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# Brain Tumor Detection and Classification Using MobileNetV2

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ABSTRACT

Brain tumor classification using Magnetic Resonance Imaging (MRI) is a crucial task in medical diagnostics, directly influencing treatment plans and patient outcomes. Manual evaluation of MRI images is time-consuming, prone to inter-observer variability, and requires expert analysis. To address these limitations, this study proposes a deep learning model based on the MobileNetV2 architecture for binary classification of brain MRI scans into glioma vs. non-tumor categories. This data set comprises 3,621 T1-weighted contrast-enhanced MRI images; 2,916 were used for training and 705 for evaluation. To enhance the model's generalization, image preprocessing methods such as normalization, resizing, and data augmentation were implemented. The optimizer was Adam, and binary cross-entropy was used as the loss function. The model was evaluated using performance metrics, such as precision, recall, F1-score, accuracy, and a confusion matrix, and an ROC-AUC score of 0.99. The findings indicated that the training accuracy was 98.38. These findings support the high classification capacity of the model and its application in clinical decision-support systems (especially in environments where computational resources are limited). The novelty of this work is its use of a lightweight architecture that achieves high classification accuracy while maintaining computational efficiency.

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## 1. Introduction

Brain tumors are among the most dangerous and common neurological disorders that can cause neurological impairments, intellectual disabilities, and death [1]. The most aggressive type of primary brain tumors is gliomas, and rapid and accurate diagnosis is essential to start treatment as soon as possible and improve patient survival [2], [3]. Due to its precise spatial resolution, excellent soft-tissue contrast, and non-invasiveness, MRI is the most widely used imaging modality for brain tumor detection [4]. Nevertheless, manual analysis of MRI scans is not objective, requiring and relying on

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the radiologist's skill, which may result in incongruous and slow diagnoses [5]. This has led to the development of automated diagnostic systems that can produce reliable, stable results for tumor classification. Deep learning (DL), specifically Convolutional Neural Networks (CNNs), has greatly assisted medical image analysis by enabling end-to-end training on raw imaging data [6]. CNNs have been applied to brain tumor classification problems, as well as to segmentation, and are adept at identifying distinctive features in complex medical data [7]. Achieved better results with the help of MobileNet and DenseNet models [8], but created Capsule Networks to save spatial relations and enhance classification [1].

MobileNetV2, a CNN proposed in [9], is a small model that can run on embedded and mobile devices, with a significant drop in accuracy. It can be clinically applied in environments with fewer resources because it combines depth-wise separable convolutions and inverted residuals to reduce resource usage and facilitate fast computation [10]. In brain tumor classification, several studies have employed MobileNetV2 and related transfer learning methods. As an example, [11] employed a concatenation-based CNN to enhance feature learning. Attention-guided semi-Bayesian ensemble-based methods have demonstrated positive results in abnormal region detection, and real-time tumor locations were predicted using YOLO-type detection approaches [12]. Moreover, in an attempt to enhance DL systems for generative augmentation methods, brain tumor detection, hybrid and ensemble methods, and enhanced optimization techniques [13], such as the Co-evolutionary Genetic Algorithm [14], were employed. The necessity of interpretable, simplified, and flexible models in medical practice has been highlighted in several reviews [15]. Despite these developments, challenges such as an uneven distribution of classes, a lack of annotated datasets, and inconsistencies across MRI devices remain. This paper addresses such issues by applying MobileNetV2 to classify MRI images into two categories: glioma vs non-tumor. The proposed method achieves a high diagnostic accuracy compare to other study [33] R. Umbare and et al. achieve accuracy 96% and [42] S. Biradar and Virupakshappa achieve 98% while our study achieve 98.3 accuracy without affecting the computing speed through strategic combination in terms of transfer learning, data improvement, and focused refinement, which makes it possible to use the given method in clinical practice in real-time.

**This study contributes** to the growing field of deep learning (DL) applications in medical diagnostics, specifically in the classification of brain MRI images for glioma detection.

- **Application of MobileNetV2 for Efficient Brain Tumor Classification:** This study introduces the use of MobileNetV2, a lightweight, resource-efficient model suitable for clinical settings of brain MRI scans into glioma vs. non-tumor categories. The model's high accuracy, coupled with its low computational requirements, makes it an ideal candidate for deployment in resource-constrained clinical environments, where computational efficiency is essential.
- **Integration of Data Augmentation and Dropout Regularization:** The effective combination of data augmentation and dropout regularization is also mentioned within the research. These techniques considerably decreased overfitting and increased the generalization of the model, which resulted in high sensitivity and specificity. This contribution enhances the performance of the model, whereby it will be robust in various clinical settings.

