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Brain Tumour Diagnosis using MRI Scans: A CNN-Based Multiclass Analysis

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Abstract: Brain tumors are among the most challenging health issues because of their complexity and the critical need for early and accurate diagnosis. Magnetic resonance imaging provides excellent spatial resolution and soft tissue contrast, making it an indispensable tool for identifying abnormalities in the brain.

It is highly used for tumor detection in the brain, but MRI scan analysis is time-consuming and prone to human errors because the appearance of a tumor may vary. This paper discusses multiclass classification for brain tumors using CNNs. The work proposes a method with a CNN model implemented in PyTorch to classify the MRI images into four categories: glioma, meningioma, pituitary, and no tumors. The experimental research was conducted using a dataset with varying tumor sizes, locations, shapes, and intensity of the images. For the rigorous evaluation of the model, the dataset of MRI scans was split into the training set and validation set. Techniques like dropout for regularization and data augmentation were used for optimizing CNN architecture to overcome overfitting. Experimental results show that the proposed model has a classification accuracy of 91.4%, which is more accurate than baseline methods. This indicates that it can be efficiently used for brain tumor diagnosis. Results obtained here highlight the potential of deep learning in clinical applications, where the technique provides enhanced diagnostic accuracy and reliability.

Keywords: Convolutional neural networks (CNNs), VGG, Brain Tumors, MRI, Image Classification, Medical Imaging.

I. INTRODUCTION

Among the most serious and complex diseases in the medical field, brain tumors present a challenge to healthcare professionals because of their diversity and varying levels of malignancy. Accurate and timely classification of brain tumors is crucial for effective treatment planning, prognosis assessment, and improvement in patient survival rates [10]. Traditionally, the classification process relies heavily on manual examination of Magnetic Resonance Imaging (MRI) [26] scans by highly trained radiologists and neurologists. Although effective, the manual procedure proves to be timeconsuming [2]; and prone to inter-observer variability and reliance on expertise. In addition, in cases where specialists are not readily available, access to proper diagnosis becomes limited, and subsequently, treatment may be initiated at a much later time than desired, affecting the results of the treatment. Magnetic resonance imaging is one of the advanced imaging techniques offering excellent spatial resolution and contrast in soft tissues [6]. The tool is vital in detecting abnormalities in the brain. It has the ability to detect several kinds of brain tumors and neurological disorders without using invasive methods [29]. Recent advances in AI and deep learning have opened new avenues to medical imaging challenges by developing automated, accurate solutions for such tasks. Among them, CNNs became one of the most powerful techniques in image-based tasks including classification, segmentation, and object detection [3]. In the context of medical diagnostics [30], CNNs performed exceptionally in analyzing complex data from imaging; they give a reliable second opinion that will efficiently enable accurate decision-making processes. The focus of this research is to apply deep learning to detect brain tumors and further classify the detected ones into three categories: gliomas, meningiomas, and pituitary tumors Rethemiotaki [3]. The approach is designed with a VGG-based CNN [4] architecture to build a system that is both scalable and efficient, thus aiding the medical fraternity in making an accurate diagnosis of brain tumors with as little human intervention as possible [18]. The model is trained and tested using a publicly available MRI dataset, which guarantees its reproducibility and further applicability [9]. This paper is organized as follows: Section 2 discusses related works in brain tumor classification and deep learning, dataset, preprocessing, and CNN architecture; Section 3 presents material and experimental process, Section 4 presents experimental results and performance metrics; and Section 4 concludes the study.

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II. LITERATURE REVIEW

Segmenting the region of interest from an object presents a significant challenge, particularly when isolating tumors from MRI brain images. Researchers globally are dedicated to advancing this field to achieve optimal segmentation of the ROI, employing a variety of distinct approaches. Currently, neural network-based segmentation is yielding impressive results, and the adoption of this model is steadily increasing.

Saeedi et al. [1] employed a dataset including 3,264 MRI brain scans, encompassing pictures categorised as gliomas, meningiomas, pituitary gland tumours, and healthy brains. Preprocessing and augmentation techniques were first applied to MRI brain images. A unique 2D Convolutional Neural Network (CNN) [23] and a convolutional autoencoder network were then developed, both pre-trained with the specified hyperparameters [24]. The 2D CNN consists of multiple convolutional layers, each employing a 2x2 kernel function inside this hierarchical structure. This network consists of eight convolutional layers and four pooling layers, with batch normalisation applied following each convolutional layer. Proposed two-dimensional convolutional neural network and convolutional autoencoder neural network. The training accuracy of the suggested 2D CNN was 96.4752%, while the validation accuracy was 93.4489%. The suggested convolutional auto-encoder achieved a training accuracy of 95.6371% and a validation accuracy of 90.9255%.

