




Multiclass classification of brain tumors using a novel CNN architecture

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Abstract

Brain tumors are a deadly condition that radiologists have a tough time diagnosing. It is critical to make treatment-related decisions based on accurate and timely categorization of malignant cancers. Several approaches for detecting brain tumors have been presented in recent years. These strategies, however, necessitate handmade feature extraction and manual tumor segmentation prior to classification, which is error-prone and time-consuming. To properly extract features and identify brain cancers, an automated tumor diagnosis approach is necessary. Despite significant advancements in the development of such systems, the techniques face challenges due to low accuracy and large false-positive values. In this study, we propose a 13-layer CNN architecture for classifying brain tumors from MRI scans. We tested the suggested model's performance on a benchmark dataset of 3064 MRI images of three different types of brain cancer (glioma, pituitary, and meningioma) and achieved the highest accuracy of 97.2%, outperforming previous work on the same database. Furthermore, we validated our model on a cross-dataset scenario to demonstrate its efficacy in a real-world scenario. The main goal is to create a lightweight CNN architecture with fewer layers and learnable parameters that can reliably detect tumors in MRI images in the shortest amount of time. The findings show that the proposed technique is effective in classifying brain tumors using MRI images. Because of its adaptability, the proposed algorithm can be easily used in practice to assist doctors in diagnosing brain tumors at an early stage.

Keywords Brain tumor · Deep learning · Convolutional neural network · Medical image analysis

1 Introduction

Brain tumors are caused by abnormal growth in brain cells. These tumors are difficult to treat and cause a substantial number of deaths worldwide. Brain cancers are classified into two

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types: primary tumors and secondary tumors. About 70% of these tumors are primary, with the remaining 30% being secondary [38]. Primary brain tumors spread only in the brain, but secondary brain tumors grow elsewhere in the body, such as the lung or kidney, and subsequently migrate to the brain [24, 27]. Glioma, meningioma, and pituitary tumors are the three most common types of brain tumors. Glioma tumors are caused by abnormal development in Glial cells and have the greatest mortality rate of all primary tumors [8]. The Glioma tumors are classified into two types: low-grade glioma and high-grade glioma. The latter is more dangerous because patients usually survive for nearly two years. Meningioma tumors form in the meninges, which serve as a protective membrane over the brain and spinal cord [22]. Pituitary tumors form in the pituitary gland, which is in charge of producing various vital hormones in the body [17]. Although this tumor is considered benign, it can induce hormonal deficits as well as irreversible eye impairment. As a result, a precise and quick diagnosis of malignant tumors is critical for a patient's health. A patient's mortality may result from a delayed or inaccurate tumor diagnosis.

Because of the variety of tumor sizes and shapes, correctly identifying brain tumors prior to therapy is a difficult undertaking. Furthermore, treatment is determined by the stage and type of tumor. Manual tumor detection from Magnetic Resonance Images (MRI) is a difficult task that heavily relies on the skill of the radiologist. Medical practitioners diagnose cancers by visually examining medical imaging and precisely marking out the tumor locations. Because of the surrounding healthy tissues, tumor borders are often unclear. The manual identification process is time-consuming and often results in tumor misinterpretation. Furthermore, the human eye is incapable of deciphering the various shades of grey shown in MRI scans. Other prevalent reasons of tumor misunderstanding include fatigued radiologists and noisy MRIs caused by imaging equipment variations. [10, 11]. Because of these issues, traditional tumor identification approaches are being phased out in favor of automated brain tumor classification systems. The deep learning-based approaches have demonstrated consistent performance across a wide range of medical image processing applications. However, there is still much opportunity for improvement. [33].

Brain tumor classification methods can be categorized in Machine learning (ML)-based methods and deep learning (DL)-based methods. Traditional ML-based techniques involve a hand-crafted feature extraction approach, in which these features must be extracted from training images before the learning process can begin. This method normally necessitates the assistance of an expert with extensive knowledge in order to identify the most important features. As a result, when working with larger databases, the detection accuracy of ML-based techniques is limited and prone to errors [15]. Meanwhile, DL-based algorithms have proven to be extremely effective in a wide range of applications, including medical imaging. The convolutional neural network (CNN) is the most commonly used DL model due to its weight-sharing nature. It can automatically extract low- and high-level features from training data. Due to these benefits, the DL-based brain tumor classification approaches have piqued the interest of researchers [21].

