

Enhanced Brain Tumor Detection Using a Lightweight CNN Model: Improved Accuracy through Advanced Preprocessing and Augmentation Techniques

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Abstract

This study presents a lightweight Convolutional Neural Network (CNN) model, designed to detect and classify brain tumors using MRI images. The model uses a dataset from Kaggle, comprising 7023 images in total, labeled into four classes: glioma, meningioma, pituitary and non-tumor. We preprocessed the data which includes: image resizing, normalization, and data augmentation to increase the size of our dataset, and make the model robust. The CNN architecture comprises 16 layers that includes - convolutional, max pooling, dropout, flatten, and dense layers. For model training, we used an adam optimization function which gave 98.20% accuracy on the test dataset. Evaluation metrics - precision, recall and F1-score validates the performance of our model, with precision scoring 98.24%, recall 98.18% and F1-score 98.18%. We further present a comprehensive analysis of the model's training and validation process through epochs vs loss and accuracy plots, confusion matrix and histogram of training and validation accuracy. The model we propose promises good results, and showcases itself as an effective tool for brain tumor detection and classification.

Keywords. Brain tumor detection, CNN, MRI images, Image preprocessing, Classification, Evaluation Metrics

1. Introduction

The abnormal growth of cells or when they start growing in bulk, in or around the brain, is a Brain Tumor. The tumor can be benign (non-cancerous) or malignant (cancerous), but the tumors affect the brain functioning and health depending upon their size and location.¹ Due to these factors, even the benign tumors can create discomfort if they grow larger and put pressure on the surrounding nerves, blood vessels, and tissues. The International Association of Cancer Registries (IARC) highlights: over 28,000 instances of brain tumors are reported in India annually, causing over 24,000 deaths. Every year, around 40,000 to 50,000 people are diagnosed with brain tumors and this case involves 20% of the children ratio.²

The early detection of brain tumors is helpful in prolonging human lives. It allows the medical professionals to provide effective treatment options and begin the treatment at a stage where the tumor is curable.³ Focusing on Glioma, Meningioma, and Pituitary among the over 150 different types of brain tumors, showcases the versatility and potential of this approach.⁴⁵ Each tumor type requires a different treatment strategy, and if the doctors are able to detect the exact type, location, and extent of the tumor, they can determine the best possible treatment. Aiming to explore the solution to this problem, a CNN architecture has been developed which is lightweight and accurate. [21]

While traditional methods are already there, an important question arises that why is there a need for AI/ML techniques. The existing methods are valuable but they lack speed and accuracy, whereas AI models can analyze a vast amount of image datasets and provide more accurate results quicker, leading to lesser chances of misdiagnosis.⁶ Machine learning and deep learning (DL) have gained increasing popularity in the past few years due to the availability of highly efficient computational systems. ML algorithms are a revolutionizing technology for fields like electronics, finances, and biomedicine.⁷ The researchers have harnessed ML's power, contributing the most to medical applications. With ML algorithms, the image analysis process becomes faster which allows quicker detection and classification of the tumor. As the world sees more of the evolving ML techniques, blending ML with biomedical

research shows a great improvement in healthcare.⁸ These models can easily improve the differentiation between different types of the tumors and that too in a shorter period of time, whereas the traditional methods are very time consuming. Moreover, the traditional methods may also lead to inconsistencies in diagnosis and treatment as the interpretation of the MRI scans can be subjective and may vary among the doctors.

1.1 Literature Review

A study conducted by Sarajit Das in 2023 used a Convolutional Neural Network in combination with Transfer Learning. This study used MRI images from Kaggle (Masoud Nickparvar), (A. Hamada) which had 7023 slices with 4 classes: pituitary, glioma, meningioma, and no tumor. The training, validation and testing set were split from the entire dataset having 90%, 5% and 5% of it respectively. This study used the EfficientNet framework which froze some top layers and then introduced new layers that were able to achieve an accuracy of 99.61%.⁶