Hossain et al. [2] suggested a technique that uses convolutional neural networks, conventional classifiers, and the fuzzy C-Means clustering algorithm to extract brain tumours from 2D magnetic resonance imaging (MRI). A real-time dataset with a range of tumour sizes, locations, forms, and intensities was used in the study. SVM, KNN, MLP, Naïve Bayes, Random Forest, and Logistic Regression are examples of traditional classifiers. With an accuracy of 97.87%, the Convolutional Neural Network (CNN) is utilized for improved performance.

Rethemiotaki [3] [28] analysed MRI pictures to identify and categorise brain tumours using computational intelligence approaches. The 3264 photos in the collection were divided into pituitary, meningioma, glioma, and healthy brain categories. Twelve convolutional neural networks were employed to classify the tumours. According to the findings, the MobileNetV2 CNN model was able to diagnose brain tumours with 99% accuracy, 98% recall, and 99% F1 score. However, the Google Net CNN model was thought to be the best option for classifying brain tumours because it had the highest accuracy (97%) of any model.

Swarup et al. [4] proposed a deep CNN model for automatically detecting brain tumor cells in MRI brain images. The model is trained using Google Net and Alex Net architectures and evaluated on a test dataset. The results show that Google Net is highly accurate and consumes significantly less parameters than Alex Net. The depth of Alex Net is 8, takes 60 million parameters, and the image input size is 227×227 . This model can be a competent alternative support tool for radiologists in clinical diagnosis due to its high specificity and speed.

Lamrani et al. [5] used machine learning and deep learning approaches in MRI images for detection of brain tumours. These algorithms facilitate decision-making and treatment selection by providing rapid prediction, reduced errors, and increased precision. A convolution neural network (CNN) for the identification and categorisation of brain tumours is proposed in this article [19]. CNN is a better method for predicting the presence of brain tumours because of its pre-trained architectural model, which delivers 96% precision and classification accuracy rates.

Martinez et al. [6] The research aimed to develop an image classifier using convolutional neural networks (CNN) to detect brain tumors in magnetic resonance imaging (MRI) [20]. Brain tumors are a major cause of morbidity and mortality worldwide, and MRI offers excellent spatial resolution and soft tissue contrast. However, accurate interpretation remains challenging due to human subjectivity and variability in tumor appearance. The best model achieved an accuracy of 97.5%, sensitivity of 99.2%, and binary accuracy of 98.2%, highlighting the potential of deep learning techniques in clinical applications.

Devkota et al. [7] developed a comprehensive segmentation process that utilises the spatial FCM algorithm and Mathematical Morphological Operations to reduce computation time. However, the proposed solution has not yet been tested beyond the evaluation stage, and the results are as follows: Cancer detection with 92% accuracy without the need for preprocessing steps. A single network achieves a dice score of 0.73, while multiple systems achieve a dice score of 0.79.

Dhole et al. [8] provides a comprehensive description of the top-tier MRI-based brain tumour division procedures. A significant number of frontal brain tumour division methods [22] operate on MRI images and utilize a variety of



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attributes to collect and organise information, as well as consider spatial information in close proximity, due to the noninterfering and extremely sensitive tissue separation of MRI.

Tumour detection and extraction are the subjects of Isunuri et al. [9][24]. The tumor's personality is assessed using the device described here, which assists specialists in the development of a treatment plan and the surveillance of the tumor's condition. Consequently, the area is partitioned. In comparison to the alternative framework, this approach improves the efficacy and spatial confinement of the image.

III. MATERIALS AND METHODS

A. Experimental Dataset

The dataset used for this paper is available on Kaggle with a license under CC0: Public Domain. It includes a mix of three datasets that are public and available for use, which are figshare dataset, SARTAJ dataset, and Br35H dataset [6]. Therefore, combining the three gives a more diversified and wider collection of brain MRI scans, ensuring that the model is quite robust. This data set consists of 7023 images that belong to four classes: gliomas, meningiomas, pituitary tumors, and no tumor. The existence of the "no tumor" class enables the generation of a more complete model that can differentiate between pathological and normal cases, which are vital in real-life scenarios of diagnosis. The images from the "no tumor" class were selected directly from the Br35H dataset.

