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Brain Tumor Detection using Convolution Neural Networks

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Abstract - Early diagnosis of brain tumor is an important for improving patient prognoses; however, traditional diagnostic methods like biopsies require invasive surgical procedures. In this study, we implemented two deep learning-based methods—a two-dimensional Convolutional Neural Network (CNN) and a convolutional auto-encoder network—that enable the accurate classification of brain tumors from magnetic resonance imaging (MRI). A data set of 7,000 T1-weighted contrast-enhanced MRI images was utilized, including glioma, meningioma, pituitary gland tumor, and normal brain samples. Preprocessing and augmentation procedures were carried out on the data set in order to enhance the generalization ability of the models. The suggested architecture of the 2D CNN includes eight convolutional layers, four pooling layers, and utilizes batch normalization with a uniform 2×2 kernel across the network. The auto-encoder architecture combines feature extraction and classification by utilizing the last output of the encoder. Experimental results show that the 2D CNN achieved a training accuracy of 96.47% with an average recall of 95%, showing good performance and efficiency in computation. The simplicity and effectiveness of the proposed CNN make it a promising tool for real-time clinical applications, offering a non-surgical and highly reliable tool for the assistance of radiologists in the diagnosis of brain tumors.

Key Words: Brain Tumors, 2D CNN, Convolutional Auto-encoder Network, MRI Images.

1. INTRODUCTION

Brain tumors, both malignant and benign, are a major health concern due to their ability to interfere with normal brain functions. There are over 200 identified types affecting the brain and central nervous system. These tumors can lead to serious or even fatal outcomes. Alarming data from the National Brain Tumor Foundation shows a 300% rise in brain tumor-related deaths over the past three decades, highlighting the growing impact of this condition [1] . If left untreated, brain tumors can progress rapidly, underscoring the critical need for early detection and prompt intervention. Currently, diagnosis heavily relies on biopsies—a procedure that is significantly more complex and riskier in the brain than in other. The complexity of brain biopsies has increased the need for non-invasive, accurate diagnostic tools. Magnetic Resonance Imaging (MRI) is the most widely used method due to its ability to capture detailed images of soft tissues, aiding in the detection of brain abnormalities. However, interpreting MRI scans requires specialized expertise, and factors like tumor variability and radiologist fatigue can lead to diagnostic errors.

As a result, computational techniques for medical image analysis have become increasingly vital. Advances in machine learning—especially deep learning—have transformed this field by enabling automatic feature extraction and classification from large datasets, reducing the reliance on manually crafted features.

CNN is a leading deep learning architecture, have demonstrated exceptional performance in medical image classification due to their ability to learn complex spatial hierarchies and extract discriminative features [2]. Autoencoders have shown promise in unsupervised representation learning and have been effectively applied in brain tumor detection tasks. However, many deep learning models proposed for brain tumor classification still face limitations. For instance, several models are computationally intensive, exclude normal brain images, or focus solely on distinguishing tumor types such as gliomas, meningiomas, and pituitary tumors—without accounting for normal cases, which are essential for real-world diagnostic scenarios [3]. Additionally, many of these approaches lack comprehensive performance comparisons, further limiting their clinical applicability [4]. Rasheed et al. have [5] proposed a specialized two-dimensional CNN model for the classification of brain tumors using MRI images to identify

three tumor types as well as normal brain images, thereby expanding its diagnostic utility. By optimizing the architecture and rigorously evaluating its performance. They developed a robust, accurate, and computationally efficient solution to support radiologists in clinical decision-making.

1.1 Related Works

Recent research on brain tumor segmentation highlights two major branches of machine learning methods: supervised and unsupervised learning. The key distinction between them lies in the need for human intervention. Supervised learning requires labeled data to train the model; it operates by making predictions on labeled inputs and refining the results iteratively to improve accuracy [6]. In contrast, unsupervised learning does not rely on labeled data, although human validation is often necessary to verify the accuracy of the outputs [7]. Among the common techniques in unsupervised segmentation are support vector machines (SVM) and fuzzy clustering approaches. These methods have demonstrated good performance in tumor detection. However, their accuracy drops when the boundary between healthy and tumorous tissues becomes indistinct. Moreover, these methods can be computationally expensive due to the large amount of edge-related feature extraction involved.

