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Brain tumor segmentation using K-means clustering and deep learning with synthetic data augmentation for classification

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Abstract

Image processing plays a major role in neurologists' clinical diagnosis in the medical field. Several types of imagery are used for diagnostics, tumor segmentation, and classification. Magnetic resonance imaging (MRI) is favored among all modalities due to its noninvasive nature and better representation of internal tumor information. Indeed, early diagnosis may increase the chances of being lifesaving. However, the manual dissection and classification of brain tumors based on MRI is vulnerable to error, time-consuming, and formidable task. Consequently, this article presents a deep learning approach to classify brain tumors using an MRI data analysis to assist practitioners. The recommended method comprises three main phases: preprocessing, brain tumor segmentation using k-means clustering, and finally, classify tumors into their respective categories (benign/malignant) using MRI data through a finetuned VGG19 (i.e., 19 layered Visual Geometric Group) model. Moreover, for better classification accuracy, the synthetic data augmentation concept is introduced to increase available data size for classifier training. The proposed approach was evaluated on BraTS 2015 benchmarks data sets through rigorous experiments. The results endorse the effectiveness of the proposed strategy and it achieved better accuracy compared to the previously reported state of the art techniques.

KEYWORDS

cancer, health systems, healthcare, synthetic data augmentation, VGG19, WHO

1 | INTRODUCTION

Medical imaging classification plays a substantial role to identify irregularity in different organs of the body, such as blood cancer (Abbas et al., 2018, 2018a, 2018b, 2018c; Rehman, Abbas, Saba, Mahmood, & Kolivand, 2018; Rehman, Abbas, Saba, Mehmood, Mahmood, et al., 2018; Rehman, Abbas, Saba, Rahman, Mehmood, et al., 2018), lung cancer (Khan, Nazir, et al., 2019; Saba, Khan, Islam, et al., 2019; Saba, Khan, Rehman, et al., 2019), brain tumor (Khan, Lali, et al., 2019; Rehman, Khan, Saba, et al., 2021), breast cancer (Mughal, Muhammad, Sharif, Saba, & Rehman, 2017; Mughal, Muhammad, Sharif, Rehman, & Saba, 2018; Marie-Sainte, Saba, et al., 2019; Saba, Sameh, Khan,

Shad, & Sharif, 2019), stomach cancer (Khan, Javed, Sharif, Saba, & Rehman, 2019; Khan, Sharif, et al., 2019), skin cancer (Javed, Rahim, Saba, & Rashid, 2019; Javed, Rahim, & Saba, 2019; Javed, Rahim, Saba, & Rehman, 2020; Javed, Saba, Shafry, & Rahim, 2020; Khan, Akram, et al., 2019; Khan, Javed, et al., 2019; Khan, Sharif, et al., 2019; Saba, Khan, Rehman, et al., 2019), Retinal image analysis (Jamal, Hazim Alkawaz, Rehman, & Saba, 2017; Saba, Bokhari, Sharif, Yasmin, & Raza, 2018; Ullah et al., 2019) and so on. The abnormality of the organ often results in rapid tumor development, which is the primary cause of death worldwide (Fahad, Khan, Saba, Rehman, & Iqbal, 2018; Rahim, Norouzi, Rehman, & Saba, 2017; Rahim, Rehman, Kurniawan, & Saba, 2017; Saba, Rehman, Mehmood, Kolivand, &

Sharif, 2018; Saba, Bokhari, Sharif, Yasmin, & Raza, 2018; Saba, Al-Zahrani, & Rehman, 2012; Ullah et al., 2019; Yousaf, Mehmood, Saba, et al., 2019; Yousaf, Mehmood, Awan, et al., 2019).

The brain tumor is the utmost perilous type of cancer as it affects the human body's main nervous system among children and adults. There are two dissimilar sorts of brain tumors: benign and malignant tumors. The benign tumor changes the cells' shape and structure that need to be treated but could not infect the other cells or spread in several parts of the brain. While malignant brain tumor is very dangerous, spreadable, grow if not treated with care and could be removed directly (Amin, Sharif, Raza, Saba, & Anjum, 2019; Amin, Sharif, Raza, Saba, & Rehman, 2019; Ejaz, Rahim, Rehman, Chaudhry, et al., 2018; Ejaz, Rahim, Rehman, & Ejaz, 2018). The detection and identification of brain tumors into malignant or benign is a complicated and sensitive task to treat the tumor accurately.

Brain tumors usually are defined as a cluster of abnormally growing brain cells. Such kinds of tumors subjected the brain tissue to decrease in size, resulting in mass harm to the brain's neurons and thus disrupts the brain's operation. Meningioma, glioma, and hysteria are forms of brain tumors that typically occur in the affected region. There is a strong malignancy in each of these tumors. Glioma is another form of brain tumor in the region of glial tissue and spinal cord (Ejaz, Rahim, Bajwa, Rana, & Rehman, 2019; Iqbal, Ghani, Saba, & Rehman, 2018).