2023 research conducted by N. Remzan used Convolutional Neural Network (CNN) to classify preprocessed MRI brain tumor images. MRI images from a dataset provided by Masoud Nickparvar, which consisted of 7019 images divided into four classes having 1620 glioma images, 1644 meningioma images, 1756 pituitary images, and 1999 normal images. It used 3 convolutional layers each followed by maxpooling and a dropout layer. The number of parameters used in this CNN approach is 1.5 million. The accuracy achieved with the model is 95.65%.⁹

Research conducted by Beyza Nur TÜZÜN in 2023 implemented Convolutional Neural Network (CNN) for brain tumor classification using MRI images from Kaggle (Masoud Nickparvar). The dataset consisted of 7022 images, of which 78% and 22% was divided into training and testing. It uses 4 convolutional layers followed by maxpooling layer, dropout layer, flatten layer and then a fully connected layer. This used 4 different models : GoogleNet having 22 layers, MobileNetV2 having 3.4 million parameters and 53 layers, InceptionV3 having 23.8 million parameters and 48 layers, and EfficientNet b0 having 5.3 million parameters and 237 layers. The best result values were obtained with the EfficientNet b0 model having 99.54% accuracy trained on 100 epochs.⁴

In a study by Güler in 2024, used a dataset that was sourced from the Brain Tumor MRI dataset available on Kaggle, which consists of 7022 brain MRI images divided into four classes: gliomas (1321 images), malignant tumors (1339 images), pituitary tumors (1456 images), and normal tissues (1595 images) to classify brain tumor. The dataset was split into 60% training and 40% testing set. It used VGG and ResNet architectures having 41 and 152 layers respectively and DenseNet, SqueezeNet as well. Among these 4 architectures with machine learning methods, DenseNet achieved the highest accuracy of 85% when combined with an SVM classification method.¹⁰

A study conducted by Syed Ahmmed in 2023 used deep learning frameworks for the classification of brain tumors using MRI images. The research worked on two architectures: ResNet 50 and Inception V3. It used 2 distinct datasets. The first dataset consisted of 3459 MRI scans containing 4 classes (glioma, meningioma, non-tumor, and pituitary) and the second dataset consisted of 3000 images with 2 classes (tumor present and tumor absent). ResNet 50 and Inception V3 are the 2 models used. An accuracy of 97.68% for the multi-class dataset and accuracy rate of 99.84% was achieved for the binary dataset.¹¹

A study conducted by Agus Eko Minarno in 2021 proposed a Convolutional Neural Network (CNN) method to classify brain tumors, including glioma, meningioma, pituitary tumors, and no tumors. The dataset used in this study comprised of 3264 MRI images, having 926 images of glioma, 937 of meningioma, 901 of pituitary, and 500 of non-tumor images. The CNN architecture included 5 conv2D layers each followed by maxpooling, and dropout layer. This was then followed by 1st dense layer having relu activation function and 2nd dense layer with softmax activation function. Between these dense layers a dropout layer was applied. In this study, 3 model scenarios with different parameters were examined and the highest accuracy achieved was 96%.³

A 2023 research conducted by Soheila Saeedi detected brain tumors in MRI images using machine learning techniques. The dataset used in this research included 3264 T1-weighted contrast-enhanced MRI images containing 926 glioma images, 937 meningioma images, 901 pituitary images and 500 non tumorous brain images. In this paper, a 2D CNN model is used with a total of 28 layers and 243,924 parameters. Another model used is Convolutional auto-encoder neural network. The accuracy of 2D CNN is 93.44%.⁸

Hence, we conclude that the accuracy of the above referenced papers ranges from 85% to 99.84% with the model's complexity varying significantly, reaching up to 23.8 million parameters. Considering all these results and conclusions, our study gives a promising accuracy of 98.24% with a model having parameters below 1 million decreasing the requirement of computational resources.

2. Proposed Model

2.1 Overview

Our proposed method begins with image preprocessing which include steps like image resizing, normalization and augmentation.⁹⁸ After preprocessing, feature extraction and reduction are performed using convolutional and pooling layers.¹² The processed and reduced features are then used to train the 2D CNN model.⁸ Subsequently, the model classifies the images as either having a tumor or not. The images identified as having brain tumor the model further classifies it into 4 types of brain tumor: glioma, pituitary and meningioma.