Further, it contains a variety of anatomical planes and image shifts, which is extremely useful for deep learning models. The diversity will reduce the chance of overfitting and the model is not very specialized to certain features or patterns. Inclusion of various imaging perspectives ensures the model generalizes better for different scenarios and enhances performance when applied to new unseen data.



Fig 1. Different samples of MRI: glioma, meningioma, no tumor, and pituitary tumour

B. Data Pre-processing

As mentioned above, some pre-processing steps are essentially vital for improving the quality and consistency of MRI images. Several key techniques are carried out to prepare data to be analyzed effectively. It began with standardizing all images by converting them to one single grayscale channel. This step made the images contain consistent intensity values without any additional color information, which is irrelevant to the task.



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All images were rescaled to 224x224 pixels so that all images are input dimensions unified throughout the dataset. The size for resolution has been chosen between a smaller resolution and a larger one for an essential preservation of characteristics, thereby being computationally balanced. CNN architectures require fixed input sizes hence requiring uniform image dimensions to maintain compatibility [13].

In addition, during the training process, random affine transformations were applied. This consisted of rotation and translation with introduced variability in the training data set, which reduced overfitting because the model is less sensitive to slight positional and orientation changes.

One example of the translated and rotated image is illustrated in Fig. 2. The augmentation processes were limited by some limits to the training datasets. There were limits placed on the horizontal and vertical translations of 3 and 5, respectively. The rotation operation was set between angles -5 and 5.



Fig 2. Translated and rotated images for the augmentation process

C. Model Architecture

The CNN based model is inspired from VGG-16 design. The architecture consisted of the following layers:

• Convolutional and Activation Layers - Convolutional Operations: Filters of size 3×3 are applied to extract spatial features.

Batch Normalization: Normalizes the output of each layer to stabilize and accelerate training.

• ReLU Activation: Introduces non-linearity to model complex relationships in the data.

• Max-Pool Layers: Used after each convolutional block to reduce feature map dimensions by retaining only the most critical features. Pooling operations reduce overfitting by providing spatial invariance.

• Dropout Layers: Dropout layers are introduced to prevent overfitting by randomly deactivating a subset of neurons during training. A dropout rate of 0.5 was used in fully connected layers.

• Fully Connected Layers: The flattened output from the convolutional layers is passed to fully connected layers, which aggregate spatial features into high-level representations suitable for classification tasks.

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Fig 3. The architecture of the 2D convolution network

D. Model Hyperparameters

The hyperparameter selection process is critical for the success of the proposed VGG based [15] multi-task learning model for brain tumor classification and segmentation. Some hyperparameters were carefully selected and fine-tuned for optimal performance. A learning rate of 1e-3 controls the step size during optimization, thereby affecting the speed and accuracy of convergence [7]. This model was trained through more than 25 epochs of complete passes over the full dataset. The batch size was taken as 32, where the balance had to be struck between efficient computation and stable gradient updates. In fully connected layers, the dropout rate applied was 0.5, with an intention to nullify overfitting during training. This was due to random deactivation of a fraction of neurons within each iteration.

The convolutional neural network (CNN) model utilizes the Rectified Linear Unit (ReLU) activation function, which is commonly employed in deep learning architectures for its ability to introduce non-linearity.

Layers	Kernel Size	Strides	Output Size	Parameters
Input	-	-	1x224x224	-
Conv2d	3 × 3	1	32x224x224	320
MaxPool2d	2×2	2	32x224x224	-
Conv2d	3 × 3	1	64x112x112	18496
BatchNorm2d	-	-	64x112x112	128
MaxPool2d	2×2	2	64x56x56	-
Conv2d	3 × 3	1	128x56x56	73856
MaxPool2d	2×2	2	128x28x28	-
Conv2d	3 × 3	1	256x28x28	295168
Conv2d	3 × 3	1	256x28x28	590080

TABLE1.	SPECIFICATION OF	F ALL LAYER	S OF MODEL
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BatchNorm2d	-	-	256x28x28	512
MaxPool2d	2×2	2	256x14x14	-
Conv2d	3×3	1	512x14x14	1180160
BatchNorm2d	-	-	512x14x14	1024
MaxPool2d	2×2	2	512x7x7	-
Flatten	-	-	25088	-
Dense	-	-	256	6422784
Dropout	-	-	256	-
Dense	-	-	128	32896
Dropout	-	-	128	-
Dense	-	-	4	516

E. **Optimizing Algorithm**

The optimization process is the most critical aspect of deep learning, where the model's parameters are adjusted to minimize the loss function and enhance the performance of the deep learning model. For this experiment, Adam optimizer was used because it is adaptive learning rate and handles sparse gradients efficiently. Adam is a combination of momentum and adaptive learning rate algorithms that are especially effective for complex tasks like multi-task learning.