In this study, we offer an automated method for classifying multi-class brain tumors using MRI scans. The objective of developing a custom CNN is to get higher performance with a simple architecture that has fewer layers and fewer parameter calculations than prior state-of-the-art approaches. We trained and evaluated our proposed method on a publically available MRI dataset [13] using multiple quantitative measures such as accuracy, precision, and recall. In addition, we assessed the suggested CNN's performance on a cross-dataset scenario [6]. The main contributions of the proposed method are as follows:

- We propose a novel end-to-end CNN architecture that can classify three types of brain tumors such as glioma, meningioma, and pituitary.
- Extensive experiments are performed to finalize the CNN layers and the hyper-parameters before reaching the final conclusion.
- The proposed low complexity method effectively reduces the number of layers and learnable parameters for tumor classification while obtaining a better accuracy.
- The proposed method is also evaluated using on a cross-dataset scenario to prove its efficacy and usefulness in real-world scenarios.

The paper is structured as follows. The related work is explained in Section 2. Proposed method is described in Sections 3, 4 and 5 are dedicated to experiments and results respectively. Section 6 concludes the suggested work.

2 Literature review

The development of an automatic model is an important research area because to the high clinical value and complexity of the brain tumor. This section provides an overview of the main works for brain tumor classification from MR images. The automated brain tumor classification approaches can be divided into two types as Machine Learning (ML)-based and Deep Learning (DL)-based methods. The ML-based systems incorporate a handcrafted feature extraction phase that inhibits the ability to take complete advantage of information embedded in the MR images [11]. Hence, the accuracy of these techniques is limited because it depends upon the quality of the extracted features [15]. Further, these systems also perform manual tumor segmentation that is error-prone because of the variation in shape, location, and intensities of the tumors. Whereas, the DL-based techniques have tried to overcome many problems being faced by ML algorithms and have shown relatively better performance in various domains including medical image analysis. These techniques are dominating the medical image diagnosis problems such as classification or segmentation. One of the prominent DL-based techniques is the Convolutional Neural Network (CNN) that can determine the significant features in a self-learning manner due to its weight-sharing nature and has gained the interest of the researchers due to its robust performance [12, 18, 39]. According to the statistics of 2016 more than 200 DL-based researches on medical images were proposed and 190 of those employed the CNNs [21]. Some of the very popular CNNs such as AlexNet [19], VGG [35] and GoogLeNet [36], etc. are currently being used in medical image classification tasks.

With an increase in population, the number of experts compared to the number of cancer patients is becoming insufficient day by day [32]. Due to which there is a shortage of automated tumor screening devices, a fully automated technique is preferred to detect the abnormalities in the brain [5]. Despite tremendous progress, the existing DL-based systems require multiple convolutional layers and kernels that increase the computational cost subsequently. Hence, an efficient method with a lesser complex network in terms of memory and computing resource usage is still a challenge for the accurate and timely classification of brain tumors [30]. These automated systems are practically proven to achieve better performance than the conventional ML-based algorithms. CNN methods have attained widespread acceptance in different research areas. In comparison with traditional ML-based methods, the DL methods embed the automatic feature extraction and classification phase.

Togacar et al. [41] developed BrainMRNET, a novel CNN to perform brain tumor classification and achieved 96.05% accuracy. Mzoughi et al. [23] designed CNN to classify High-Grade Glioma (HGG) and Low-Grade Glioma (LGG) in MRI images from BraTS 2018 dataset. The system achieved 96.49% accuracy. The authors in Khawaldeh et al. [16] suggested a CNN model to classify brain MR images as normal or abnormal, as well as high-grade and low-grade glioma tumors. They improved the AlexNet CNN model and used it as the basis for their network architecture, achieving 91% accuracy. Despite the tremendous work being done in this area, finding a strong and practical strategy to classify brain MR images still requires more effort. The major drawback of the studies presented in [16, 23, 41] is that they only perform binary classification of brain tumors and ignore multiclass classification, so further analysis is required to determine the type of tumor.

Various researchers have successfully applied transfer learning to brain tumor classification tasks. For example, the authors in Sajjad et al. [31] classified brain tumors using a fine-tuned VGG-19 model and achieved 94.5% accuracy. The images were segmented using Input Cascade CNN. The system performs both the segmentation and classification via CNNs which is computationally exhaustive. Waghmare et al. [42] employed VGG16 architecture to classify brain tumor images. The images were preprocessed and augmented before supplying to the CNN. The system achieved 95.71% accuracy. Swati et al. [37] employed a transfer learning architecture i.e. AlexNet, VGG19 and VGG16 to perform brain tumor classification and achieved the highest accuracy of 94.8%. The authors in Saxena et al. [34] employed various transfer learned models such as ResNet, Inception-V3 and VGG-16. The system obtained highest accuracy of 95% via ResNet. However, the pre-trained CNN architectures mentioned in AlexNet [37], VGG16 [42], VGG19 [31] and ResNet [34] are computationally complex as they contain millions of trainable parameters. Such large networks are usually slower and can result in overfitting.

