

Brain Tumor Detection using VGG16 CNN with Data Augmentation

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Abstract— Brain tumors represent a critical condition characterized by the abnormal growth of cells in specific brain regions, potentially forming life-threatening masses. Early diagnosis is crucial for prompt treatment, yet the laborious and time-consuming human analysis of magnetic resonance imaging (MRI) can cause significant delays. Recent advancements in deep learning have revolutionized healthcare and medical diagnostics, offering promising solutions to these challenges. Given the constraint of limited datasets, improving deep learning algorithms, particularly convolutional neural networks (CNNs), becomes essential. Data augmentation techniques effectively address dataset limitations, enabling the training of various CNN architectures such as VGG16, EfficientNetB0, MobileNetV2, and DenseNet121. These models are compared using evaluation metrics like accuracy and other standard classification metrics, with the VGG model demonstrating superior performance, achieving a notable 97% accuracy rate. This research underscores the potential of deep learning and CNNs in accelerating brain tumor identification from MRI images, emphasizing the advantages of different CNN architectures in medical applications.

Keywords— Machine Learning, CNN, Image Classification, Deep Learning, Brain Tumor Detection

I. INTRODUCTION

In the US, there were 89,158 new instances of primary brain and central nervous system tumors year between 2015 and 2019. The age-adjusted mortality rate was almost 24.25 per 100,000 individuals annually. Magnetic Resonance Imaging (MRI) is a crucial imaging technique in classifying brain tumors and plays a vital role in diagnosis and treatment planning. Magnetic Resonance Images is an essential imaging technique for classifying brain tumors. Of the cases, 63,889 were benign and 25,269 were malignant [1]. According to the National Brain Tumor Foundation (NBTF), emerging countries have seen a 300% increase in the incidence of brain tumor-related mortality over the past three decades [2]. Brain tumors grow quickly, their size doubles roughly every 25 days. The age of the patient and the type of brain tumor are two factors that can greatly affect the survival rates of people with malignant brain tumors [3].

In recent years, the utilization of magnetic resonance images (MRI) increased due to its high-resolution, multiplanar imaging, and non-invasive nature. Seeing the increasing number of cases, medical experts have claimed that it is difficult to keep detecting brain tumors in clinics. Better and more dependable procedures are therefore required, such as CAD [3, 4]. These CAD techniques have been helpful in various healthcare fields to distinguish between healthy tissues and non-healthy ones. The aim is to research and make a CNN model that could classify brain tumor images into positive and negative images utilizing data augmentation [5]. The goal is to evaluate and compare different CNN architectures that help improve the accuracy of classifying brain MRI images. This work provides profound insights into the possibilities of CNN and deep learning, and it is highly relevant in deep learning and medical image classification.

Research has demonstrated the efficacy of machine and deep learning methods, such as CNN, Adaptive Neuro-Fuzzy Interference Systems (ANFIS), and SVM, in precisely and efficiently categorizing brain tumors [6]. Feature Extraction methods such as wavelength transformation and statistical texture analysis are used to enhance the working of the classification models, improving the model's precision. The development of segmentation models mainly using CNN helped a lot in separating the tumor from the MRI which helps a lot in the treatment of the tumor. But issues with model optimization, computational resources, and the results' interpretability draw attention to the need for more study to overcome these shortcomings.

The focus is on bridging the gap in neurology and medical imaging by developing precise techniques for identifying brain tumors. The goal is to close gaps in the literature by creating a CNN model for brain MRI image classification using deep learning techniques. The efficacy of many CNN models, including VGG16, EfficientNetB0, MobileNetV2, and DenseNet121, in identifying brain tumors from MRI data was studied. Notably, VGG16, with an impressive accuracy score of 97.0%, emerged as the leader. Building on this important finding, the study aims to

understand the architecture of VGG16 further and explore the usefulness of data augmentation methods for improving brain tumor diagnosis. Overall, the study may provide medical professionals with a useful tool for precisely identifying brain tumors, streamlining clinical procedures, and enhancing patient outcomes while treating brain tumors.

The contribution of this work comes in three folds:

- a) The research uses deep learning and CNNs to identify brain tumors from MRI images, potentially speeding up diagnosis and treatment.
- b) It evaluates CNN architectures like VGG16, EfficientNetB0, MobileNetV2, and DenseNet121, finding VGG16 with the highest accuracy at 97%.
- c) By using data augmentation, the research addresses limited datasets, improving the training and performance of CNN models in medical imaging.