F. Batch Normalization and Dropout

The Batch Normalization layer enables each layer of the architectural model to learn more independently. The main purpose of this layer is to normalize the output of the layer that has been used previously. It can be used in order to avoid the problem of overfitting and, therefore, can help with regularization. The work of the layer is to standardize input and output of the sequential model. This layer can be fed to the model at different points. It can be at after creating the sequential model, in between layers or even after the convolution and pooling layer. Dropout was applied to the fully connected layers to introduce stochasticity during training in order to avoid overfitting [11]. A dropout rate of 0.5 was chosen, which means that 50% of the neurons are randomly deactivated during each training iteration. This prevents the model from relying too heavily on specific neurons and encourages it to learn more generalized feature representations. Along with the optimization strategy and batch normalization, dropout contributed considerably to how well the model generalizes to unseen MRI scans and still performs robustly for the task. Overall, these techniques helped to establish the reliability and effectiveness of the proposed model.

IV. RESULTS

A. Performance Stats

The performance of the brain tumor classification model was evaluated through analysis of the trends of training loss and validation loss over 25 epochs. Training loss steadily decreased across all epochs, indicating the effective learning of the model in minimizing the error of the training data. Training loss steeply declined within the initial epochs, representing fast optimization since the model has captured most of the important features from the MRI images.

The validation loss, which refers to the performance of the model on unseen data, also decreased in a similar manner, which indicates the good generalization ability of the model. The parallel drop of both training and validation loss in the first epochs indicates that there is no overfitting. Can be seen, minor fluctuations in the validation loss in later epochs are probably due to the variability in the validation dataset. However, these fluctuations did not reflect any major deviation of the training loss and the validation loss.

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Fig 4. Loss Curve of Proposed Method

B. Evaluation Metrics

The performance of the brain tumor classification model was evaluated using a confusion matrix and metrics such as accuracy (A), precision (P) and recall (R) [6]. The confusion matrix provides a detailed insight into the classification performance by showing the true labels versus predicted labels for the four classes: Glioma, Meningioma, No Tumor, and Pituitary. The formulas for accuracy, precision and recall involve the values of false-positive (FP), false-negative (FN), true positive (TP), and true negative (TN) within the confusion matrix [13].

$$A = \frac{TP + TN}{TP + TN + FP + FN} \qquad \qquad R = \frac{TP}{TP + FN} \qquad \qquad P = \frac{TP}{TP + FN}$$

The diagonal elements of the confusion matrix represent the number of correctly classified instances for every type of tumor, while off-diagonal elements signify misclassifications. A model that has an accuracy of 91.4% means that it is very accurate in its predictions over the entire dataset. Precision as high as 91.1% means that a model is very accurate in preventing false positives. With a recall of 91.7%, the model correctly identified 91.7% of the actual positive instances, and so it proved effective in reducing false negatives and catching most true positive cases. Altogether, these metrics highlight the balance of the specificity and sensitivity of the model. Precision and recall were calculated for all individual classes and The confusion matrix below shows the accuracy of each label and the errors of the classifier, including both false positives and false negatives. The code for this layout of a Seaborn confusion matrix is here on GitHub.



Fig 5. Confusion Matrix Analysis of Proposed Model

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V. CONCLUSION

This research introduces a comprehensive framework for the detection and classification of brain tumors based on Convolutional Neural Networks (CNNs) on MRI images. A multi-task approach was utilized to identify tumor types such as glioma, meningioma, pituitary tumors, and no tumors with an overall accuracy of 91.4%. This would ensure generalization of the model to many scenarios due to the preprocessing techniques of data, which include image resizing, grayscale conversion, and data augmentation. Other optimization strategies applied include the Adam optimizer, batch normalization, and dropout regularization to further improve the model's performance, reducing overfitting and improving convergence. The evaluation metrics, including a precision of 91.1% and a recall of 91.7%, signifies the reliability and capability of the proposed model in handling challenging classification tasks. These results indicate that the approach is not only accurate but also effective in maintaining a balance between precision and recall, making it suitable for real-world medical applications. Future work can explore the integration of advanced architectures like Vision Transformers or hybrid models, leveraging additional datasets to improve performance further. Additionally, extending this framework to other medical imaging domains or tumor grading can enhance its applicability, ultimately contributing to improve healthcare diagnostics and patient outcomes.

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