Commonly, neurologist segments the abnormal regions manually at each slice of MR-imaging modalities (Nazir, Khan, Saba, & Rehman, 2019; Norouzi et al., 2014). The early and accurate detection of any type of disease is a keystone in the cure of patients, increasing the survival possibilities. The manual segmentation of brain tumor is subjective, consume more time, and error-prone. However, early and accurate detection of the tumor is a process that involves the intervention of experts in the evaluation processes of the patient (Iqbal, Khan, Saba, & Rehman, 2017). This is costly and nearly impossible to be achieved for a huge number of patients. The main purpose of semi-automatic or automatic segmentation techniques of brain tumors is to detect efficiently and segment accurately abnormal regions from the brain rapidly for a significant number of patients. The two main grades of brain tumors are low-grade glioma (LGG) and high-grade glioma (HGG; Ramzan, Khan, Iqbal, Saba, & Rehman, 2020; Ramzan, Khan, Rehmat, et al., 2020; Saba, Mohamed, El-Affendi, Amin, & Sharif, 2020; Saba, Haseeb, Ahmed, & Rehman, 2020; Tahir et al., 2019;). HGG is aggressive while LGG less aggressive. The patients suffered from HGG have an average life expectancy of 1 year, while in LGG this expectancy is 5 years. A brain tumor is treated based on surgery, radiation, and chemotherapy. Therefore, an automatic or semi-automatic framework for specific brain tumor segmentation is enormously needed. The first stage of tumor detection could be achieved in the proposed system automatically using the K-means clustering algorithm. The magnetic resonance imaging (MRI) system generates the brain images, while machine learning will detect any different sections or areas in the brain like a tumor. The system will assist the human expert in generating the first report of tumor-associated possibilities. Computer mediated cancer detection

techniques could play a significant role in brain cancer detection (Amin, Sharif, Raza, Saba, Sial, et al., 2019).

1.1 | Background

Different challenges have been identified over the years to speed up research in medical image exploration and classification (Mughal et al, 2017; Saba, 2019). The BraTS challenge is one of the most popular appeared in 2020 with precise brain tumor segmentation, overall endurance likelihood of patients and the distinction between pseudo progression and accurate tumor recurrence (Pennsylvania University, 2020). Besides BraTS, the researchers also face many other challenges by using machine learning from various imaging methods for automated diagnosis. Different computer-aided diagnostic systems have been reported in state of art to improve brain tumor segmentation, classification, and related issues. These systems automatically perform different tasks, like image segmentation, to find the cancerous part, whether the brain tumor is benign or malignant, brain tumor type recognition, and degree. Deep learning has overtaken classical machine learning techniques for the above-mentioned tasks (Mashood Nasir et al., 2020; Saba, 2017; Saba, 2020; Sadad, Munir, Saba, & Hussain, 2018).

Generally, the brain tumor classification task consists of four phases; preprocessing, segment the tumor in MRI, extraction of rich features followed by suitable features selection, brain tumor classification (Amin, Sharif, Yasmin, Saba, & Raza, 2019; Hussain et al., 2020; Khan, Sharif, et al., 2020).

Fidon et al. (2017) offered a novel scalable multimodal deep learning architecture for brain tumor detection. They achieved dice scores for the leather board are 0.77, 0.64, and 0.56 for the whole core and enhance respectively on BraTS 2013 data set. A deep CNN system for programmed brain tumor recognition and degradation was proposed by Seetha and Raja (2018). Fuzzy-C-means (FCM) employed for brain tumor segmentation and texture, shape features extracted from segmented regions. Finally, these features are fed to DNN and SVM fused classifiers and attained 97.5% precision. A noninvasive graduation scheme of brain glioma tumors was introduced by Khawaldeh, Pervaiz, Rafiq, and Alkhawaldeh (2018) using an updated form of AlexNet CNN. The regression was achieved for entire-brain MR images and image labeling was not pixel level, but with the image level. The experimental findings show that 91.16% of the method achieved a reasonable performance. Sajjad et al. (2019) proposed a comprehensive method for brain tumors gradings. For this purpose, tumorurs region after data augmentation was fed to pre-trained VGG-19 CNN. The grading accuracy 87.38 and 90.67%, respectively, claimed for data beforehand and afterward the augmentation. Özyurt, Sert, Avci, and Dogantekin (2019) merged CNN with the full fuzzy specialist (NS-CNN) neutrosophic, confident entropy to diagnose brain tumors. These images were then added to the CNN for the extraction of characteristics and finally, extracted features are fed in the SVM classification to be classified as benign or malignant with an averaged 95.62% accuracy.