On the other hand, Abiwinanda et al. [1] proposed five CNN architectures to classify brain tumors and obtained the highest validation accuracy of 84.1%. However, very simple CNNs are unable to extract high-level deep features, resulting in a poor overall accuracy. The authors in Afshar et al. [3] identified and classified brain tumors using Capsule Networks with a 90.89% accuracy. It may be noted that the CapsNets are very sensitive to the image backgrounds and perform better if segmented images are input into the model. Hence resulting in a complex architecture. Anaraki et al. [2] utilized the Genetic Algorithms (GA) to find an appropriate CNN architecture with lesser computation cost for brain tumor identification. The system achieved an accuracy of 94.2% to classify three types of brain tumors in MRI images. However, the GA was unable to find optimal CNN architecture thus resulting in a poor overall accuracy. Using the Bayesian fuzzy clustering (BFC) technique, Raja et al. [29] suggested a hybrid deep auto encoder (DAE) for brain tumor classification. To eliminate the noise from the image, they first employed a non-local mean filter. After that, the BFC method is used to segment brain tumors. They extracted the features using scattering transform, information-theoretic measurements, and wavelet packet Tsallis entropy. Finally, for brain tumor classification, a hybrid DAE strategy was used, which yielded good accuracy. This technique that it takes a long time to compute and is computationally inefficient.

3 Proposed method

The methodology of the suggested method for identifying and classifying brain tumors using a novel CNN architecture is presented in this section. The proposed technique consists of two

major components. The first stage is to prepare the dataset, and the second is to create a Custom CNN for extracting deep features and conducting brain tumor classification. Initially, we normalized and resized MRI images. These images are then supplied to the proposed 13 layered CNN architecture. Figure 1 shows the generic workflow of the proposed method.

3.1 Data preprocessing

The images are min-max normalized before being fed into the proposed CNN architecture, as shown in Eq. (1).

$$f(x, y) = \frac{f(x, y) - Z_{\min}}{Z_{\max} - Z_{\min}} \quad (1)$$

Where brain image is denoted by f , x and y is the location of the pixel in an image, the minimum pixel value is indicated by Z_{\min} , and the maximum pixel value by Z_{\max} . Images before and after min-max normalization are shown in Fig. 2. The intensity normalization scales the intensity values between $[0, 1]$ and then resizes them to 227×227 before passing them on to the CNN architecture. The preprocessing steps aid network training by speeding up the learning process and resolving memory issues.

3.2 Convolutional neural networks

CNN's remarkable discoveries have not only increased its appeal among scholars, but have also inspired them to solve challenging tasks that were previously thought to be unsolvable. Several CNN architectures have been developed in recent years by researchers to handle various problems in numerous research domains, including medical image diagnosis domain. CNNs are made up of multiple layers that are stacked together to fulfil specific tasks. The network training begins in a feed-forward fashion from the input layer to the last layer, which is the classification layer, whereas backpropagation occurs from the classification layer to the very first convolution layer. It may be noted that the CNNs automatically identifies relevant features and performs classification based on them. [4, 10].

In this study, we suggest a unique CNN architecture, which is depicted in Fig. 3. The suggested design has 13 layers in total, including the input layer that holds the normalized images, two convolution layers and a ReLU, two Batch Normalization layers, and two Max Pooling layers. In order to avoid the problem of overfitting, a dropout layer is also introduced.