This is how the rest of the paper is organized. Part 2 has the relevant work. The model's architecture and construction techniques are described in detail in Section 3. The experimental setup, a description of the dataset, and measurements are presented in Section 4. The research's conclusion and findings are presented in Section 5, and a repository for related works and citations is provided in Section 6.

II. LITERATURE REVIEW

Research has demonstrated the efficacy of machines and deep learning methods, such as CNN, ANFIS, and SVM, in precisely and efficiently categorizing brain tumors [6,7]. Combining SVM models with extraction methods like wavelet transformations has shown really good results in classifying healthy and unhealthy brain images [7]. However, the research conducted by Haifeng Wang and Dejin Hu pointed out that the substantial time and memory resources needed for optimization have hindered the SVM adopted in big datasets [8]. In their paper, Auria, Laura, and Moro explained that Support Vector Machines (SVM) may lack transparency in some situations. However, they also discussed that SVMs are reliable and can produce accurate classification results based on a strong theoretical foundation. They also discussed both the advantages and disadvantages of SVMs in solvency analysis [9].

In a study conducted in 2016, S Roy et al. [10] found that the ANFIS could classify MRI brain pictures more quickly and accurately than the previous techniques. A multimodal strategy may be used to improve neuroimaging, which can result in better patient care and diagnostic performance. Fuzzy logic and neural networks were discussed along with their advantages and disadvantages by Pezeshki and Mazinani (2019). They noted that although fuzzy logic is easier to employ, model creation and parameter selection may provide difficulties [11].

In 2018, Avizenna, Soesanti, and Ardiyanto reported achieving 100% accuracy, sensitivity, and specificity in categorizing brain FLAIR MRI images using statistical texture analysis [12]. This method highlights the effectiveness of statistical texture analysis in accurately classifying tumor and normal brain MRI images, thereby enhancing diagnostic precision. Chen and Konukoglu (2018) developed an unsupervised lesion detection method for brain MRI images that accurately identifies lesion locations without extensive annotated datasets [13]. Their

approach leverages prior knowledge of brain appearance to achieve human-level anomaly detection using shallow-level autoencoders, promising advancements in clinical abnormality detection.

CNNs were investigated by Chattopadhyay and Maitra in 2022 for their potential to separate brain tumors from MRI images. Its findings showed that CNNs were dependable and robust in this regard [14]. Their work addresses the critical need for effective and dependable methods in clinical brain tumor segmentation, significantly contributing to automated segmentation literature. Comparably, a work on CNNs for brain tumor segmentation by Bhandari et al. (2020) offered insights into the potential of deep learning methods for accurate tumor delineation [15]. Together, these studies showcase significant advancements in automated segmentation methods, promising improvements in the accuracy of MRI image classification systems.

A. LIMITATIONS

The following limitations are recognized from the existing work:

- 1) SVM cannot automatically identify and extract hierarchical features from unprocessed picture data,
- 2) The ANFIS struggles with handling high-dimensional image data and complex feature extraction.
- 3) Statistical texture analysis is limited in capturing complex spatial hierarchies and features in images.
- 4) A simple CNN lacks the depth and complexity to extract detailed hierarchical features from images.
- 5) EfficientNet and InceptionNet, while more computationally efficient, may require more complex training processes and tuning.

To overcome the above-mentioned limitations, a comparative analysis is done in this research using various deep neural networks.

III. MATERIALS AND METHOD

The current research focuses on developing a computer-aided diagnosis (CAD) system utilizing CNNs and MRI images. An extensive summary of the preparation procedures and research architecture is given in this section.

A. PREPROCESSING

1) Data Preparation

In order to be ready to train the CNN, the pictures were loaded into two categories: positive, which includes MRI scans showing tumors, and negative, which includes scans showing no tumors. To guarantee uniformity, every picture is imported using *Keras* preprocessing routines and scaled to (224,224) pixels. After that, they were transformed into a NumPy array and uploaded to the dataset, labeling the positive photos as 1 and the negative ones as 0. These procedures ensure that the dataset is prepared for training.