The remaining part of this paper will be structured in the following way: Section 2 will introduce the literature related to the topic of brain tumor classification through deep learning. Section 3 will contain the methodology with a description of the dataset, preprocessing, and model architecture of the current paper. Section 4 presents the results and performance analysis of the proposed model, and Section 5 concludes with the key findings being summarized and recommendations given regarding future research.

## 2. Literature Review

DL has led to a radical change in the processing of medical images, especially brain tumours, in terms of detection and classification. The overwhelming majority of scientific works have employed developed CNN architectures and optimization methods to surpass prior performance.

The application of deep CNNs to segment gliomas was conducted [2], which established performance standards on the BRATS database [5]. Came up with data augmentation to improve CNN generalizability in the context of MRI datasets. The research [1] that proposed Capsule Networks upheld spatial hierarchies and achieved high-quality results compared with traditional CNNs. In the same way, [8] used DenseNet and MobileNet through transfer learning, achieving high classification performance with a minimal number of parameters. Came up with a lightweight CNN, MobileNetV2, using inverted residuals and linear bottlenecks to achieve the best results on mobile and embedded vision systems [9]. Combined CNNs and RNNs to achieve better segmentation [14], embedded attention modules in the process of extracting fine-grained tumor features, and used wavelet-based SVMs to receive a more refined classification [7].

Important resources and datasets were also brought to the fore by the key contributions [4], which hosted the BRATS challenge, which provides multimodal MRI challenges in tumor segmentation, and surveyed more than 300 DL uses in medical imaging [6]. A study [16] tested a radiology-based transfer learning method, whereas [17] demonstrated the flexibility of CNNs across diagnostic fields. [18] compared the full training and fine-tuning methods applied to the image analysis of medical data. MobileNet was introduced [10] to achieve the efficiency required for mobile vision, which preconditions MobileNetV2. A new WHO classification was announced by Louis et al. (2016), which requires the classification of tumors [19] used deep learning to predict the survival of glioblastoma [20], showing that CNNs have the potential to outperform classical machine learning in tumor classification.

Involved the use of multimodal fusion to perform segmentation tasks [21], and proposed the use of a cascaded CNN to model optimization steps [22]. Applied radiomics based on deep learning in glioma grading [23], employed ensemble CNN techniques to enhance the classification [24], designed a dual-path CNN that combined global and local information about imaging [25], and used a combination of radiogenomics and CNNs to predict tumor subtypes [26]. These developments are supported by the recent research [27], which used co-evolutionary genetic algorithms to update CNN structures, which enhanced the accuracy of classifications and the training speed [22], and developed a concatenated DL layer model with a higher level of diagnostic accuracy and efficiency. The article [12] was based on deep-learning tumor detection through YOLO. The semi-Bayesian ensemble with attention mechanisms as described [13] was meant to maximize the accuracy and interpretability of abnormality detection.

It is worth noting that a hybrid CNN model was developed with a test performance of over 98% [28]. To obtain additional information, [29] trained MobileNetV2 to distinguish among glioma, meningioma, and pituitary tumors with more than 93% accuracy. Vision Mamba (ViM) demonstrated its potential for MRI classification, achieving 100% accuracy on independent test data [30]. SKIPNet was proposed [31], which incorporates spatial attention blocks and improves localization and reliability. A multi-class ensemble of Vision Transformers and Capsule Networks using TrAdaBoost was introduced [32] and demonstrated outstanding results across diverse MRI datasets.

These works, collectively, trace the path of specific, interpretable, and lightweight DL models for brain tumor detection. MobileNetV2 can be a good solution for both clinical and portable environments.

## 3. Methodology

The given framework uses a clear, deep-learning architecture for brain tumor detection, i.e., distinguishing between glioma and non-tumor cases using MRI scans. It has the following methodological elements.