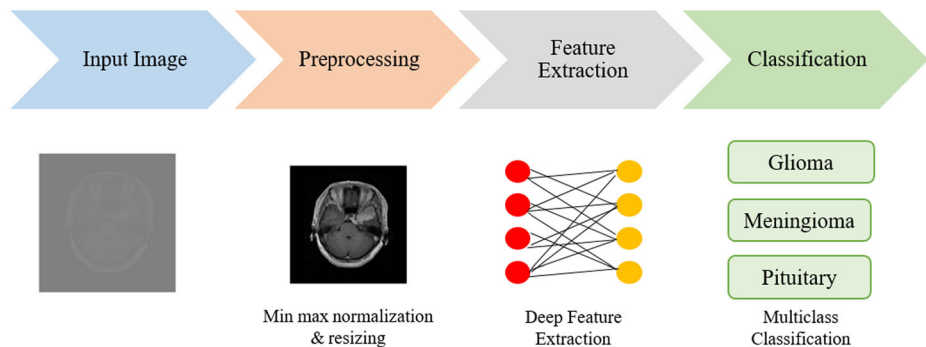


Fig. 1 Workflow diagram of the proposed method

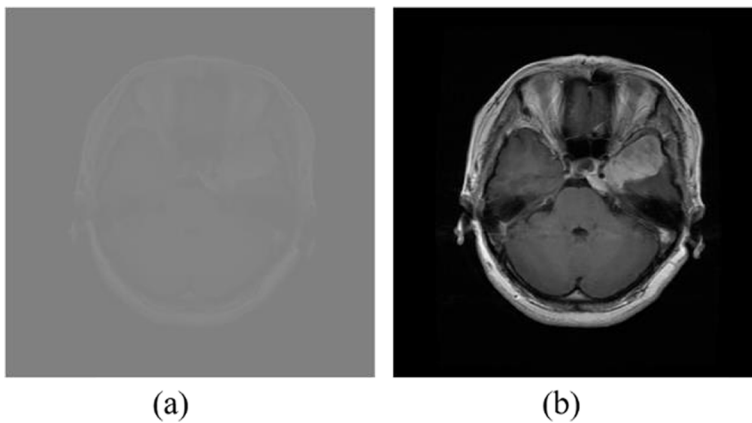


Fig. 2 MRI before and after normalization

It is followed by a fully connected (FC) layer, a softmax layer, and eventually a classification layer to classify the input image.

The first layer of the designed architecture is the input layer to read the preprocessed MRI images of size 227×227 . Following the input layer is a Convolution layer, which is made up of numerous convolution filters that are in charge of convolving an image with kernels to generate feature maps [26]. The kernel slides over the image to compute the dot product of the weights [38]. The involved parameters for the convolution layers are as follows: Filter Size = [5 5], Stride = [1 1], No. of convolution filters = 32, 64 for convolutional layers 1 and 2 respectively. Figure 4 shows an example of convolution layer.

Each convolution layer is followed by its activation function (ReLU in our case) which applies an activation function in an element-wise manner to the output from the previous layer [25]. The ReLU function is shown in Fig. 5.

$$f(z) = \max(0, z) \quad (2)$$

ReLU is described in Eq. (2) as a function of z , in which the output value is equal to the input value when z is positive and 0 for other values.

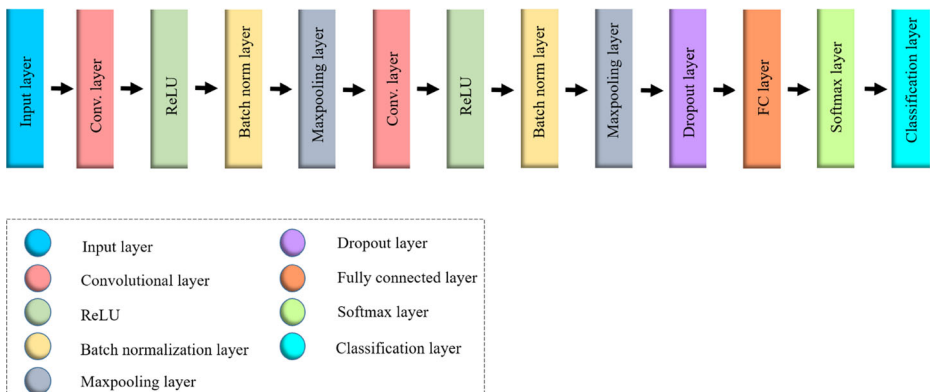


Fig. 3 Proposed CNN architecture

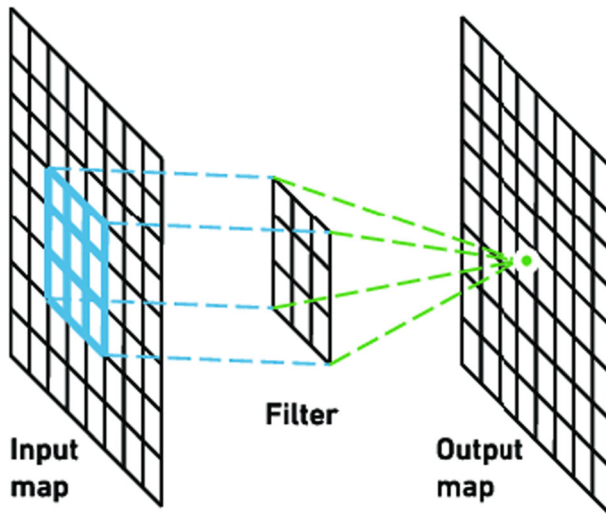


Fig. 4 Convolution layer [43]

The Maxpooling layer is the next layer in the architecture that reduces the computational load on the subsequent stages. This layer decreases the image's dimensionality by dividing it into small rectangles (3×3 in the suggested structure) [2]. The neighboring features are then combined by making the representation of redundant features minimal in this layer. [20, 26]. Max Pooling layer is shown in Fig. 6.

For the purpose of stabilizing the learning process, the batch normalization layer standardizes the inputs to each mini-batch. It speeds up network training by lowering the number of epochs needed to train the model. Whereas, the dropout layer speeds up the network training process and reduces overfitting by discarding random nodes while training the network (example shown in Fig. 7) [4]. In our proposed structure, we found a dropout rate of 0.5 most suitable.