Segmentation, which involves dividing an image into meaningful regions, is one of the most critical and challenging tasks in computer-aided clinical diagnostics. Traditionally, brain tumor segmentation is performed manually. However, this is not only time-consuming but also prone to inter-observer variability [8]. Therefore, developing an automatic and reliable segmentation method would significantly benefit brain tumor diagnosis and treatment.

CNNs provide a promising solution, as they automate both segmentation and feature extraction with high precision. Unlike traditional machine learning techniques, CNNs do not require manual intervention for these tasks. However, CNNs come with the drawback of high computational complexity, necessitating powerful GPUs for training due to the large number of parameters involved [9]. A CNN typically performs two main tasks: feature extraction through convolution and pooling layers, and classification through fully connected layers [10].

For instance, Febrianto et al. compared two CNN models for brain tumor detection: one with a single convolutional layer and the other with two. The results showed that increasing the number of convolutional layers improved performance, achieving a 93% accuracy and a loss value of 0.23 [11].

Another popular approach is transfer learning, which allows researchers to leverage pre-trained CNN architectures instead of building models from scratch. These pre-trained models are adapted to the specific task, thereby reducing training time and improving accuracy [12]. Transfer learning models offer robust performance with minimal expert input, and the weight-sharing mechanism helps the network automatically detect tumors from MRI images [13]. Nazir et al. implemented three transfer learning models—VGG19, Inception V3, and MobileNet V2—and reported accuracy rates of 88.22%, 91%, and 92%, respectively, with MobileNet V2 proving to be the most efficient [10].

Using artificial neural networks (ANNs), Soesanti et al. worked on classifying MRI images into benign and malignant tumor classes. They applied filters for preprocessing, followed by the average color moment technique to extract features. The ANN then classified the images with an accuracy of 91.8% [14]. In a different study, Khan et al. used histogram statistical equalization to transform pixel values by computing features like mean, variance, entropy, and dissimilarity. This approach was tested on low-grade and high-grade cervical glioma images, achieving an accuracy of 83.6%, sensitivity of 80.88%, and specificity of 86.84% [15].

In the present work, a 2D CNN and an autoencoder network are used to classify brain tumors into four categories: pituitary, glioma, meningioma, and no tumor.

2. DATA AND METHODS

2.1 Data collection and pre-processing

Our research utilized three publicly available brain tumor MRI datasets from Kaggle. The details of the datasets and their divisions (i.e., training and testing) are listed in table 1. The table presents three MRI datasets, their respective class distributions, and the number of images in the training and testing sets. Dataset 2 includes classes labeled as yes and no, with 239 images. The training set of Dataset 2 comprises 201 images, and the testing set contains 38 images. Dataset 3 focuses on the tumor classes, with 1500 images. The training set of Dataset 3 has 1200 images, and the testing set consists of 300 images. Dataset 3 also has an additional set of 3000 images, with 2400 in the training set and 600 in the testing set. Dataset 1 contains images of glioma, meningioma, pituitary, and no tumor classes, with a total of 7023 images. The training set of Dataset 1 consists of 5712 images, while the testing set has 1311 images.

Table -1: Dataset Distribution

Dataset 1				Dataset 2				Dataset 3			
Class	Images	Train	Test	Class	Images	Train	Test	Class	Images	Train	Test
Glioma	1621	1321	300	Yes	155	135	20	Yes	1500	1200	300
Meningioma	1645	1339	306	No	84	66	18	No	1500	1200	300
Pituitary	1757	1457	300								
No Tumor	2000	1595	405								
Total	7023	5712	1311	Total	239	201	38	Total	3000	2400	600

A set of procedures was utilized to preprocess the MRI scans, thus allowing accurate identification of brain tumors and producing meaningful results. The procedure addressed issues associated with inconsistencies in image resolutions and intensity levels contained in the dataset. Normalization of intensity levels, using techniques like z-score normalization and scaling of pixel intensities to a target range (e.g., 0 to 1), enhances the accuracy of machine learning models. Since there were inconsistencies in patient positioning and image orientation, it was important to register the scans to a standard reference frame. Image registration techniques were utilized to enable spatial consistency, thus allowing for more reliable comparisons and analyses. Additionally, artifacts and interferences caused due to patient movement or inconsistencies in the equipment were dealt with. Denoising algorithms like Gaussian smoothing and non-local means filtering were utilized to remove unwanted distortions without degrading essential image characteristics.