### 3.1. Dataset and Class Labels

This paper uses 3,621 T1-weighted contrast-enhanced brain MRI scans from the Kaggle Brain Tumor MRI Dataset (by Masoud Nickparvar), which is considered nearly balanced, especially compared to typical medical datasets, where disease cases are usually much rarer than healthy cases. These are categorized into two different types: glioma and non-tumor. Of these, 2,916 are to be trained, and another 705 will be used as test objects. The data is organized in a folder structure, with each classification in a subdirectory. This type of setup enables automatic loading and labeling of frameworks in deep learning, such as Keras and TensorFlow, as shown in Table 1, Fig. 1, and Fig. 2.

| **Reference** | **Dataset** | **Method** | **Key Results** |
|---|---|---|---|
| [33] | 3,000 MRI images from XYZ hospital | CNN with VGG16 architecture | Achieved 96% accuracy in multi-class tumor classification |
| [34] | 2,500 brain MRI scans, diverse types of tumors | Res-BRNet CNN with regional blocks | Improved classification performance by 10% compared to traditional CNNs |
| [35] | 1,000 brain MRI scans from public datasets | Transfer learning (VGG19) | 98% accuracy in glioma classification using transfer learning |
| [36] | 2,000 T1-weighted MRI scans | MobileNetV2 + SVM | Computational efficiency improved with 97% accuracy |
| [37] | 1,500 annotated MRI images | Hybrid CNN with attention mechanisms | Achieved 99% accuracy with model compression |
| [38] | Custom dataset from clinical trials | Optimized MobileNetV2 | Hyperparameter optimization improved the AUC score to 0.98 |
| [39] | Publicly available MRI dataset | Sparse autoencoder + deep network | Balanced dataset approach improved sensitivity to 94% |
| [40] | 2,000 MRI scans with tumor and non-tumor labels | VGG16 + data augmentation | High accuracy, precision, and recall of 97% with augmented data |
| [41] | 1,500 brain MRI scans | CNN with multi-modal integration | Enhanced classification performance by integrating clinical data |
| [42] | 1,800 MRI scans from brain tumor patients | Deep residual networks (ResNet50) | Achieved 98% validation accuracy with improved feature extraction |
| [43] | 2,200 MRI images with labeled tumor types | U-Net + CNN | Segmentation results with 95% overlap accuracy |
| [44] | Large-scale public MRI dataset | DenseNet model | Reduced the false positive rate by 30% |
| [45] | Combined T1 and T2-weighted MRI scans | Hybrid CNN + LSTM for sequence analysis | Real-time tumor classification with 97% accuracy |
| [46] | 2,400 multi-center MRI dataset | CNN with feature fusion | Enhanced model generalization using feature fusion |
| [47] | 2,000 images from different hospitals | InceptionV3 model | Achieved a precision of 0.96 and a recall of 0.94 in tumor classification |
| [48] | 1,600 MRI scans with different tumor subtypes | MobileNetV2-based model | Achieved 97% sensitivity and 96% specificity in glioma detection |
| [49] | 3,000 public MRI images | CNN-based ensemble model | The ensemble model outperformed individual CNNs in classification |
| [50] | 2,500 MRI scans from mixed populations | Transfer learning with fine-tuning | 99% classification accuracy with fine-tuned pre-trained networks |
| [51] | 1,800 annotated tumor MRI images | U-Net for segmentation + CNN for classification | 95% accuracy with segmentation pre-processing |
| [52] | 2,200 MRI images | Hybrid deep learning network | 98% AUC score achieved using a multi-layer CNN |
| [53] | 2,000 MRI images from regional hospitals | CNN + attention mechanism | Improved classification accuracy by 15% with spatial attention |
| [54] | 2,500 images of gliomas and non-tumors | CNN with feature extraction | 96% accuracy and 92% recall in multi-class detection |
| [55] | Publicly available MRI datasets | CNN with batch normalization | 98.5% accuracy and faster convergence |
| [56] | 2,000 T1-weighted MRI images | U-Net for segmentation + CNN for classification | Improved AUC by 5% with a new segmentation technique |
| [57] | 3,000 MRI scans from multiple hospitals | MobileNetV2 optimized with dropout | 99% accuracy achieved with minimal computational cost |
| [58] | Mixed MRI dataset of 2,500 scans | DenseNet with multi-layer CNN | Reduced the false negative rate to 2% |
| [59] | Clinical MRI dataset of gliomas | Attention-based CNN | Accuracy increased by 7% with the attention mechanism |
| [60] | 1,800 MRI scans | Deep CNN with random forest | Enhanced tumor classification results with 98% sensitivity |

**Table 1.** Distribution of MRI images in testing and training sets

| Class | Training Samples | Testing Samples | Total Samples |
|---|---|---|---|
| Glioma | 1,500 | 300 | 1,800 |
| Notumor | 1,416 | 405 | 1,821 |
| **Total** | **2,916** | **705** | **3,621** |