Saba, Haseeb, et al., 2020 used GrabCut technique to derive MRI texture features to classify brain tumors. 98.78, 99.63, and 99.67% precision testified on (BraTS) 2015, 2016, and 2017, respectively with VGG-19 (CNN architecture). Ejaz et al. (2020) suggested the use of MICCAI BraTS data set for hybrid SOM pixel labeling with reduced cluster membership and deterministic role clustering for brain tumor detection. Cluster obtained for the segmentation of brain tumors using three unendorsed learning procedures. They evaluated the method using the index of dice overlap, the index of jaccard tanimoto coefficient, mean squared error and the ratio of Peak signal to noise. The results acquired were 98%, respectively, 96% 0.06, 18 lb.

For brain tumor segmentation, Iqbal et al. (2019) proposed a deep learning model by integrating short-term memory (LSTM) and coevolutionary neural networks (ConvNet). Of note, 75% accuracy for ConvNet, 80% accuracy for LSTM-based network and cumulative accuracy, 82.29% reported on BraTS 2018 data set.

Recently, Rehman, Khan, Saba, et al. (2021) employed pretrained 3D CNN for brain tumor classification. Three data sets BraTS data sets 2015, 2017, and 2018 experimented and 98.32, 96.97, and 92.67% accuracy claimed, respectively.

So far, research has focused on a patch-based approach and uses traditional segmentation methods such as GrabCut, Gabor, K-Means, and so forth. These procedures, however, are inadequate for a significantly large number of classifications of brain tumors. However, accurate, efficient, and consistent methods are still needed to recognize and classify MR images' tumors (Khan, et al., 2021).

1.2 | Main contributions

In the proposed study, we present a research framework for brain tumor segmentation and classification using synthetic data augmentation concept for better classification accuracy to support medical practitioners. Accordingly, a four-stage system is proposed to classify brain tumors. The first stage preprocessed the images to generate pipelines from the input MRI modalities and normalize their intensities. In the subsequent stage, K-means clustering is applied to the segment region of interest (ROI). Thirdly, rich features are mined from the segmented ROI. A finetune CNN model VGG19 is trained to categorize the tumor to its respective categories, that is, benign/malignant. The technique is evaluated using without tumor segmentation and with a segmented tumor, and the results were equated with state-of-the-art techniques. The key offerings of the proposed work are summarized as such:

1. In the method suggested, first the MR data is standardized and unbiased using SimpleITK technique. K-means clustering technique is applied to the segment region of interest/brain tumour.
2. The proposed finetuned CNN model, VGG19, is integrated with MRI data to classify brain tumors in their respective categories (benign/malignant). Results are computed with and without synthetic data augmentation.

The remaining article has three main sections. Section 2 presents the proposed methodology: experimental results and discussion in Section 3. Finally, Section 4 concludes the research.

2 | PROPOSED METHODOLOGY

Medical image analysis and classification have become an emerging field in the last few decades, including health-related applications that could assist medical experts and radiologist in diagnosing different chronic diseases such as chest cancer, brain tumour, diabetes prediction, and cardiac murmurs evaluation (Fahad et al., 2018; Husham, Alkawaz, Saba, Rehman, & Alghamdi, 2016; Iftikhar, Fatima, Rehman, Almazayad, & Saba, 2017; Liaqat et al., 2020; Marie-Sainte, Aburahmah, Almohaini, & Saba, 2019; Mittal et al., 2020; Perveen et al., 2020; Qureshi, Khan, Sharif, Saba, & Ma, 2020). This research presents a hybrid approach based on k-means clustering and a finetuned CNN model assisted with synthetic data augmentation. The proposed technique consists of three main stages: (a) normalize and unbiased the intensities of MR modalities; (b) segmenting tumor area using k-means clustering; and (c) synthetic data augmentation followed by deep features extraction from ROI and classification of brain tumor into its relevant categories benign or malignant using a finetuned CNN model. CNN model followed training steps: (a) convolution, (b) ReLU Layer (c) pooling, (d) flattening, and (e) full connection. The complete process is presented in Figure 1.

2.1 | Pre-processing

Pre-processing of data set images is a mandatory step to enhance the accuracy and smooth line supplementary stages. Since different types of noises are observed in MRI, such as salt pepper noise, Gaussian noise, and so forth. Additionally, in few cases, images are taken using different scanners, and therefore, image intensities also normalized (Khan et al., 2018; Lung, Salam, Rehman, Rahim, & Saba, 2014; Nodehi et al., 2014).