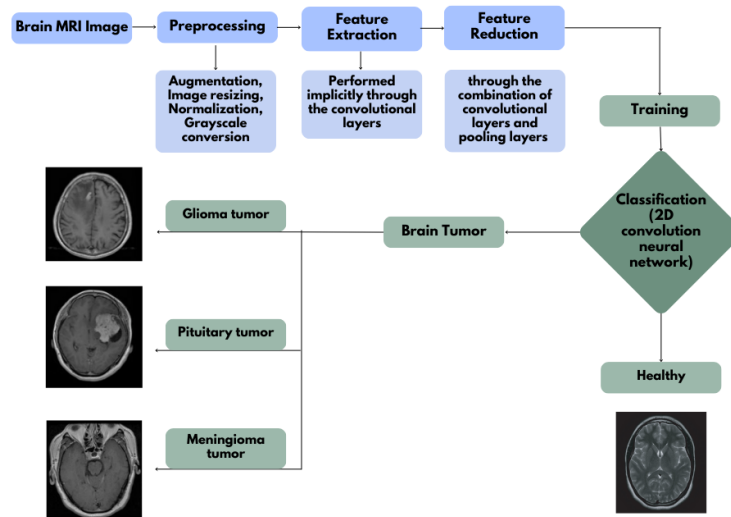
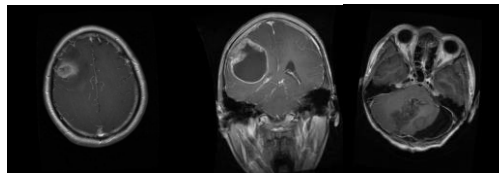


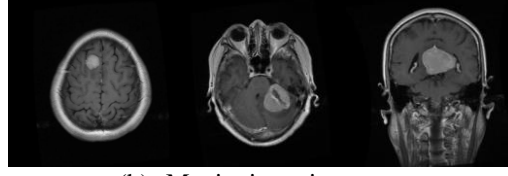
Fig 1. Flowchart depicting the steps involved in detecting brain tumors.

2.2 Dataset

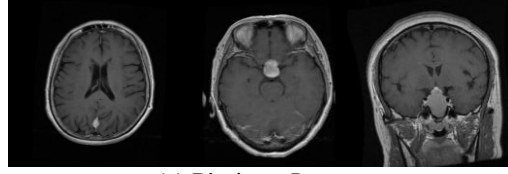
The dataset is sourced from Kaggle and is a diverse collection of 7023 medical images in JPG (Joint Photographic Group). This dataset is labeled into classes: glioma (1621 images), meningioma (1645 images), pituitary (1757 images), and non-tumor (2000 images). The dataset is a fusion of three different sources: figshare, SARTAJ, and Br35H. The non-tumor class images were obtained from the Br35H dataset, however the SARTAJ dataset presented a challenge, as the images from Glioma class are not categorized accurately, which causes an impact on the overall integrity of the dataset. Hence the images on the figshare site are preferred instead.



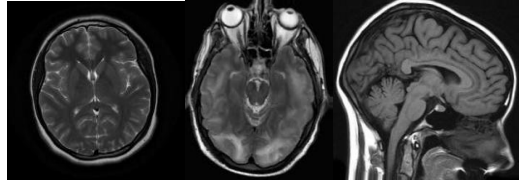
(a) Glioma images



(b) Meningioma images



(c) Pituitary Images



(d) Non-Tumor Images

2.3 Preprocessing

Data augmentation

Using this technique, a new version of the dataset is created to increase the size and diversity of images, and various transformations are made. To our dataset, rotations are applied to a range of 10 degrees; height-shifts are introduced with a range of 0.1 which is maximum of 10% of the height; images are flipped horizontally; and a “fill_mode” is set to the nearest which makes sure that any if any area of the images that become empty after these transformations, they are filled with the nearest pixel values. These techniques then improve the model robustness and prevent overfitting.¹³

Resize

Image resizing refers to the process of adjusting the dimensions or scale of an image. It involves changing the number of pixels used to represent the image, either increasing or decreasing its size. To maintain the consistency across the dataset, the images are resized to a uniform size. By doing this, every image would be processed in the same way.¹⁴