A fully connected layer is in charge of generating class scores from classification activations [25]. In this layer, features from preceding levels is turned into a 1D matrix. Before the final Classification layer, Softmax is applied that is responsible of carrying out the probabilistic computation created on the network in order to generate a specific value for each class [4]. An example of the FC layer and Softmax layer is presented in Fig. 8. The classification layer is the

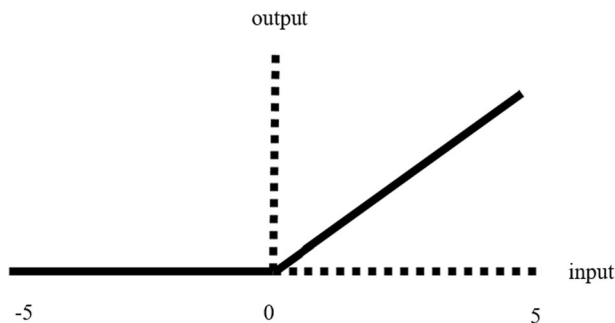


Fig. 5 Example of ReLU activation function

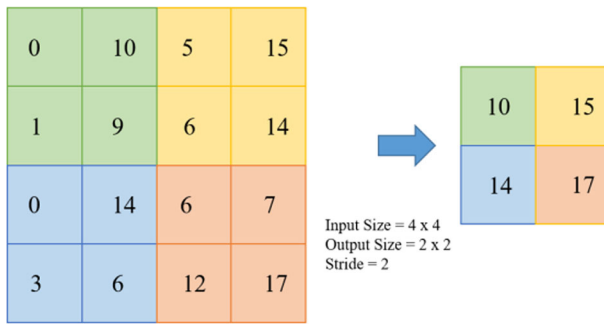


Fig. 6 MaxPooling layer

last layer of the architecture. The output value for this layer equals the number of classes in the dataset (3 in the proposed study).

4 Experiments

4.1 Datasets

4.1.1 Figshare dataset

A publically available dataset is used to conduct this study. Tianjin Medical University collected the data from 2005 to 2010, and Jun Cheng published it online in 2017. The dataset consists of 3064 T1-weighted CE images of Glioma, Meningioma, and Pituitary tumors obtained at three different planes, namely Coronal, Sagittal, and Axial of 233 patients [13]. Figure 9 depicts several types of tumors and planes in this dataset. The images in the dataset are sized 512×512 whereas the size of each pixel is $49 \text{ mm} \times 49 \text{ mm}$. [13]. Table 1 provides a thorough description of the dataset.

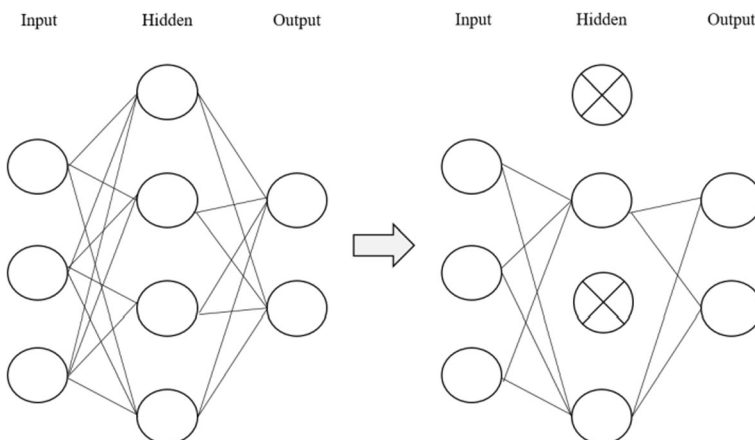


Fig. 7 Dropout layer

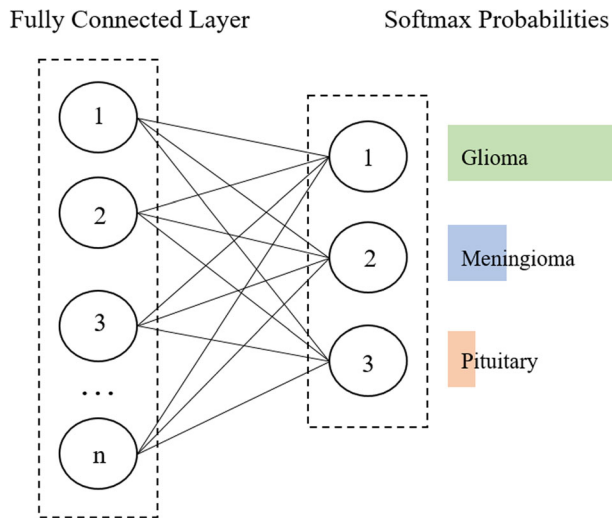


Fig. 8 Example of FC and softmax layer

4.1.2 Kaggle dataset

The second dataset is obtained from Kaggle website. This database also contains three types of brain tumors such as Glioma, Meningioma and Pituitary as well as Normal samples. The dataset is divided in two portions mainly training samples and testing samples. The images in this dataset were obtained from numerous web resources and released online after being verified by a medical practitioner [6]. We only used this dataset to evaluate the proposed CNN on a cross-dataset scenario.