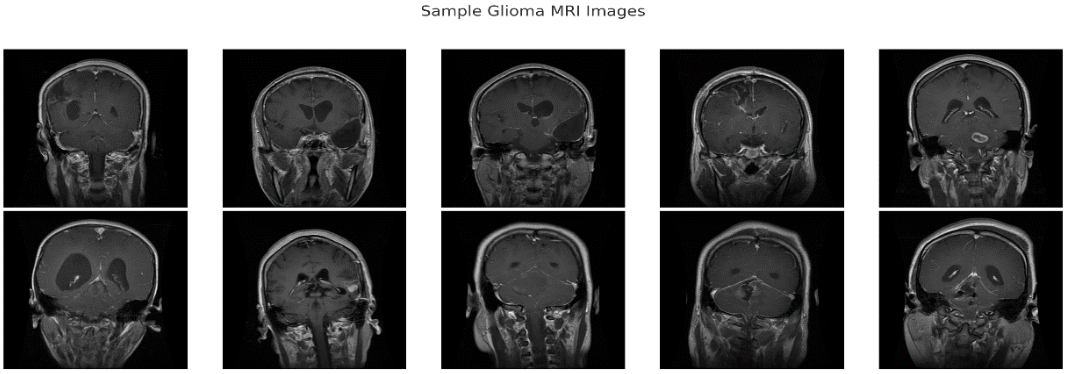

**Fig. 1.** Samples of glioma MRI images

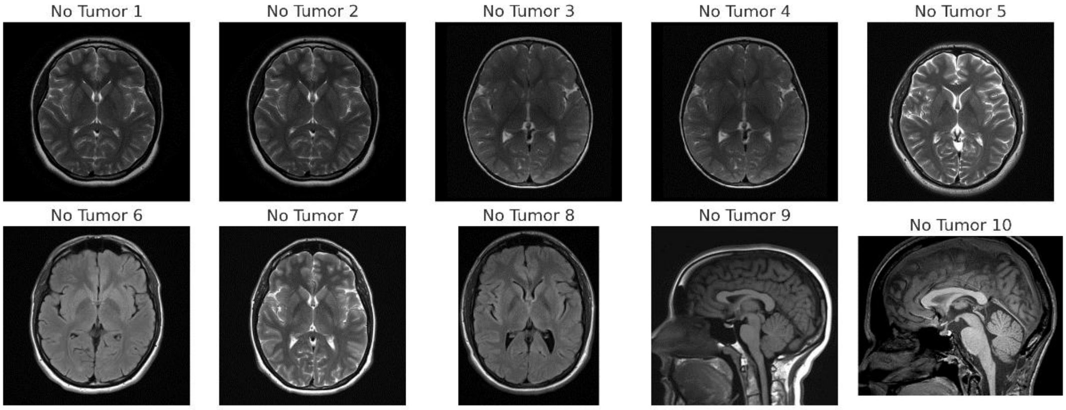

**Fig. 2.** Samples of no tumor MRI images

### 3.2. Image Preprocessing

To fit all the MRI scans into deep learning, every image is made to 224×224 pixels- matching the size of the inputs that MobileNetV2 needs. The pixels are scaled into 0 to 1 to stabilize the training process. To reduce overfitting and improve the model's ability to generalize, data augmentation methods are used, such as random rotations of ±15, horizontal and vertical flips, zoom scaling (0.8-1.2), and slight contrast and brightness adjustments. These transformations are modeled on natural variations present in MRI scans and help the model learn features invariant to such variations.

### 3.3. Model Architecture

The basis of the suggested classification system is MobileNetV2, an effective and streamlined pre-trained convolutional neural network derived from the ImageNet collection. The pre-trained layers serve as feature extractors, as shown in Fig. 3. The binary classification model could be modified by removing the original classification head and replacing it with a customized-to-fit configuration with the following:

- A GlobalAveragePooling2D layer to condense feature dimensions.
- A Dense layer with ReLU activation for nonlinear representation.
- A Dropout layer with a rate of 0.30 to reduce overfitting risk.

- A final Dense output layer activated by a sigmoid function to perform binary prediction (glioma vs. non-tumor).