Normalization

Normalization is used to make sure that the pixel values are consistent and easy to analyze. Adjusting the pixel intensities to a particular range is important because this helps us to accurately interpret the image features. The typical formula for normalization transforms the original pixel values (r) to normalize values (s) using:

$$s = (r - \text{Min Pixel Value}) / (\text{Max Pixel Value} - \text{Min Pixel Value}) \quad (1)$$

In equation (1), we figure out the Min and Max Pixel Values from the entire set of images. Normalization not only deals with variations in image intensity but also sets up a standardized scale. Applying normalization to MRI brain tumor images significantly improves image quality and ensures trustworthy results in the field of medical image processing.¹⁵

2.4 Algorithm

The dataset used in this study consisted of MRI images in different sizes. To bring consistency in the dataset and to increase the speed of the processing we resized each image to 120*120. Normalization was applied on each image

and was augmented using the augmentation techniques discussed above. We augmented each image 4 times resulting in a total of 28,092. The dataset was splitted into training data (22097) and testing data (5242) i.e 80% training data and 20% testing data. Further training data was splitted into training data (18363) and validation data (4544) i.e 80% training data and 20% validation data.¹³

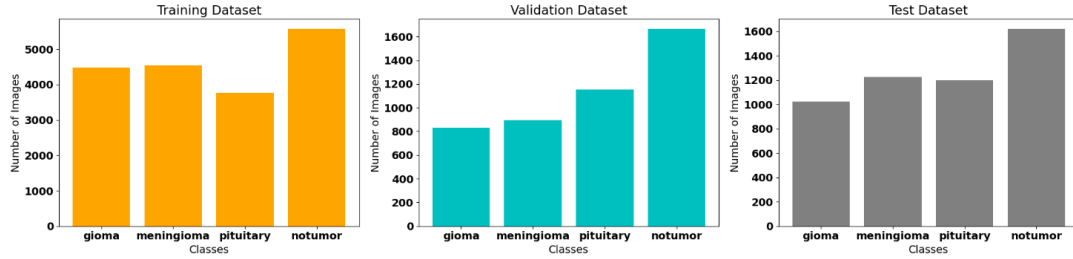


Fig 2. Split of dataset into training, validation and testing

The proposed model has several layers including convolutional layers, max pooling layers, dropout, Flatten and dense. A total of 18 layers were used in this architecture as shown in Figure 2, starting with a convolutional layer having 16 filters each of size 3*3. The padding used in each convolutional layer of this architecture was “same” along with ReLU activation function. First layer was followed by a max pooling layer of size 2*2 and each max pooling layer had a striding of 2*2. Another convolutional layer was used but with 32 filters instead of 16 filters. It was followed by a batch normalization layer (0.5) and a max pooling layer of size 2*2. Next two layers were convolutional layers having 64 filters each. These two layers were followed by another max pooling layer of size 2*2. Two more convolutional layers with filter size of 128 were used and were followed by another max pooling layer. Dropout layer was used after every max pooling layer except for the second max pooling layer in order to prevent overfitting⁶

A flatten layer was used to convert the multi- dimensional output given by the convolutional and max pooling layers into a single dimensional array. Finally a dense layer was used with 256 units so that the learning capacity of the model is balanced and it could learn complex patterns while preventing overfitting. Dense layer was followed by a dropout layer with a 0.5 dropout rate meaning that half of the layers will be turned off during training iteration. Eventually another Dense layer with 4 units along with sigmoid activation function was used signifying the 4 different classes in our dataset.⁸

To increase the efficiency of the model, Adam was used as an optimization function and different values including 0.1, 0.01, 0.001, 0.002, 0.0001 were used but 0.0001 with a decay rate of 0.77 per epoch⁸. For the training to complete, 100 epochs were used and a batch size of 64 along with it. Seed was set to 2680 which is a process where a fixed value is set for the random number generator, and it ensures reproducibility in the preprocessing steps¹⁶. In simple words, it means that the same sequence of random operations will be applied every time and it ensures the consistency.^{17, 8}