We used four modalities (T1, T1c, T2, and FLAIR) as input with its ground truth in the proposed framework. The pipeline generation consists of three steps: (Step 1); conversion of modalities to slice co: four modalities of different patients are used as input and convert each modality of each patient to slices using SimpleITK (Marstal et al., 2016). Each patient has four modalities, and each modality contains 155 slices, so for each patient, the total slices are; $4 \times 155 = 620$, and having dimension is 240×240 . (Step 2) generation of brain pipeline: brain pipelines are created for each patient's modality with the same slice and ground truth, that is, 155 pipelines and having dimension $240 \times 1,200$. (Step 3) normalizing the intensities: Generally, MR images contain noise and their intensities levels vary as they might be scanned at different intensities. This difference in intensity substantially weakens the efficiency of subsequent MRI processing, such as segmentation and classification. Hence, to normalize pixel intensities, a statistical approach is applied by taking the

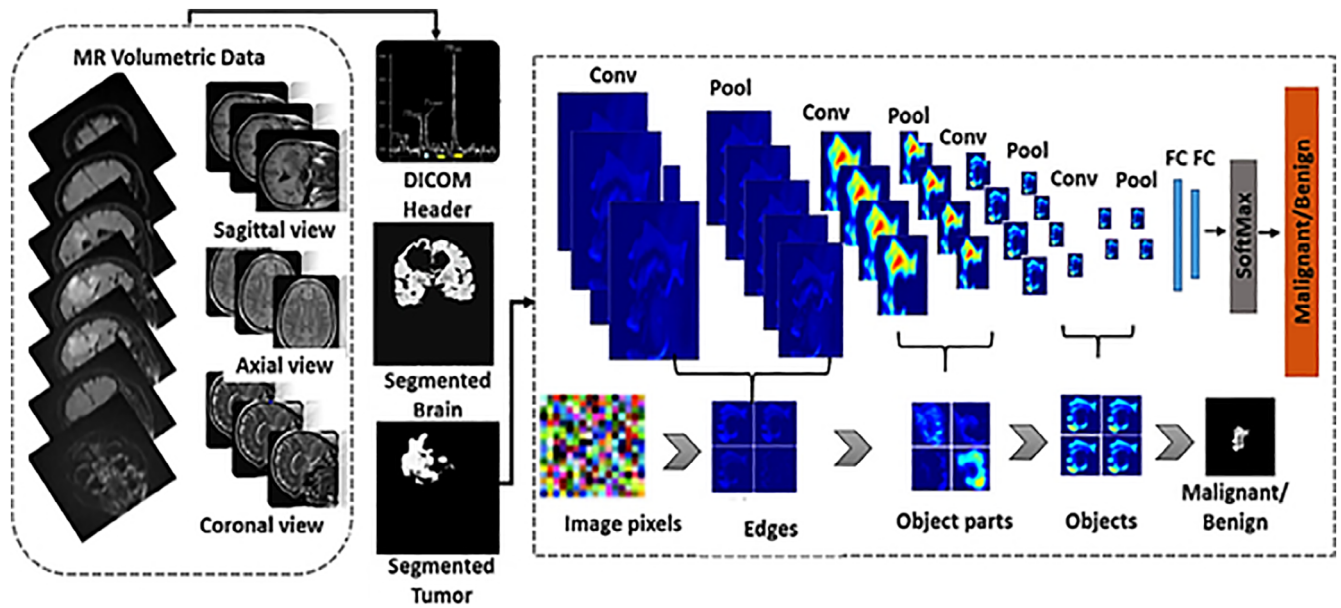


FIGURE 1 Brain tumor segmentation and classification process using magnetic resonance imaging [Color figure can be viewed at wileyonlinelibrary.com]

mean of the slices and subtracting it from each slice's intensity value divided by the standard deviation of the slices (Shinohara et al., 2014). Mathematically represented in Eq. (1).

$$\text{Normalized intensities} = \frac{(\text{Pipeline} - \text{Mean}(\text{Pipeline}))}{(\text{StDev}(\text{Pipeline}))} \quad (1)$$

2.2 | Segmentation of brain tumor regions using K-means clustering

Image segmentation is a method to divide an image into various coherent and semantically related regions also known as ROI for 2D image data or volume of interest (VOI) for 3D image data. ROI or VOI is performed to extract the most relevant regions in the image, which is further incorporated in feature extraction (Rehman, 2020; Saba, 2019). The clustering-based approach is very beneficial in MR tumor segmentation; it splits pixels into groups based on the same group's highest similarity, that is, categorizing the pixels using certain features. In the clustering approach, the training is completed by employing the pixel attributes with each group's properties (Rehman, Khan, Mehmood, et al., 2020; Saba, 2016).