Algorithm: Fine-Tuning of CNN Hyperparameter

Step1: Find the best hyperparameters to train the model

Step2: Develop new model instances for the best hyperparameters

Step3: Train the model with specified parameters

Step4: Test and evaluate the CNN model.

Step5: Find the best performance metrics

2.2 Methodology

The research process of this study is explained in Figure 1. The key steps of the research are selecting an appropriate brain tumor dataset, pre-processing the MRI images, feature extraction, and classification through different models

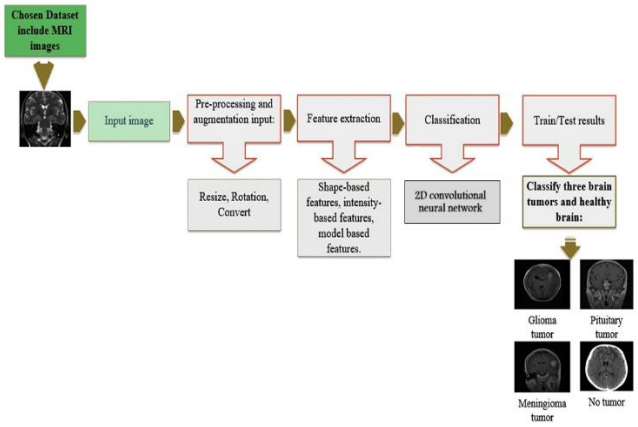

Fig-1: Stages of the proposed methodology

2.2.1 2D CNN

The design of the proposed two-dimensional CNN (2D CNN) architecture is explained in this research. Training and testing were performed on a database of 7,000 MRI images, 90% (6,300 images) of which was used for training and the rest, 10% (700 images), was used for testing. The network consists of various layers, among which some are convolutional layers—two having 64 filters, another set with 32 filters, and some other layers designed with 16 filters. The last two convolutional layers have filters of an 8-dimensional size. All the convolutional layers utilize a 2×2 kernel for spatial feature extraction. The CNN is hierarchical in structure, connecting convolutional layers with periodic pooling and fully connected layers. Note that not all convolutional layers have a pooling layer following them, as is evident with the structure. The network in total has eight convolutional layers and four pooling layers. The last pooling layer's output is flattened into a one-dimensional vector to be fed into the fully connected layers. Padding is carried out using the same values in neighbouring cells so that the dimensions of the output of the convolutional layers and edge information are preserved. In the classification stage, the network architecture consists of a fully connected layer of 1024 neurons and then a layer of 4 neurons corresponding to the four provided output classes. The last classification stage uses a softmax activation function. Batch normalization layers are used after each convolutional layer for enhancing the training stability and avoiding overfitting. Dropout layers with a rate of 0.1 are also used after each pooling and dense layer for regularization. ReLU activation function is used in all the layers except the last dense layer. The model is optimized with Adam optimizer, and some different learning rates (0.01, 0.001, 0.0001) are tried out to determine the most effective setting. It was found that the optimal learning rate is 0.001. The training process was performed over 100 epochs total, batch size 16, each epoch lasting about 7 seconds. The feature

extraction that occurs through the convolutional layers results in input to the first dense layer Ufc = 1024 neurons. Computation of the weights (Wconv) of the dense layer is derived from the dimensions of the convolution output (y1 × y2), the number of filters (k), and the dense layer number of neurons. Wconv = y1 × y2 × k × Ufc = 5 × 5 × 8 × 1024 = 204,800

Including the biases (1024), the first dense layer's total number of parameters is 205,824. The total number of trainable parameters in the entire network, calculated by summing all layer parameters, is 243,924. All of these parameters are optimized during training.