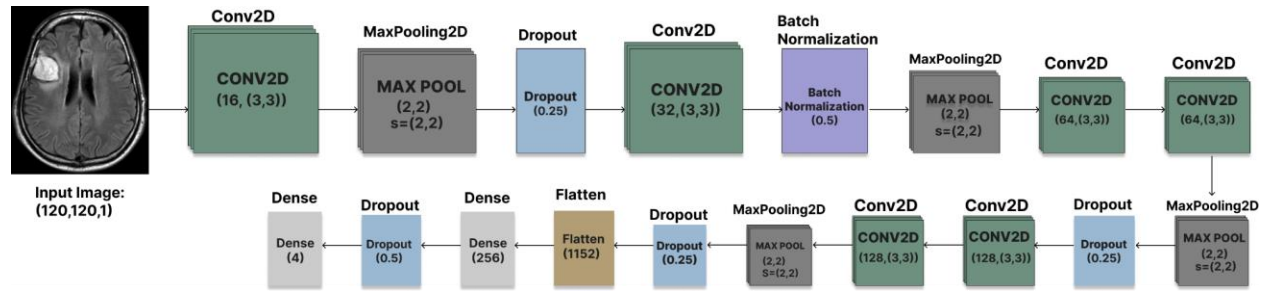


Fig. 2. Diagram illustrating the architecture of our proposed brain tumor detection model

A summary of parameters is shown in Table 1 from which we can conclude that our proposed model has total parameters of 578,248, making it lightweight in comparison with the other proposed methods mentioned in the literature review.

Table 1. Layers Utilized in the Proposed Brain Tumor Detection Model

Model: “sequential”		
Layer (type)	Output Shape	Param (#)
conv2d (Conv2D)	(None, 120, 120, 16)	448
max_pooling2d (MaxPooling2D)	(None, 60, 60, 16)	0
dropout (Dropout)	(None, 60, 60, 16)	0
conv2d_1 (Conv2D)	(None, 60, 60, 32)	4640
batch_normalization (BatchNormalization)	(None, 60, 60, 32)	128
max_pooling2d_1 (MaxPooling2D)	(None, 30, 30, 32)	0
conv2d_2 (Conv2D)	(None, 15, 15, 64)	18496
conv2d_3 (Conv2D)	(None, 15, 15, 64)	36928
max_pooling2d_2 (MaxPooling2D)	(None, 7, 7, 64)	0
dropout_1 (Dropout)	(None, 7, 7, 64)	0
conv2d_4 (Conv2D)	(None, 7, 7, 128)	73856
conv2d_5 (Conv2D)	(None, 7, 7, 128)	147584
max_pooling2d_3 (MaxPooling2D)	(None, 3, 3, 128)	0
dropout_2 (Dropout)	(None, 3, 3, 128)	0
flatten (Flatten)	(None, 1152)	0
dense (Dense)	(None, 256)	295168
dropout_2 (Dropout)	(None, 256)	0
dense_1 (Dense)	(None, 4)	1028
Total params: 578276 (2.21MB)		
Trainable params: 578212 (2.21 MB)		
Non-trainable params: 64 (256.00 Byte)		

2.5 Evaluation Metrics

Precision

Precision is one indicator of a machine learning model's performance, the quality of a positive prediction made by the model. Precision is defined as the ratio of correctly classified positive samples (True Positive) to a total number of classified positive samples (either correctly or incorrectly) as shown in equation (2).¹⁸

$$Precision = TP / (TP + FP) \quad (2)$$

Recall

The recall measures the model's ability to detect positive samples. It is calculated as the ratio between the numbers of Positive samples correctly classified as Positive to the total number of Positive samples as shown in equation (3).¹⁸

$$Recall = TP / (TP + FN) \quad (3)$$

F-measure score

The F-measure score is a metric used to evaluate the accuracy of a classification model. It is calculated by taking the harmonic mean of precision and recall as shown in equation (4). It gives equal weight to both precision and recall, making it a useful metric for evaluating models when both false positives and false negatives are important. It ranges from 0 to 1, with higher values indicating better performance.¹⁸

$$F1 \text{ Score} = 2 / (1/Precision + 1/Recall) \quad (4)$$

Or

$$F1 \text{ Score} = 2 * Precision * Recall / (Precision + Recall)$$

3. Results and Discussion

The main objective of this study is to develop a CNN model to bring ease to the medical field so that the professionals can accurately detect and classify the brain tumors using MRI scans. The model was trained over 100 epochs each taking approximately 28 seconds/step, and achieved a total of 0.0096 training loss and training accuracy of 0.9967 which means that the model is well-fitted to the training data.⁸ The validation accuracy and loss is 0.9957 and 0.0150 respectively, indicating that the model is performing well on both training and validation data.⁹