2) Data Augmentation

The *ImageDataGenerator* function was used to augment the data in order to compensate for the lack of data and improve the model's accuracy. In order to add diversity to the dataset, a number of transformations were applied,

such as `rotation_range = 20`, `width_shift_range = 0.2`, `height_shift_range = 0.2`, `horizontal_flip = True`, and `zoom_range = 0.1`. These adjustments include rotation (up to 20 degrees), flipping the image horizontally, shifting the image horizontally and vertically (up to 20% of the width and height), and zooming (up to 10% of the image). These improvements strengthen the dataset's resilience and diversity, which boosts the CNN model's performance.

3) Splitting data

Using the "train_test_split" function from the scikit-learn library, the dataset was divided into training and testing data after the data preparation stage. This function allocates the samples into the respective train and test sets randomly, ensuring the model's performance can be assessed on unseen data. Specifying a Random State parameter further ensures reproducibility among different lines of code.

B. Model Used

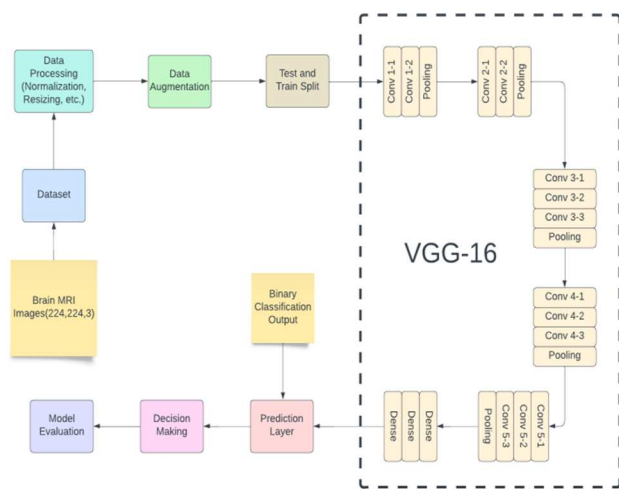


Fig.1. Block Diagram of VGG16 Model.

The CNN model's block design, as seen in Figure 1, starts with the dataset of brain MRI pictures that have been divided into two folders in accordance with section 3.1's instructions. These photos are scaled to match the CNN model in order to guarantee consistency. The goal of data augmentation is to increase the diversity and durability of the model. The dataset is divided into training and testing sets, and then the data is fed into a pre-trained model. The preprocessed photos are fed into a pre-trained model after the data is split. To extract spatial information from all feature maps, a global average pooling layer is attached. For binary classification, a prediction layer employing the sigmoid activation function is added [16]. The model is assembled using the Adam optimizer and binary cross-entropy function, with accuracy chosen as the assessment metric. An early stopping function with a patience of 5 is used to avoid overfitting. The preprocessed training data is used to train the model in batches, and the validation data is used to monitor performance. Finally, the model is evaluated using measures such as F1 Score, Accuracy, Recall, and Precision.

EfficientNetB0

EfficientNetB0, introduced by Google Brain in 2019, uses the compound scaling method to balance model complexity and computational efficiency by uniformly

scaling width, depth, and resolution dimensions [17]. It achieves high accuracy with fewer parameters compared to traditional CNNs. EfficientNetB0 incorporates components from MobileNetV2, such as the Mobile Inverted Bottleneck Conv (MBConv), and Squeeze and Excitation (SE) optimization, which enhance accuracy with minimal parameter overhead, making it ideal for resource-constrained devices [18].

MobileNetV2

MobileNetV2, introduced by Google, is significant for mobile and embedded systems [19]. It uses linear bottlenecks and inverted residual blocks to enhance speed and efficiency. Depthwise separable convolutions reduce computation while maintaining complexity, and the linear bottleneck design ensures smooth information flow. Its standout feature is adaptability through the compound scaling method.

DenseNet121

DenseNet121 is known for its dense connectivity pattern and effectiveness with datasets like Cifar-10 and SVHN [20]. A recent hybrid model for brain tumor segmentation combined DenseNet121 with UNet, omitting the fully connected layer and adding up-sampling layers for segmentation [21]. This design uses DenseNet121 as an encoder with skip connections to maintain spatial information, enhancing feature extraction for segmentation tasks.