K-means algorithm is vigorous, fast, and simpler to measure. It is an unsupervised learning technique for clusters. K-means algorithm provides a remarkable outcome when data points are well separated from one another. In this approach, initially, “K” centroids are marked randomly or using some heuristic but must be positioned distantly from one another. Then select a data point and assign it to the nearest centroid until no data point is remaining. After completing the first step, the centroids of k

clusters are recalculated to form new “K” centroids and allotting must be achieved among the new centroid and nearest data points. This process remains to continue until centroids do not relocate anymore. The main objective of this algorithm is to minimize the objective function as below (Sadam, Munir, Saba, Hussain, 2018).

$$\text{obj}(X) = \sum_{u=1}^c \sum_{v=1}^{c_u} \|p_u - x_v\|^2$$

where $\|p_u - x_v\|^2$ represents the Euclidean distance among p_u and x_v . “ c_u ” denotes the number of points in the u th group and “ c ” denote the group centers.

The followings are the main steps of this algorithm.

Consider $X = \{x_1, x_2, x_3, \dots, x_c\}$ is a set of group center and $P = \{p_1, p_2, p_3, \dots, p_n\}$ is data elements.

Step 1: Choose group centers “ c ” randomly.

Step 2: Compute the distance among group centers and each data element.

Step 3: Assign the element to the group center whose distance from the group center is the lowest of all the group centers.

Step 4: Re-compute the latest group centroid through

$$x_v = \left(\frac{1}{c_u} \right) \sum_{v=1}^{c_u} p_u$$

where, “ c_u ” denotes the number of points in the u th group.

Step 5: Re-compute the distance among each data element and newly achieved group centroids.

Step 6: Repeat Step3 until centroids do not relocate anymore.

2.3 | VGG19 based brain tumor classification

In the proposed method, the concept of transfer learning is utilized in VGG19 CNN model. The use of finetuned CNN helps to minimize training time and increase predictive accuracy. Moreover, we finetuned the weights of fully connected layers of the CNN model VGG19 to classify brain tumors into its respective two classes. Generally, the pre-trained VGG19 model involves 19 layers, 16 are convolutional and 3 fully connected layers (Yu et al., 2016). In VGG19, the first and second convolution layers of the group of two layers followed by max-pooling layers, and next eight convolution layers are a group of four layers followed by max-pooling with same filter size, that is, 3×3 , the last three are dense layers, contain 4,096 and 1,000 features followed by SoftMax function, as shown in Figure 2.

The last FC-8 layer is passed as a features vector with 1,000 dimensions to softmax function to predict brain tumor class. In the proposed technique, we incorporated VGG19, since in this model the filter size is minimum, that is, 3×3 , which were same for all the convolution layers and with stride 1, while in other CNN models, filter size is 11×11 or 7×7 with 4–5 strides (Bernal et al., 2019). Such type of kernels having larger strides might ignore important information and also increase the model parameters.

2.4 | Synthetic data augmentation

Deep learning techniques necessitate a significantly large amount of labeled data for training purposes. Unfortunately, labeled medical images are usually not enough in quantity and it causes problems while training, especially using deep learning techniques. However, data augmentation strategy presents a solution to this problem by increasing the available data for training (Sadat et al., 2019, 2020).

Synthetic data augmentation is the process of extending data using different techniques such as cropping, padding, and horizontal flipping to train large CNN (Sajjad et al., 2019). The synthetic data augmentation techniques used in the proposed technique are; random rotation, zoom, geometric transformations, sharpening, noise addition and contrast. In the proposed framework, to improve classification accuracy, data size is increased by synthetic data augmentation for MRI segmentation before the effective deployment of deep learning models. Accordingly, to enhance the model's performance, six augmentation techniques and 20 parameters are employed to increase each segmented image into 20 images of the used data set.

3 | EXPERIMENTAL RESULTS

3.1 | Data set

BraTS 2015 benchmark data set is employed for experiments (Menze et al., 2014). However, the synthetic data augmentation technique is also programmed to escalate the size of the labeled data set. Experiments are conducted with and without data-augmentation and results are equated with each other and previously available benchmarks. Table 1 presents the detail of labeled classes before and after data augmentation.

3.2 | Classification results using synthetic data augmentation

This section presents an experimental assessment of the proposed brain tumor classification in detail. Several experiments were