Finally, our test model shows promising results of 0.9820 accuracy and 0.0906 loss on the test data. Table 2 gives key performance metrics for a classification model across different datasets: training, validation, and testing.¹⁰

Table 2. Results obtained using the proposed CNN model

	Accuracy	Loss
Training Data	0.9967	0.0096
Validation Data	0.9947	0.0150
Testing Data	0.9820	0.0906

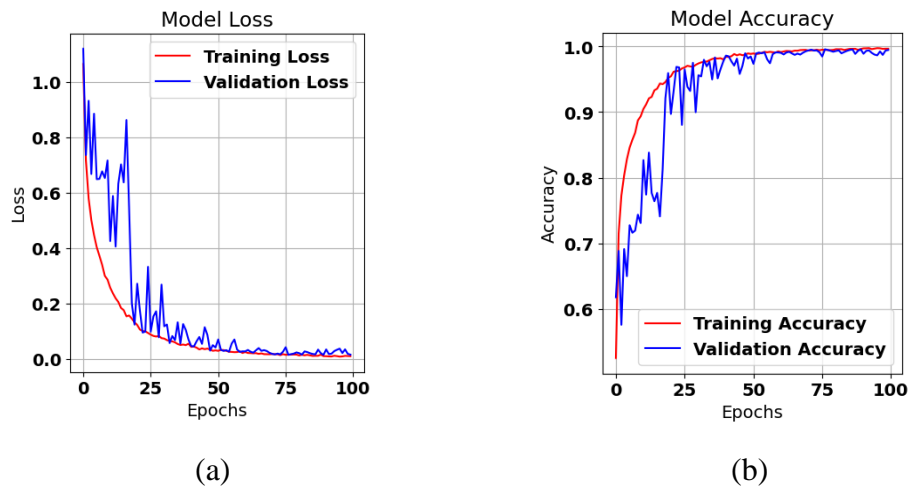
The Table 3 shows the precision, recall and f- measure score of test data each being 98.24%, 98.18 and 98.18%.

Table 3. Precision, Recall and F1 Score of Training, Validation and Testing Data

	Precision	Recall	F1-score
Training Data	0.9968	0.9967	0.9965
Validation Data	0.9949	0.9945	0.9946
Testing Data	0.9824	0.9818	0.9818

In this study, we plotted an epochs vs Model Loss and Model Accuracy graph, where x-axis represents Model Loss and Model Accuracy in the respective graphs. In Fig. 3, we can see two lines: red for training loss and blue for validation loss. The left plot shows the model's loss over the epoch where the training loss was initially high, indicating a poor fit to the training data and then decreased rapidly within the first 20 epochs which means that the model eventually started learning quickly and fit the training data well. After approximately 20 epochs, the training loss stabilizes and remains low, meaning that the model has come to a point with a good fit to the data. Similarly, the validation loss was high at the beginning but then rapidly decreased along with the training loss, and finally became stable. However, the validation loss shows more fluctuation in comparison to the training loss, indicating that even if the model was performing well on the unseen data, there were still some variabilities in the performance.

The right plot shows the model's accuracy over the epochs. Here the training accuracy starts low which means that the model's performance was poor in the beginning, but then it increases rapidly within the first 20 epochs. Finally the training accuracy plateaus near 1.0, which means that the model has now learned to classify the training data really well. Similar to training accuracy, the validation accuracy also starts low and increases rapidly along with the training accuracy, and finally stabilizes and stays high along with showing more fluctuations than the training accuracy. Even with these fluctuations, the model is able to generalize the unseen data along with minor variabilities. Overall, the model shows a steady improvement in both loss and accuracy which means that the model learns effectively and it is fit to the training dataset. The validation matrix also improves with some variabilities compared to the training metrics.