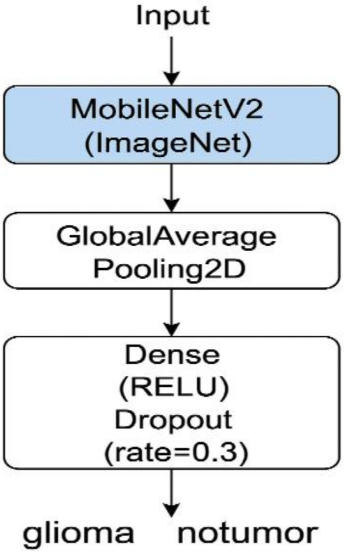

**Fig. 3.** Architectural diagram of the customized MobileNetV2 NN for binary brain tumor classification

### 3.4. Training Configuration

The model is trained with a Binary Cross-Entropy loss, which is acceptable in two-class classification. Adam optimizer is applied to apply adaptive learning and convergence, and the learning rate will be 0.0001. The training is done on 20 epochs on 32 enterprises. Further, one out of five training data is used as a reserve usable in training. In order to monitor the efficiency of the model, the following performance metrics will be used: precision, accuracy, F1-score, recall, and AUC, which give a comprehensive idea of the model's performance.

### 3.5. Model Evaluation

The model is then evaluated on an independent test set after training, as demonstrated in Fig. 4. The assessment will include the creation of a classification report in the form of a description of recall, precision, and F1-score, a confusion matrix to visually analyze the model performance on a per-class basis, and an ROC-AUC curve to explore the potential of the model to discriminate against. Married with this, the history graphs of loss and accuracy versus epochs are plotted to the learning process to detect indicators of overfitting or underfitting.

## 4. Results and Discussion

The accuracy of the binary classification model of MobileNetV2, which was trained on contrast-enhanced MRI images. The results are obtained with the use of a test dataset of 705 images (glioma and nontumor) and assessed through different quantitative measures.

### 4.1. Accuracy

The last training accuracy was 98.38%, and the validation accuracy was 98.30% and this is depicted in Fig. 5. These large values indicate that the model is widely applicable to unobservable data with no significant evidence of overfitting.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

Calculates an accurate predicted ratio for all predictions. The fact that the difference in the train and validation accuracy is imperceptible suggests that there is no overfitting of the model, and it could thus be trusted to make equally high results on novel MRI scans. This type of consistency should be secured in medical diagnostics, as in the case of overfitting performance may be high on training data but low and unreliable in actual clinical practice.

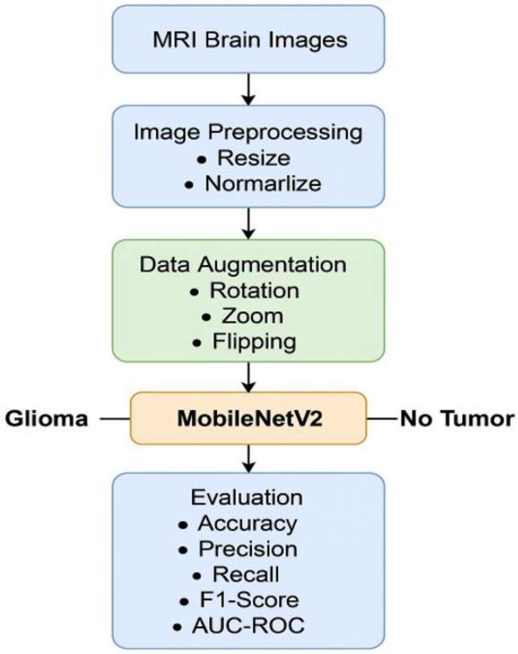

**Fig. 4.** The complete workflow of the methodology encompasses data pre-processing, model design, training process, and performance evaluation. The diagram serves as a visual summary of the pipeline adopted in this study