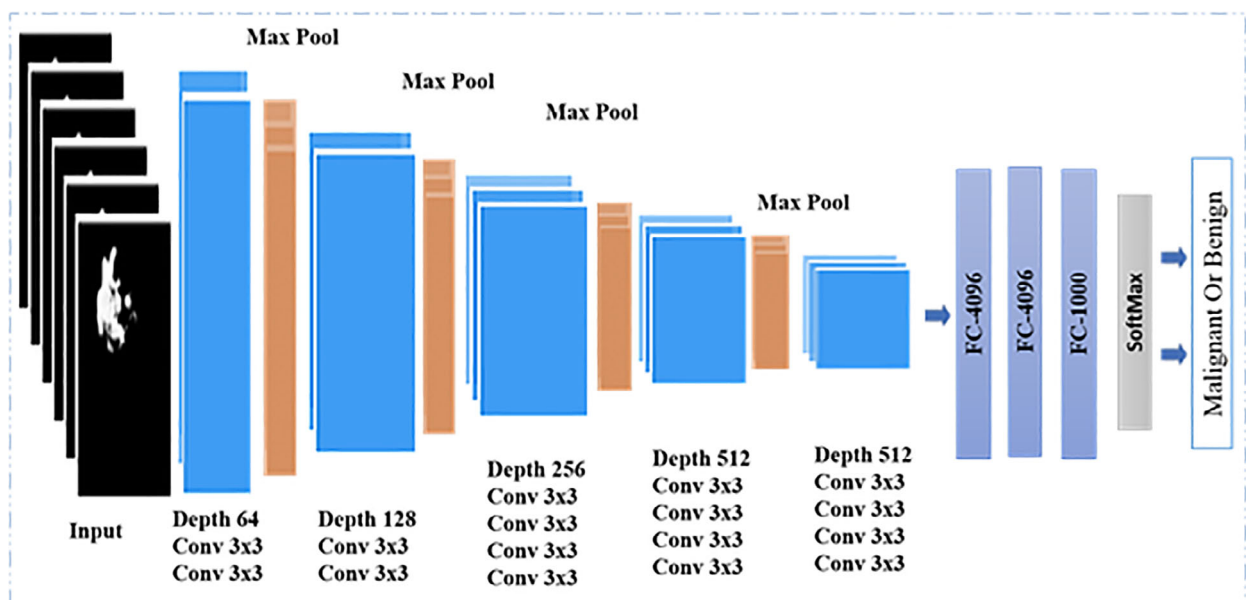


FIGURE 2 The proposed finetune VGG19 CNN model for brain tumor classification [Color figure can be viewed at wileyonlinelibrary.com]

performed on BraTS 2015 benchmark data set. The data set is collected with ground truth, which contains two classes, and labeled as benign/malignant (Louis et al., 2016). In the proposed technique, following preprocessing, we segmented brain tumor using k-means clustering and segmented image sample increased to 20 samples per image, using different data augmentation techniques, to improve classification accuracy. Figure 3 presents the segmentation results. For evaluating the proposed system, all experiments were conducted on BraTS 2015 data set using NVIDIA GTX-1070 system.

Performance measurements on BraTS 2015 benchmark data set are shown in Tables 2 and 3 individually. The overall accuracy is 90.03% before data augmentation and 94.06% after synthetic data augmentation. Finally, experimentally it is perceived that the proposed method's overall accuracy has been improved in training and testing phases using different data augmentation techniques, as shown in Figure 4.

TABLE 1 Brain tumor data set (Abiwinanda et al., 2019) along with its class labels

Brain tumor classes	Before augmentation	After augmentation	Sub-grades
Malignant	99	1980	Grade-I, II, III, IV, Meningiomas, Glioma
Benign	121	2,420	
Total	220	4,400	

3.3 | Analysis and comparison

A significant part of the recently published brain tumor classification literature used deep learning methods rather than traditional machine learning. Many researchers used pre-trained CNN architectures and finely tuned them for the classification of brain tumor tasks. Some data scientists have proposed/experimented and trained novel architectures from abrasion. The majority of the CNNs used were 2D but some used 3D CNN architectures (Khan, Ashraf, et al., 2020; Rehman, Khan, Saba, et al., 2021). However, in the era of deep learning, the main issue is the unavailability of large enough labeled MRI data for CNN training. We covered this issue using synthetic data augmentation.

Proposed three convolutionary autoencoders (for three MR sequences) for brain tumor classification followed by fusion, and then a fully linked layer. Sajjad et al. (2019), tumor area fed to pre-trained VGG-19 CNN after extensive data augmentation, which was finetuned for grade classification.

Khan, Ashraf, et al., (2020) suggested a fusion of pre-trained CNN models (VGG16 VGG19) to classify multimodal automated brain tumors with linear contrast stretching, a transition of learning-based extraction functions, features correntropy-based collection. Finally, fed the fused matrix to the extreme learning machine (ELM) to detect brain tumor. The proposed methodology validated on the BraTS data sets and attained a precision of 97.8, 96.9, and 92.5% for BraTs 2015, BraTs 2017, and BraTs 2018, respectively. Recently, Rehman, Khan, Saba, et al. (2021) proposed a 3D CNN architecture to classify brain