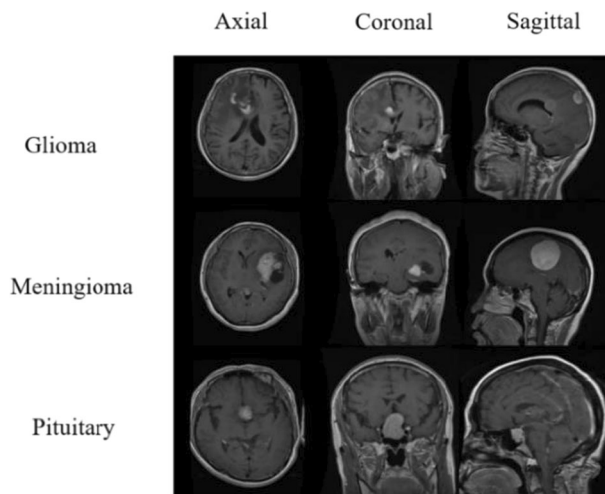


Fig. 9 Depiction of normalized MRIs at different planes

Table 1 Total no. of plane wise slices in each tumor type along with the number of patients

Type of tumor	No. of patients	No. of images	No. of axial samples	No. of coronal samples	No. of sagittal sample
Glioma	91	1426	494	437	495
Pituitary	60	930	291	319	320
Meningioma	82	708	209	269	231

4.2 Experimental configuration

This section discusses the suggested method's experimental setting. The proposed study's experiments are conducted on an Intel Core i5 6300 CPU with 8 GB RAM using Matlab 2019a. The dataset was randomly divided into two parts: a 70% training set for training the proposed CNN and a 30% validation set for providing an unbiased evaluation of a trained model.

We conducted several experiments on the MRI dataset by testing different CNN architectures and hyper-parameters before reaching the optimal technique with the highest performance. These parameters are explained in Table 2. We scaled the image intensities between [01] and resized them to 227×227 to avoid overfitting issues during the network training procedure of our suggested technique. Furthermore, we employed a dropout layer to eliminate the hidden units at random. In this research, we initially trained and evaluated different CNN architectures on single parameter setting (such as 10 epochs and 10 mini batch size using SGDM optimizer) before reaching the final architecture of the CNN. Then, the final CNN architecture was trained and evaluated on various hyper-parameters to reach the final conclusion. The optimal values for CNN architecture and hyper-parameters are highlighted in the table.

Table 2 Hyperparameters and architectures tested before reaching the final model

Factor (s)	Value (s)
Convolutional Layer+ReLU	1, 2 , 3
Batch Normalization Layer	1, 2 , 3
Dropout Layer	1 , 2
Cross channel normalization layer	0 , 1, 2
Fully Connected Layer	1 , 2
Grouped Convolution Layers	0 , 1, 2
Pooling Layers	Max , Average
Dropout Rate	0.25, 0.5
Learning Rates	0.0001, 0.0002, 0.0003 , 0.0005
Optimizers	Adam , SGDM
No. of Epochs	10, 20, 30 , 40
Mini batch size	4, 8, 10
No. of convolution kernels	32 , 64 , 128, 256
Convolution kernel size	2, 3, 5
Image Size	128×128, 227×227

Bold entries shows the optimal hyper-parameter values and final architecture at which the highest performance is obtained

5 Results and discussion

5.1 Evaluation metrics

The proposed method is evaluated via Precision, Recall, and Accuracy. Precision is mentioned in Eq. (3), Recall in Eq. (4), and Accuracy in Eq. (5).

$$\text{Precision} = \frac{TP}{FP + TP} \quad (3)$$

$$\text{Recall} = \frac{TP}{FN + TP} \quad (4)$$

$$\text{Accuracy} = \frac{TN + TP}{TP + FN + TN + FP} \quad (5)$$

Where, TP denotes the True Positives, TN denotes the True Negatives, FP denotes the False Positives and FN denotes False Negatives.

5.2 Proposed method results

This section discusses the results obtained from the presented framework. Our proposed method achieved an overall 97.2% classification accuracy. The confusion matrix for the proposed approach is presented in Fig. 10. The X-axis of the matrix presents the target class whereas the Y-axis shows the output class.