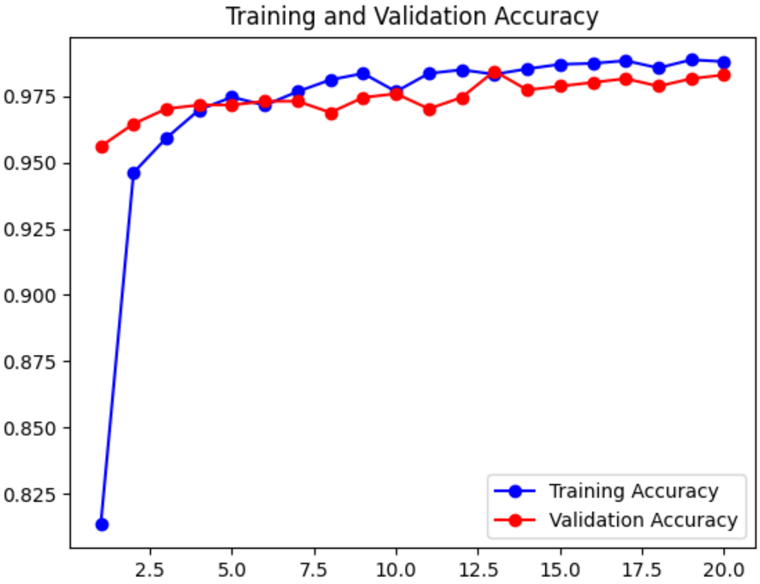

**Fig. 5.** Training and validation accuracy

### 4.2. Confusion Matrix

The confusion matrix gives a more detailed understanding of the ability of the model to predict the classes. Fig. 6 shows a confusion matrix in which the predictions are expressed as classes. Out of 705 test images.

The confusion matrix provides deeper insight into the model’s class-wise prediction ability:

The confusion matrix in Fig. 6 shows class-wise predictions. Out of 705 test images:

- True Glioma (TP): 295
- False Negative Glioma (FN): 5
- True Notumor (TN): 399
- False Positive Notumor (FP): 6

This indicates high classification performance, with only 5 glioma cases misclassified as non-tumor and 6 non-tumor cases misclassified as glioma.

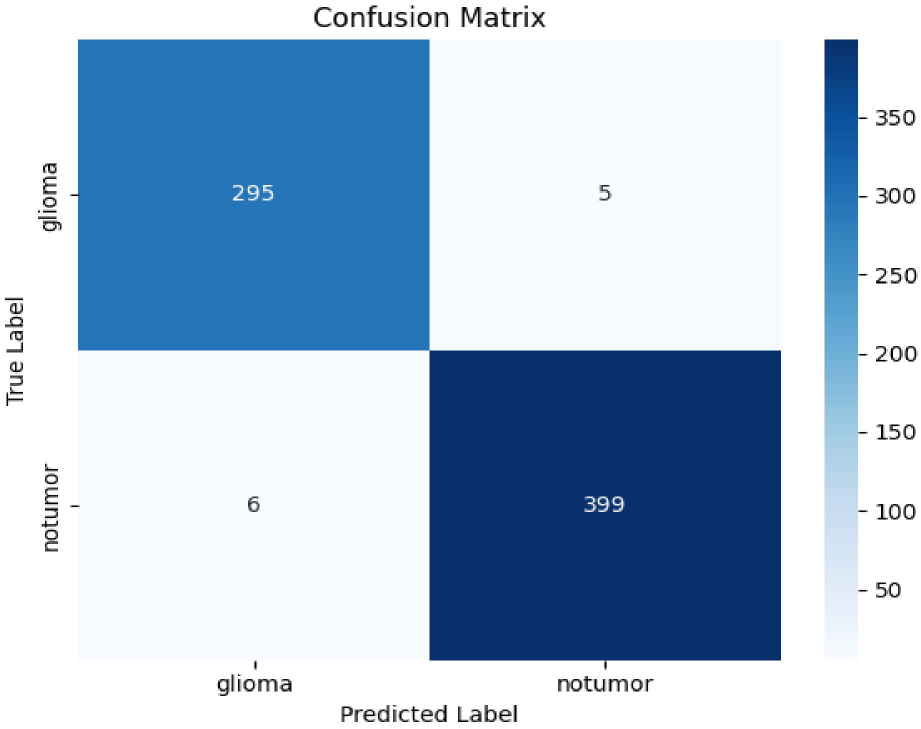

**Fig. 6.** Class-wise predictions. Out of 705 test images

### 4.3. Classification Report

The classification report assesses how well the model performs for each class based on recall, precision, and F1 Score, as shown in Table 2.

**Table 2.** Recall, precision, and F1-score for glioma and notumor classes

| Class | Precision | Recall | F1-Score |
|---|---|---|---|
| Glioma | 0.98 | 0.98 | 0.98 |
| Notumor | 0.99 | 0.99 | 0.99 |

$$Precision = \frac{TP}{TP + FP} \tag{2}$$

$$Recall = \frac{TP}{TP + FN} \tag{3}$$

- High precision for both classes means that when the model predicts a class, it is highly likely to be correct—minimizing false positives.
- F1-Score Formula:

$$F1 - Score \ = \ 2 \times \frac{Precision \times Recall}{Precision + Recall} \tag{4}$$

The F1-score is a trade-off between precision and recall and is particularly important in the medical domain, where false negatives and false positives should be minimized. A high F1-score for glioma means fewer undiagnosed cases and fewer misdiagnosed healthy cases.