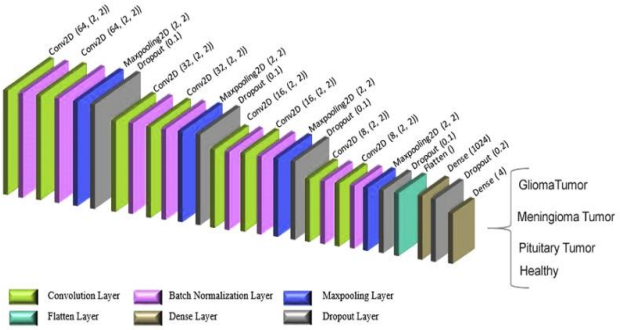

Fig -2: Architecture/ Layers of CNN

The depicted architecture is a deep CNN tailored for brain MRI image classification into four categories: Glioma Tumor, Meningioma Tumor, Pituitary Tumor, and Healthy. The network sequentially stacks multiple convolutional layers (green) for feature extraction, each followed by batch normalization (purple) to stabilize and accelerate training. MaxPooling layers (blue) are interleaved to reduce spatial dimensions and computational load, while dropout layers (gray) are incorporated to prevent overfitting by randomly deactivating neurons during training.

After several convolutional and pooling blocks, a flatten layer (light green) converts the multidimensional data into a one-dimensional vector. This vector is then processed by dense layers (yellow), which perform the final classification. The last dense layer outputs probabilities for each of the four classes. The architecture's color-coded design clearly distinguishes each layer type, facilitating understanding and reproducibility.

This CNN structure effectively combines convolutional operations for hierarchical feature learning, normalization for training efficiency, pooling for dimensionality reduction, and dropout for regularization, making it well-suited for robust and accurate brain tumor classification in medical imaging applications.

3. RESULTS & DISCUSSION

Several standard evaluation metrics are generally introduced to evaluate the performance of the system, among these metrics there is Accuracy, Precision, Recall, F1_score, confusion matrix and Receiver Operating Characteristic curve (ROC).

3.1 Performance evaluation metrics:

Several common measures of evaluation are used to measure the performance of the system. Some of them are Accuracy, Precision, Recall, F1-score, Area Under the Curve (AUC), the Confusion Matrix, and the Receiver Operating Characteristic (ROC) curve. Each one provides a different perspective on the performance of the model. The definitions and the corresponding mathematical equations for these measures are explained in the next section.

3.1.1 Confusion Matrix:

predictive A confusion matrix is a tabular display describing the output of a classification model's predictions. The matrix aids in differentiating correctly classified instances from misclassified instances, making it possible to identify potential errors made by the model. Being a performance-measuring tool, it categorizes predictions into four fundamental categories: true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN). These categories of information are critical in describing the ability of the model and are presented in Table 2.

Table – 2: Elements of confusion matrix

Element	Description
TP	Images containing the tumor and correctly classifies
NP	Images not containing the tumor and correctly classified.
FP	CNN classifies images as containing tumors but that does not contain any tumor
FN	CNN classifies images as not containing any tumor but are containing a tumor

3.2 Loss Function:

A loss function quantifies the extent to which the outputs of the predictions of the NN are distant from the values in the training set. The performance of the network enhances as the loss function value decreases. Minimization of the function is done by minimizing the difference between the predicted and actual values, and this is done by the adjustment of the internal weights of the network during training.

3.3 Training Results:

The CNN model was trained using a notebook on the Google Colab platform, which provides access to widely used Python libraries such as TensorFlow and Keras. Colab executes the code on Google's cloud infrastructure, utilizing high-performance hardware. This significantly boosts training efficiency which is particularly beneficial given the large number of parameters in the proposed CNN architecture. The progression of accuracy and loss over the training and validation phases is illustrated in Fig. 3 and Fig. 4, respectively.

The accuracy plot in Fig. 3 shows the trend during both training and validation. It is evident that the training accuracy consistently outperforms the validation accuracy. Similarly, as seen in the loss curve presented in Fig. 4, the training loss is lower than the validation loss throughout. These observations indicate that the model generalizes well and does not suffer from overfitting.

