quality as the original image. The "eLU" activation feature is present in every layer since the LuNet model does not exclude negative pixels.

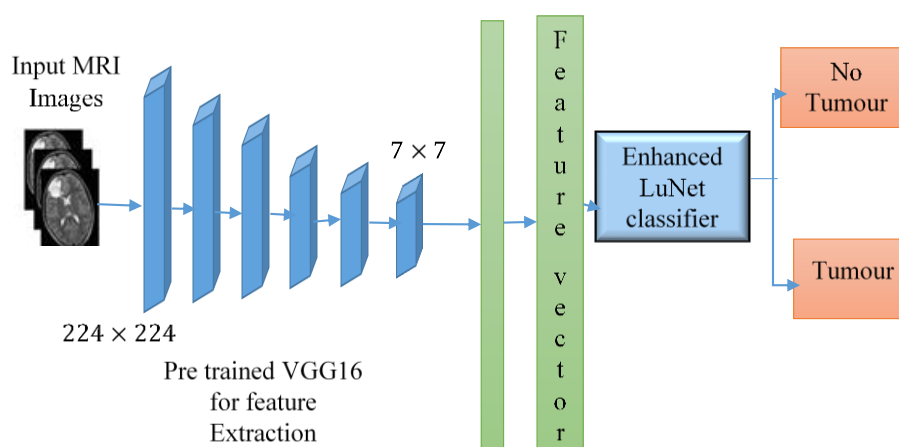


Figure 3: Suggested hybrids architecture of the LuNet classifier

A sigmoid activation function and up-sampled data are used in the final stage to connect two eventually connected layers. Figure 3 displays each tier's table and graph structures for the proposed model (LuNet).

Since the proposed LuNet model is viewable, it only consists of four layers for the sigmoid activation function, two layers for the encoder, two layers for the decoder, and two ultimately coupled layers. The U-Net model serves as the foundation for the suggested model structure; yet, because to its six levels, the model is distinct, straightforward, and quick.

3.5 Performance Evaluation criteria

Four popular classification measures are utilized to assess the performance of the proposed network: F1-score, accuracy, recall, and precision. The primary determinant of the overall precision of the model is its accuracy. Using equation (6), this assessment measure can be calculated as follows:

$$\text{Accuracy} = \frac{TP+TN}{TP+FP+TN+FN} \quad (6)$$

The accuracy is calculated as the number of correctly predicted positive cases divided by the total number of expected positive cases. This assessment metric is determined using equation (7), as shown below:

$$\text{Precision} = \frac{TP}{TP+FP} \quad (7)$$

It is possible to evaluate the correctness of the suggested Hybrid KFCM-LuNet testing by utilizing the F1-score, which is the harmonic median of precision and sensitivity (recall). As demonstrated below, equation (8) can be used to calculate this evaluation metric:

$$F - \text{score}(\%) = 2 \times \frac{\text{recall} \times \text{precision}}{\text{recall} + \text{precision}} \quad (8)$$

The number of true positives divided by the number of genuine positives (TP + FN) yields this figure. The model's recall measures its ability to identify every pertinent positive case. Recall can be calculated using:

$$\text{Recall} = \frac{TP}{TP+FN} \quad (9)$$

4. RESULT AND DISCUSSION

4.1 Dataset

The experimental results of the tumor segmentation and classification techniques, along with a comparison analysis, are shown in this section to demonstrate the efficacy of the Hybrid KFCM-LuNet approach. MATLAB 2018b, a software program with an Intel core processor, 4 GB of random access memory (RAM), and Windows 7 was used to implement the Hybrid KFCM-LuNet technique. Using the T1-W CEMRI dataset, the suggested approach was verified. This sample contains 116 images of pituitary tumors, 105 images of meningiomas, and 118 images of gliomas, as shown in Table 1.