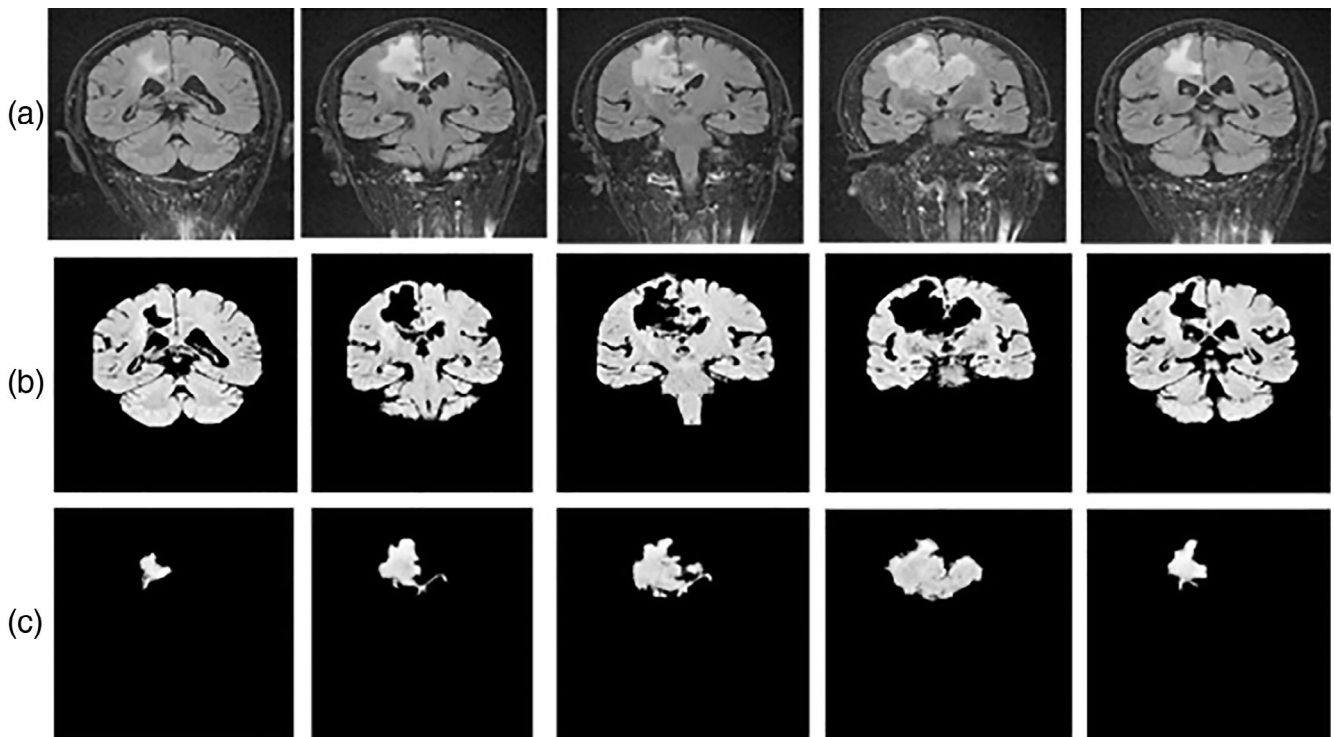


FIGURE 3 Visual results, (a) original MR images, (b) segmented brain, and (c) segmented tumor

TABLE 2 The performance measure of the proposed system before data augmentation using the BRATS 2015 benchmark data set in terms of sensitivity, specificity, and accuracy

Brain tumor classes	Training set		Testing set	
	Sensitivity %	Specificity %	Sensitivity %	Specificity %
Malignant	84.07	93.03	84.03	90.04
Benign	95.01	87.02	91.05	89.08
Overall accuracy	90.03%			

TABLE 3 The performance measure of the proposed system after synthetic data augmentation using BRATS 2015 benchmark data set in terms of sensitivity, specificity, & accuracy

Brain tumor classes	Training set		Testing set	
	Sensitivity %	Specificity %	Sensitivity %	Specificity %
Malignant	88.09	96.01	89.09	90.01
Benign	99.05	90.05	96.05	93.05
Overall accuracy	94.06%			