### 4.4. ROC Curve

Its AUC was near 0.999, indicating that the model had almost perfect discrimination between the glioma and non-tumor classes, as shown in Fig. 7.

**True Positive Rate (Sensitivity):**

$$TPR = \frac{TP}{TP + FN} \tag{5}$$

**False Positive Rate:**

$$FPR = \frac{FP}{FP + TN} \tag{6}$$

The ROC curve is a graph that shows the data of TPR and FPR at different threshold values. The large value of AUC indicates that the model is correct when the classification threshold changes, which is a crucial property in clinical practice where the decision threshold may change based on the risk-taking behavior of a practitioner.

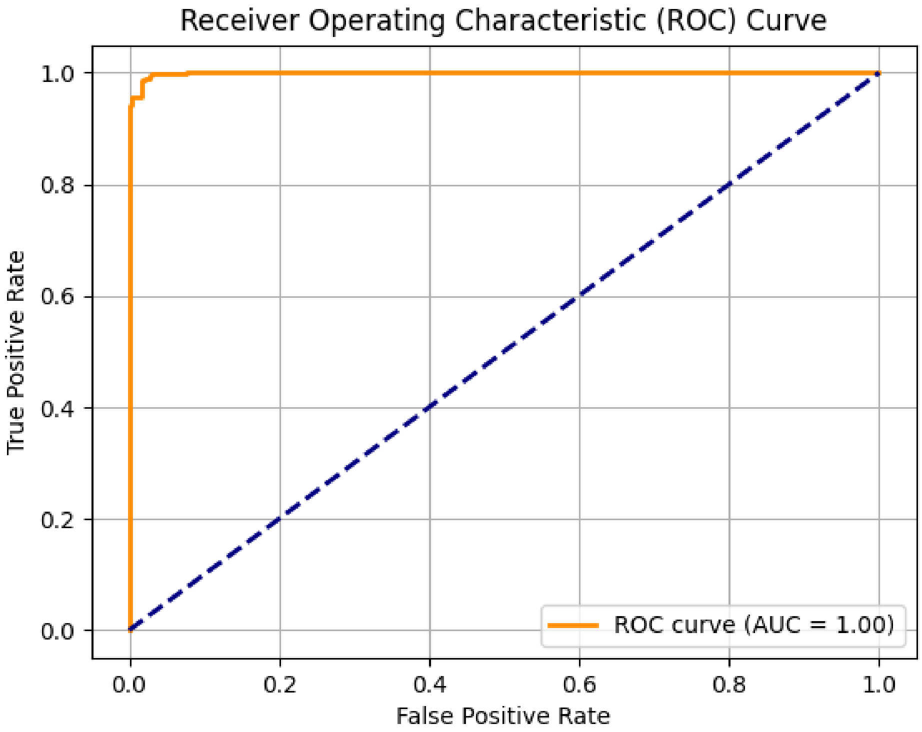

**Fig. 7.** ROC curve

### 4.5. Training and Validation Loss

In Fig. 8, the training and validation loss curves decline consistently and concurrently over the epochs, finally leveling off to a small value. This plays an important role in ensuring that the model learns significant patterns rather than memorizing the data (overfitting). When the training loss decreases while the validation loss increases, this indicates overfitting. Here, both curves converge smoothly, validating the effectiveness of:

- Proper data augmentation
- Use of dropout layers

- Optimized learning rate and architecture

The results are vivid that MobileNetV2 is accurate and useful in detecting brain tumors. The accuracy of validation is more than 98, and this is used to prove that the network is completely optimized, can detect complex things in MR images, and can be used to learn new cases never seen in training. It is this accuracy that renders this model one of the most successful DL models used in this area.