Output Class	Glioma	413	9	6
	Meningioma	2	175	6
	Pituitary	0	2	277
		Glioma	Meningioma	Pituitary
		Target Class		

Fig. 10 Confusion matrix of the proposed method

Table 3 Different metrics obtained from the confusion matrix

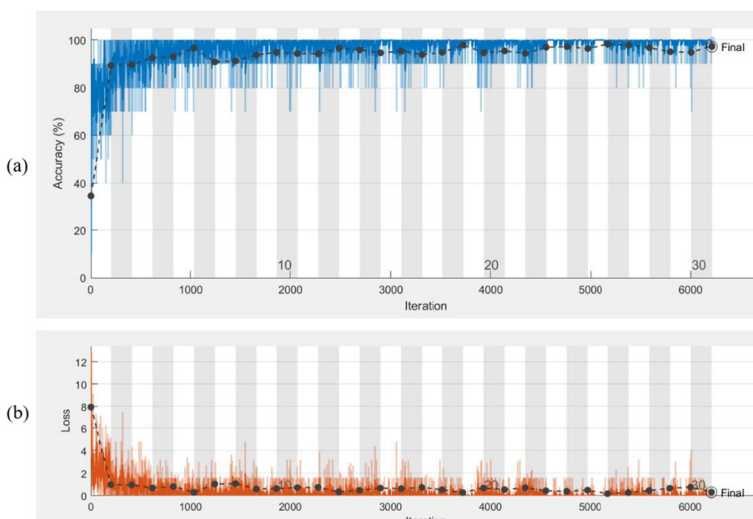
Tumor type	Accuracy	Precision	Recall
Glioma	98.09%	0.96	1.0
Meningioma	97.87%	0.96	0.94
Pituitary	98.43%	0.99	0.96
Average	97.2%	0.97	0.96

The evaluation metrics extracted from confusion matrices are shown in Table 3. The table discusses the values of Accuracy, Precision, and Recall for each class. The proposed method achieved classification accuracy values of 98.09% for Glioma, 97.87% for Meningioma, and 98.43% for Pituitary tumor. The proposed CNN obtained an average accuracy of 97.2%, an average precision value of 0.97 and average recall value of 0.96.

Figure 11 presents the network learning curve of the proposed CNN. A learning curve is a plot that represents the learning performance of the model over time. This plot shows (a) the progress in accuracy and (b) the loss percentage during the validation phase. Y-axis measures accuracy and loss percentages whereas the X-axis represents the number of epochs and iterations. The plot (a) shows that the accuracy curve rose sharply and almost hit almost 100% several times. Whereas, the loss graph (b) drops sharply and slightly fluctuates due to a smaller mini-batch size (10 in our proposed study). However, the loss curve almost hits zero several times. During the validation phase, the proposed method obtained an overall 97.2% accuracy.

5.3 Cross dataset validation

In this section, we evaluate the performance of our proposed method on a cross-dataset scenario using MRI images from Kaggle database [6]. The dataset contains 100 images for Glioma, 115 images for Meningioma and 74 images for Pituitary tumor. The fundamental purpose of cross-dataset analysis is to determine the generalizability of our proposed approach

**Fig. 11** Network learning curve of the proposed CNN

Output Class	Glioma	96	4	0
	Meningioma	1	114	0
	Pituitary	0	4	70
		Glioma	Meningioma	Pituitary
		Target Class		

Fig. 12 Confusion matrix for cross-dataset validation scenario

on other datasets. The proposed CNN classified total of 289 MRI images in 14 s with a 96.9% accuracy. Figure 12 depicts the confusion matrix for the cross dataset validation scenario. These findings show that our proposed approach is capable of efficiently classifying brain cancers from unseen samples.

5.4 Comparison with state-of-the-art deep learning based techniques

Table 4 presents a broad comparison of our proposed system with existing brain tumor classification techniques that employ deep learning techniques. This comparison is done based on classification accuracy as a metric. Our proposed method achieved 97.2% accuracy to classify Glioma, Meningioma, and Pituitary from MR images. Afshar et al. [3] classified brain tumors using a capsule network (CapsNet) architecture with a 90.89% accuracy. However, the CapsNet architectures are very sensitive to image backgrounds and this property can affect the performance of the architecture negatively. Moreover, they provided tumor boundaries as an additional input for better results thus, requiring manual localization of tumors before classification via CNN. Sultan et al. [38] developed a 16 layer CNN architecture to classify brain tumors in MRI images and achieved 96.1% accuracy. They trained the network on an artificially augmented dataset. However, the network can be fine-tuned to classify a small number of images. To find optimal CNN architecture, Anaraki et al. [2] used GA and achieved

Table 4 Performance based comparison of the proposed method with the existing systems

Reference	Technique	Layers	Accuracy
Sultan et al. [38]	CNN	16	96.1%
Anarkari et al. [2]	CNN	17	94.2%
Deepak et al. [9]	CNN	7	95.8%
Proposed CNN	CNN	13	97.2%

Table 5 Performance based comparison of the proposed method with transfer learning based models

Reference	Technique	Parameters	Accuracy
Sajjad et al. [31]	VGG19	138 M	95.4%
Swati et al. [37]	AlexNet	61 M	89.9%
Pundir et al. [28]	VGG16	138 M	91.8%
Proposed CNN	CNN	0.59 M	97.2%

an accuracy of 94.2% for classifying brain tumors. However, GA was unable to determine the best possible CNN for brain tumor classification that resulted in lower overall accuracy. Whereas, the proposed CNN architecture contains only 13 layers and is lightweight and robust than the existing systems.