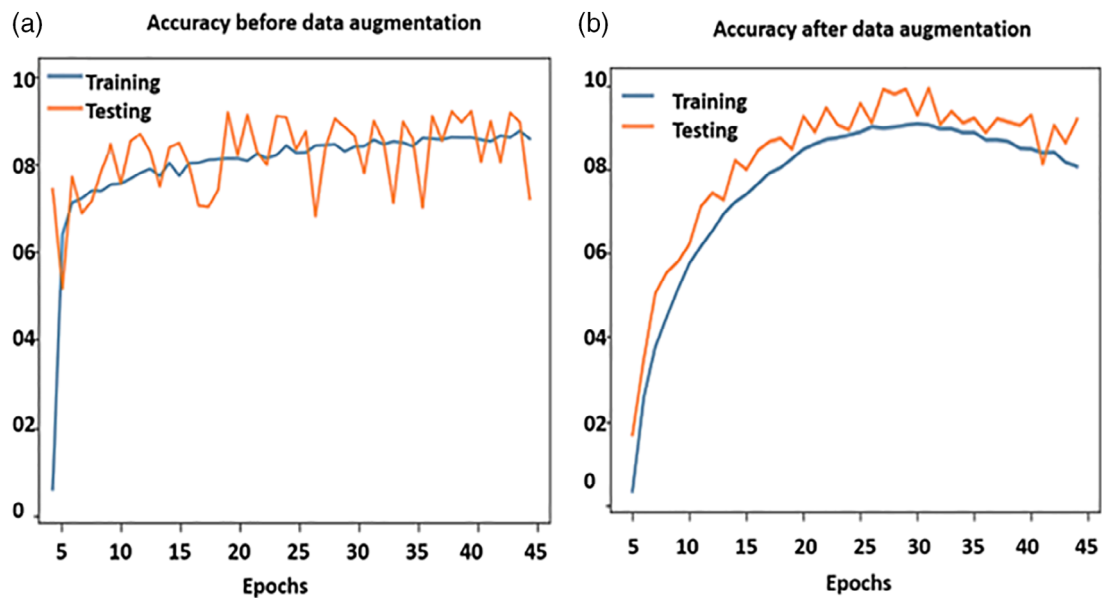


FIGURE 4 Training and testing accuracy of the proposed finetuned CNN model for brain tumor classification, before and after synthetic data augmentation [Color figure can be viewed at wileyonlinelibrary.com]

tumors using a pre-trained CNN model. An accuracy of 98.32, 96.97, and 92.67% reported on BraTS 2015, 2017, and 2018. The detailed comparison of the proposed approach in comparing state of the art techniques is presented in Table 4.

4 | CONCLUSION

This article has exhibited a comprehensive brain tumor segmentation system and classification using VGG19 CNN model on MRI data. To enhance the accuracy of the classifier synthetic data, augmentation concept is introduced. The proposed technique first converts each input MR modality to slices, and intensities are preprocessed using a statistical normalization approach.

K-means clustering approach is implemented to segment brain tumors to focus ROI for precise feature extraction. Finally, to classify brain tumors into their two general classes (benign/malignant); a finetuned VGG-19 CNN model is trained perfectly using synthetic data augmentation techniques. The proposed CNN based method is evaluated by conducting rigorous experiments on BraTS 2015 data set. Thus, the results show that the proposed technique could assist the radiologist and medical experts in detecting brain tumors and classifying them into their respective classes (benign/malignant). The proposed computer analysis's efficiency and accuracy to design (CAD) system are compared with recent existing methods and the results exhibited that the proposed technique exhibited better accuracy.

TABLE 4 CNN based techniques for brain tumor segmentation

Reference	CNN model	Preprocessing	Segmentation	Augmentation	Data set	Accuracy
Pereira et al. (2018)	Novel 2D CNN	N/A	Convolutional network using UNet	N/A	BraTS-2017	92.98%
(Seetha & Raja, 2018)		N/A	FCM segmentation, texture and shape feature fed to SVM and DNN	N/A	BraTS-2015	97.5%
	Novel 3D CNN	Scaling	Ground truth	Yes (flipping)	BraTS-2017	89.47%
(Sajjad et al., 2019)	Pre-trained VGG-19	N/A	Pre-trained cascade CNN	Yes (shear, flip, rotation, skew, Gaussian blur, edge detection, emboss and sharpening)	BRATS-2016	With augmentation: 90.67%, without augmentation: 87.38%
(Özyurt et al., 2019)		N/A	NS-CNN feature fed to SVM classifier	N/A	TCGA-GBM	95.62%
	Pre-trained inception V3	Contrast stretching using PlaL	N/A	N/A	BraTS 2013, 2014, 2017, 2018	98.3% 97.8% 96.9% 92.5%
Rehman, Khan, Saba, et al. (2021)	3D CNN	Yes	Yes	N/A	BraTS 2015, 2017, 2018	98.32% 96.97% 92.67%
Proposed	Fine tuned VGG19	Normalized intensities	K-means clustering	Yes (random rotation, zoom, geometric transformations, sharpening, noise addition and contrast)	BraTS 2015	90.03% before data augmentation and 94.06% after synthetic data augmentation

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ETHICAL APPROVAL

No experiments are conducted on animals/humans; only publicly available data sets are used for experiments, analysis and comparisons.

CONFLICT OF INTEREST

All authors have equal scientific contributions and no conflict for this article.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are openly available in [MICCAI 2013 Challenge on Multimodal Brain Tumor Segmentation] at <https://www.smir.ch/BRATS/Start2015> reference number [Menze et al. 2015].

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