3.4 Testing Results:

The performance of the proposed methodology was evaluated by the measures of precision, specificity, accuracy and, above all, the ROC curve for two classes (normal and abnormal brains) and compared to the performance of other classifiers, the metrics mathematical equations are detailed below. Also, the confusion matrix as shown in fig 5 shows how well the model is able to classify and detect true positives and true negatives.

$$Specificity = \frac{TN}{TN+FP} \quad (1)$$

$$Sensitivity = \frac{TP}{FN+TP} \quad (2)$$

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (3)$$

$$Precision = \frac{TP}{TP+FP} \quad (4)$$

$$F1-Score = 2 * \frac{Precision*Sensitivity}{Precision+Sensitivity} \quad (5)$$

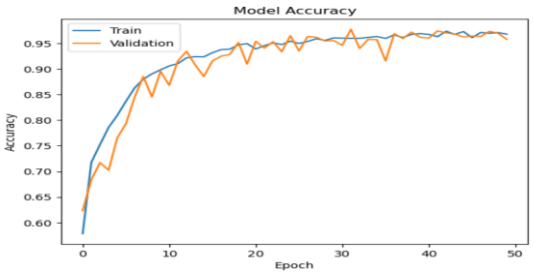

Fig -3: Model Accuracy Graph

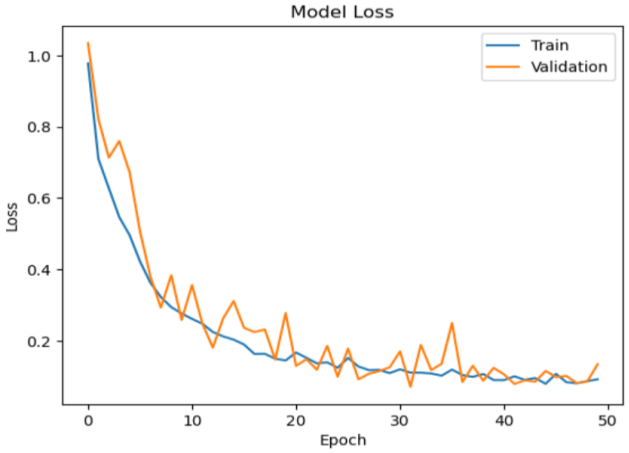

Fig -4: Model Loss Graph

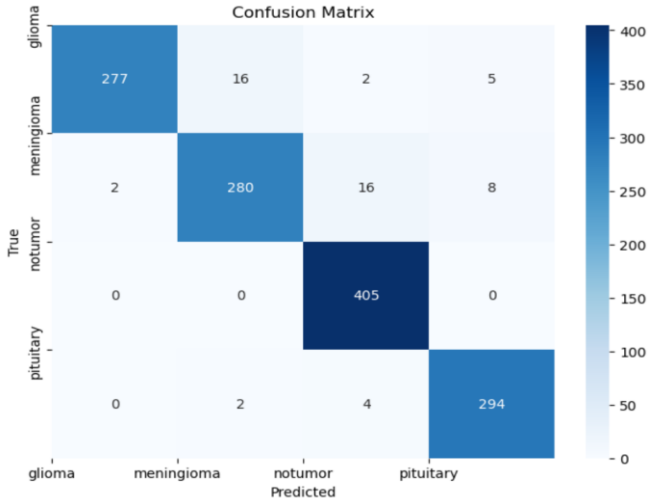

Fig -5: Confusion Matrix

4. CONCLUSION & PERSPECTIVES

In this study, we developed and evaluated a novel 2D CNN architecture, alongside traditional machine learning models, for the accurate classification of brain tumors using T1-weighted, contrast-enhanced MRI scans. The proposed CNN model demonstrated high training accuracy of 96.47% and effectively distinguished between three tumor types—glioma, meningioma, and pituitary—as well as healthy brain images. Comparative analysis showed that the CNN outperformed conventional classifiers such as KNN, Random Forest, and SVM in both accuracy and execution time, highlighting its efficiency and generalization capability.

Furthermore, we validated the model on an extensive MRI dataset, where preprocessing and normalization played a key role in enhancing performance. The CNN achieved superior results in segmentation and classification tasks, with overall

accuracy rates reaching up to 97%, outperforming other existing models across various evaluation metrics. These outcomes confirm the robustness of CNN-based architectures in medical image analysis and support their use as reliable decision-support tools for radiologists in clinical settings.

Future work will focus on refining the proposed architecture and assessing its scalability and performance across larger, more diverse datasets to further strengthen its applicability in real-world diagnostics.

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