**Fig. 3.** Training and validation analysis over 100 epochs. (a) Loss v/s Epochs graph (b) Accuracy v/s Epochs graph

The confusion matrix is useful in breaking down the performance of the model in terms of: True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). These terminologies help us calculate precision, recall, and F1-score as: Precision - equation 2, Recall - equation 3, and F1-score - equation 4.¹⁰⁹ The matrix in Fig. 4 indicates an accurate model with very few errors in both false positives and false negatives, indicating the model's effectiveness in diagnosing brain tumors based on MRI images.

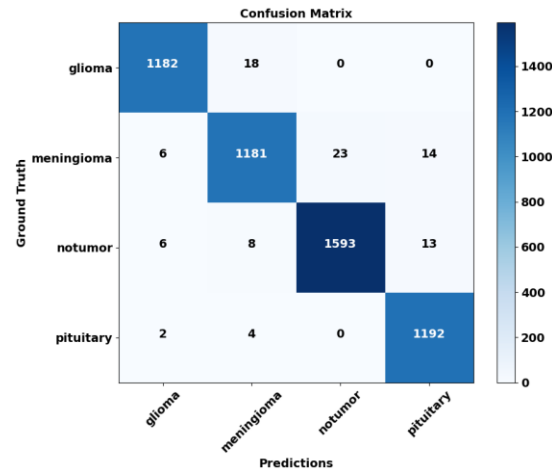


Fig. 4. Confusion matrix analysis representing TP, TN, FP, FN

The developed CNN model gives a high overall testing accuracy of 98.20% with a loss of 0.0906, with key performance parameters including precision, recall, and F1-score, each being 98.24%, 98.18% and 98.18%. These parameters validate the effectiveness of the model in detecting and classifying the brain tumor accurately. The study makes a detailed analysis through training and validation metrics, and the confusion matrix. This highlights that the model's performance is robust with a very few errors in FP and FN.

The CNN model is lightweight and shows outstanding accuracy, while remarkably reducing the need for extensive computational resources. This enables the model to run effectively on ordinary hardware or with the limited memory, making the model valuable for medical professionals as compared to the other resourceful models.

4. Conclusion

Our proposed model, a lightweight Convolution Neural Network (CNN), using MRI scans, successfully tackles the problem of brain tumor classification. The model's architecture, consisting of 16 layers including convolution, max-pooling, dropout, and dense layer, was carefully designed to ensure high performance. By applying preprocessing steps such as image resizing, normalization, and augmentation, we ensured the dataset was prepared for training. The model was trained on a diverse dataset from Kaggle, including 7023 images from four classes: glioma, meningioma, pituitary, and non-tumor.

With parameters less than 1 million, our model achieved an accuracy of 98.20%. This performance is better than many state-of-art models, which range from 85% to 99.84% accuracy, but often involve significantly higher complexity, with some models reaching up to 23.8 million parameters. This trade-off between high accuracy and low complexity makes our model suitable for real-world medical diagnostics. Our model's effectiveness is further demonstrated by its precision, recall, and F1-score, all exceeding 98%, indicating minimal errors in classification. The model's confusion matrix also reflects high accuracy by distinguishing between 3 types of tumor (glioma, meningioma, and pituitary) and healthy (non-tumor) cases.

The study by N. Remzan(2023) utilized a CNN model with 1.5 million parameters, achieving an accuracy of 95.65%. Compared to our model's 98.20% accuracy, our model not only outperforms in accuracy but also uses fewer

parameters, enhancing its efficiency and practicality. The study by Beyza Nur TÜZÜN (2023) implemented an EfficientNet b0 model with 23.8 million parameters, achieving an accuracy of 99.54%. Although this model has higher accuracy than ours, it comes at the cost of increased complexity. Our model with fewer than 1 million parameters, offers much lower complexity. Hence, making it a valuable tool for medical professionals, by making quicker and accurate brain tumor diagnosis, resulting in potentially improving patient's health through timely and appropriate treatment.

5. References

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