Tumor Type	Training Images	Testing Images	Total Images
Glioma	92	26	118
Meningioma	79	26	105
Pituitary	89	27	116
Total	260	79	339

Table 1: Dataset Features: MRI Image Counts of Brain Tumors

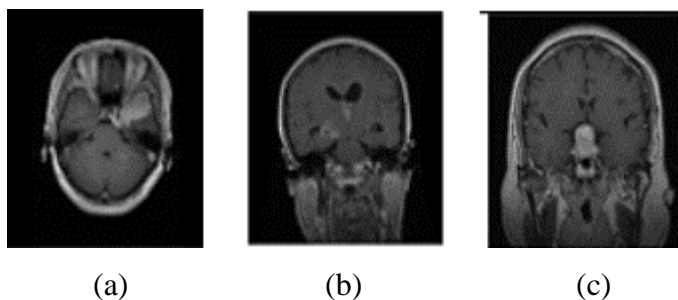


Figure 4: The T1-W CEMRI dataset provides the following input images: (a) Meningioma, (b) Glioma, and (c) Pituitary.

MRI scans of the pituitary, glioma, and meningioma brain tumor types are shown in Figure 4. The T1-W CEMRI dataset provided these pictures, which form the basis for additional preprocessing, segmentation, and classification.

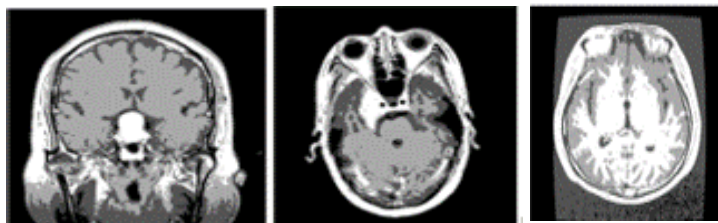


Figure 5: Three pictures of brain tumors (pituitary, glioma, and meningioma) clustered

The Hybrid KFCM clustering technique is used to show the clustered output of different forms of brain tumors: meningioma, glioma, and pituitary (Figure 5). The preprocessed MRI images' tumor regions are efficiently highlighted and segmented by the clustering, allowing for easy visual discrimination between the various tumor kinds and supporting the classification step that follows.

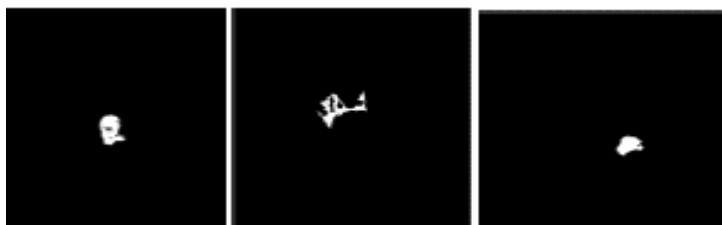


Figure 6: Segmented of three brain tumour images

The segmented output of brain tumor pictures using the Hybrid KFCM algorithm is displayed in Figure 6:

4.2 Classification

Hence, propose a LuNet architecture based on deep learning for the classification of brain cancers, such as meningioma, pituitary, and glioma diseases. Various metrics, including precision, F1-score, sensitivity, accuracy, and specificity, are employed to assess the suggested model's classification performance. Additionally, a ROC curve and confusion matrix were constructed for this procedure.

26	0	0
0	25	1
1	0	26

Figure 7: KFCM-LuNet Classifier Confusion Matrix

The classifier's best performance on the test set was demonstrated by the confusion matrix for the third approach, Hybrid LuNet. Each matrix item showed the proportion of samples that the classifier correctly or erroneously identified. Glioma, meningioma, and pituitary were displayed in the matrix's three rows and columns. The number of photographs identified was determined by how many of the diagonal elements in each class accurately mirrored the photos. The off-diagonal portions showed the quantity of inappropriately

classified photos. The classifier accurately identified 27 images as pituitary, 26 as meningiomas, and 26 as gliomas inside the combined technique's confusion matrix (Fig. 7).