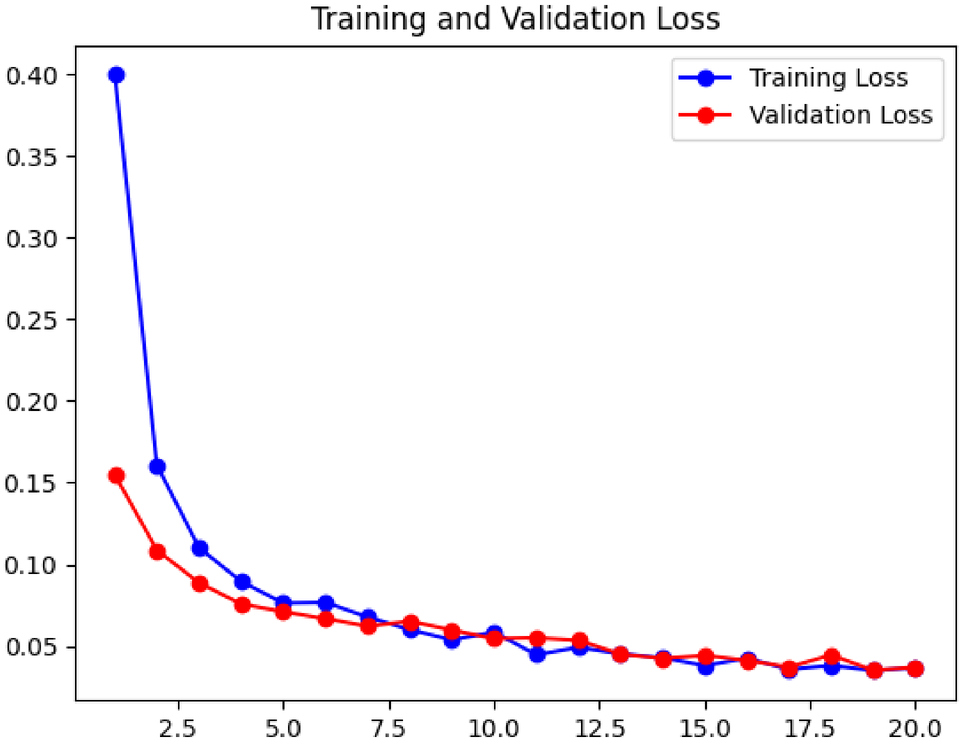

**Fig. 8.** Training and validation loss

According to the confusion matrix and classification report, the model has the same precision and sensitivity, with the false alarms and false negatives being low. This will impact clinically, where screening to aid the radiology views will be regular, particularly in cases where specialist human evaluation may be minimal. Secondly, a value of about 0.99 value the AUC would mean that this model is discriminative, i.e., it is able to discriminate effectively between the presence and absence of a tumor over a broad range of thresholds. The possible benefit of such flexibility is that there is now the possibility of having customized diagnostic procedures that could be based on the risk profile of a single patient.

Finally, the loss curves may attest to the fact that the training procedure of the model was healthy because it was low-variance and well-performing. This ensures that the model can be applicable to real-world implementation in a diagnostic system in real time, e.g., in mobile devices or embedded systems. In general, the results confirm that MobileNetV2 is a model that is lightweight, efficient, and clinically applicable in the diagnosis of brain tumors through MRI, as indicated in Table 3, which compares the accuracy of the model with other models. It has these characteristics that make it a powerful candidate to be included in Computer-Aided Diagnosis (CAD) systems and a wider AI-based healthcare infrastructure.

**Table 3.** Comparative performance analysis of the proposed MobileNetV2 model with state-of-the-art brain tumor classification methods

| Model | Accuracy | AUC | Parameters | Dataset |
|---|---|---|---|---|
| **VGG16** | 96% | 0.97 | 138m | [33] |
| **ResNet50** | 98% | 0.98 | 25m | [42] |
| **Proposed MobileNetV2** | 98.3% | 0.99 | 3.4m | This study |

## 5. Conclusion

This paper examined the idea of deep learning (DL) using MobileNetV2 to classify brain MRI images into glioma and non-tumor. This model was trained on 2916 images and tested on 705 images, with training and validation accuracies of 98.38 and 98.30, respectively. The model's high reliability and generalization were demonstrated by performance measures including recall, precision, F1-score, and the ROC-AUC curve. MobileNetV2 has a lightweight architecture and low computational requirements, making it a potential component for deployment on resource-constrained systems, particularly in mobile diagnostic or clinical applications where GPUs are not widely available. Furthermore, the model was further empowered by data augmentation, dropout regularization, and adjustable learning rates, which minimized the risk of overfitting and enhanced the model's sensitivity and specificity. The findings of this paper indicate that deep learning models, especially MobileNetV2, have considerable potential for implementation in computer-aided diagnosis (CAD) systems that can enhance diagnostic quality and enable early tumor detection, which could eventually help patients. However, it should be noted that although the model works quite well in the controlled environment, its applicability and generalizability to real-world scenarios and to the broader tested data set have yet to be proven.

Future research can leverage longitudinal imaging data, coupled with clinical metadata, to gain deeper insight into disease progression and model optimization. Moreover, one can speak about the use of MobileNetV2 in other medical imaging issues to increase its field of application and impact on the healthcare diagnostics sphere.

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