5.5 Comparison with transfer learned architectures

We also compare the performance of the proposed architecture with well-known transfer learning models as shown in Table 5. Swati et al. [37] fine-tuned AlexNet, VGG16 and VGG19. The system obtained accuracy of 89.9% via AlexNet. Waghmare et al. [42] classified brain tumors by employing a pre-trained VGG16 network and achieved 95.7% accuracy. Sajjad et al. [31] classified brain tumors using a fine-tuned VGG-19 model and achieved 94.5% accuracy. The images were segmented using Input Cascade CNN. The system performs both the segmentation and classification via CNNs which is computationally exhaustive. However, the pre-trained CNN architectures mentioned in AlexNet [37], VGG16 [42], VGG19 [31] and ResNet [34] are computationally complex as they contain millions of trainable parameters. Such large networks are usually slower and can result in overfitting. Whereas, the proposed CNN architecture is lightweight because it contains fewer learnable parameters than the existing CNNs.

5.6 Comparison with traditional ML based techniques

In this section, we compare the performance of our proposed CNN with non-DL based brain tumor classification methods as shown in Table 6. Kaplan et al. [14] proposed a method employing Local Binary Pattern (LBP) as a feature extraction technique and K-nearest neighbor (KNN) as a classification technique. The system obtained highest accuracy of 95.5%. Thejaswini et al. [40] segmented images using Adaptive Regularized Kernel based Fuzzy C-Means Clustering (ARKFCM) method and extracted first order and second order statistical features from segmented area. The system obtained a success rate of 91.4% using the SVM. Chen et al. [7] investigated the efficacy of three distinct feature extraction methods on

Table 6 Comparison with traditional ML techniques

Reference	Feature vector	Classifier	Accuracy
Kaplan et al. [14]	LBP	KNN	95.5%
Thejaswini et al. [40]	ARKFCM	SVM	91.4%
Chen et al. [7]	BoW, GLCM, Density Histogram	SVM, KNN	91.4%
Proposed	CNN	Softmax	97.2%

the brain tumor classification problem: density histogram, grey level co-occurrence matrix (GLCM), and bag of word (BoW) model. The authors classified the handcrafted features using SVM/ KNN and achieved the highest accuracy of 91.4% using BoW features and SVM classifier. Traditional procedures, on the other hand, necessitate manual tumor segmentation and feature extraction, which is not only time-consuming but also error-prone. Before classification, these manual algorithms require the use of an expert with significant knowledge to attempt various segmentation and feature extraction strategies.

5.7 Discussion

Our proposed method was trained and validated on Figshare dataset that achieved 97.2% accuracy. Moreover, to assess the robustness of the suggested CNN on unseen samples, it was validated on 289 MRI images from Kaggle dataset and achieved 96.9% accuracy. The obtained results clearly suggest that our proposed strategy outperforms existing methods in tumor identification and classification. It is crucial to note that the compared algorithms used deep CNNs, which can easily over fit and are computationally and memory intensive. The proposed method, on the other hand, is efficient and lightweight due to fewer layers and very less trainable parameters than the existing architectures. Furthermore, because the suggested CNN does not require segmentation prior to classification, we may conclude that our approach is both robust and successful for brain tumor classification.

6 Conclusions

In this study, we propose a novel CNN based method for identification and classification from MRI images. The proposed system can classify the tumors into three classes i.e. Glioma, Meningioma, and Pituitary. The architecture contains a total of 13 layers including 2 Convolution layers, Batch normalization layers, Maxpooling layers. The architecture is also composed of a dropout layer to prevent overfitting followed by an FC layer, a Softmax layer to predict the output, and finally Classification layer to produce the predicted class. The presented framework is evaluated using Precision, Recall, and Accuracy. Our proposed method obtained 97.2% accuracy on 3064 MRI images from the publically available Figshare dataset. Whereas, the proposed method attained 96.9% accuracy on a cross-dataset scenario. The suggested CNN architecture is robust and eliminates the need for manual lesion segmentation prior to classification. As a result of the findings, it is demonstrated that our suggested method is more efficient than existing methods and that it can be used by doctors to detect and classify the type of tumors from MRI scans in real-time. Despite the promising performance of our proposed strategy, in the future we will try to investigate different databases with different imaging modalities in order to increase the network's generalization capability.

Declarations

Conflict of interest Authors declare that there is no conflict of interest between them.

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