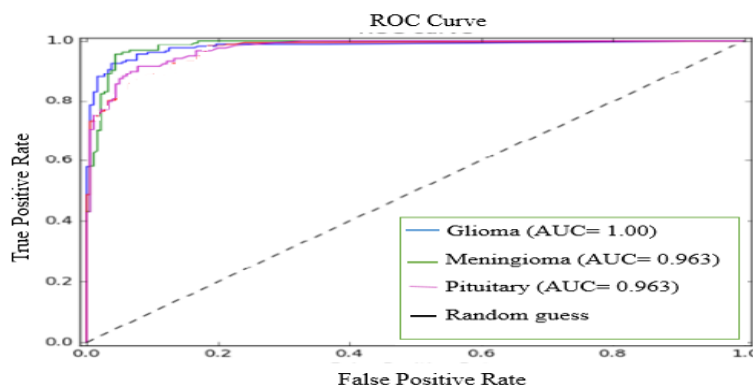


Figure 8: ROC Curve of LuNet Classifier

The AUC values for glioma, meningioma, and pituitary using this method were 100%, 97%, and 97%, respectively, as Figure 8 illustrates. The brain tumor classification model achieved an overall accuracy of 98% on the dataset, demonstrating good performance in distinguishing between meningioma, glioma, and pituitary tumors.

Table 2: Evaluation of the suggested technique's performance

Performance measures	Meningioma	Glioma	Pituitary
Precision	0.9630	1.0	0.9630
Accuracy	0.9630	1.0	0.963
Recall	1.0	0.9615	0.9630
F1 score	0.9811	0.9804	0.963

The precision, F1 score, and recall of Glioma were 1.00%, 0.98%, and 0.97%, in that order. According to the findings, the Meningioma had a 0.96% F1 score, a 1.00% recall, and a 0.97% precision. Thus, the pituitary's F1 score, precision, and recall were, respectively, 0.987%, 0.97%, and 0.97%. Table 2 lists the results of the performance analysis.

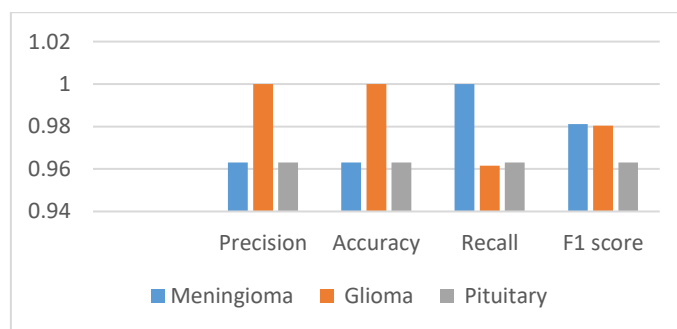


Figure 9: Performance of proposed classifiers

A graphic depiction of the suggested approach's performance is shown in Figure 9. The average outcomes of testing the existing method are shown in Table 3.

Table 3: Performance metrics for various strategies

Model	Dataset	Accuracy
(Nalawade et al., 2019) DenseNet-161 [26]	TCIA	90.5
Çinarer et al. (2020) DNN [27]	TCIA	96.15
SVM [28]	T1-W CEMRI	91.14
CNN [29]	T1-W CEMRI	84.16
Proposed Hybrid KFCM and LuNet	T1-W CEMRI	98%

5. CONCLUSION

Using enhanced MRI images, this study proposed a hybrid deep learning-based approach for brain tumor classification and segmentation. Through noise removal, scaling, and grayscale conversion, the preprocessing pipeline improved the quality of the images. The technique combines a lightweight LuNet classifier for effective tumor type classification with Hybrid Kernelized Fuzzy C-Means (KFCM) clustering for accurate tumor segmentation. According to experimental data, the suggested framework was able to successfully identify pituitary tumors, meningiomas, and gliomas with a high classification accuracy of 98%. This method works well for clinical diagnosis since it is accurate and computationally efficient. Future improvements could include adding support for multi-modal MRI inputs (such T2, FLAIR, and T1c) to the suggested model to increase segmentation robustness across a range of tumor types and imaging settings. Instead of using 2D slices, 3D volumetric analysis could improve clinical relevance and spatial understanding. Finally, real-time deployment for usage in remote diagnostics and smart healthcare can be investigated on cloud platforms or embedded devices.

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