VGG16 Model

To set the VGG16 architecture apart from its predecessors, Simonyan and Zisserman created it. Three fully linked layers are positioned after five convolutional blocks in the VGG16 architecture. Block 1 is composed of two convolutional layers (CL) with 64 3x3 filters, and a 2x2 max-pooling layer (MPL). Both of Block 2's CL are made up of 128 3x3 filters, followed by a 2x2 MPL. Block 3 consists of a MPL with dimensions of 2x2 and three CL with 256 filters of size 3x3. Block 4 is composed of a MPL with dimensions of 2x2 and three CL with 512 filters of size 3x3. Block 5 reflects Block 4 and has three CL with 512 3x3 filters each, followed by a 2x2 MPL. The completely connected layers are made up of a final layer (4) with 2 neurons for binary classification and two levels with 4096 neurons each. These stacks of 3x3 matrices offer several benefits, such as increased non-linearity and fewer parameters utilized. A 1 x 1 convolution layer is also added to improve performance, as it increases non-linearity even more while maintaining the same spatial dimensions. Below is the algorithm for the VGG16 architecture.

Pseudocode

Step 1: Input Layer

Input: Image of size 224x224x3 (height, width, RGB channels)

Step 2: Convolutional Layers

For each convolutional layer l:

For each position (i, j) in the output:

$$Z_{ij}^{(l)} = 0$$

For each filter k:

For each m in range(1, K):

For each n in range(1, N):

$$Z_{ij}^{(l)} = W_m^n k^{(l)} * X_{(i+m-1)(j+n-1)} k^{(l-1)} + b_k^{(l)} \quad (1)$$

Step 3: ReLU Activation Function

For each convolutional layer l:
For each position (i, j) in the output:

$$A_{ij}^{(l)} = \max(0, Z_{ij}^{(l)}) \quad (2)$$

Step 4: Pooling Layers

For each pooling layer l:
For each position (i, j) in the output:

$$P_{ij}^{(l)} = \max\{X_{(i+m)(j+n)}^{(l)}\} \quad (3)$$

Step 5: Fully Connected Layers

For each fully connected layer l:

$$Z^{(l)} = W^{(l)} * X^{(l-1)} + b^{(l)} \quad (4)$$

Step 6: Softmax Layer

For each input vector z_i :

$$\text{softmax}(z_i) = \frac{e^{z_i}}{\sum_{j=1}^C e^{z_j}} \quad (5)$$

where,

$Z_{ij}^{(l)}$ is the output (1) of the lth layer at position (i, j),

$W_{mnk}^{(l)}$ are the weights (filters) of the lth layer,

$X_{(i+m-1)(j+n-1)}^{(l-1)}$ is the input from the (l-1)th layer,

$b_k^{(l)}$ is the bias term,

$A_{ij}^{(l)}$ is the output of the ReLU (2) activation function,

$P_{ij}^{(l)}$ is the output of the pooling layer (3),

$W^{(l)}$ and $b^{(l)}$ are the weights and biases of the fully connected layer,

C is the number of classes and

z_i is the input vector's ith element.

IV. EXPERIMENTAL SETUP & RESULT

A. Experimental Setup

An Intel i7 Evo CPU from the 12th generation with 16GB of RAM is used. A 512 GB hard drive in the Intel Iris Xe storage is used and it has a GPU with 7.8 GB of RAM. The setup runs on Windows 11 and uses the Jupyter Notebook as the IDE. Python 3.8.2 is used for programming tasks, whereas TensorFlow 2.4.0 is used for machine learning processes. Pre-processing activities are handled with the help of the OpenCV package, while Matplotlib helps in doing visualization.

B. Dataset Description

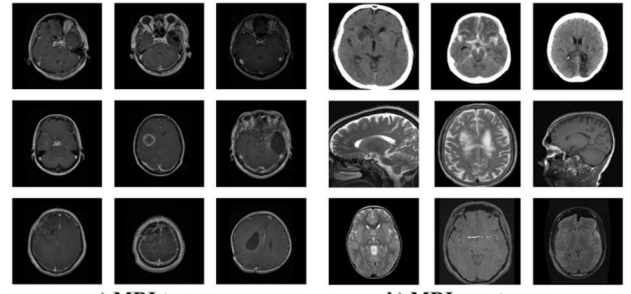


Fig.2. Samples from the dataset.

In this research, brain MRI scans publicly available on Kaggle were utilized, comprising a dataset of 5,266 images and sample images are shown in figure 2. Among these, 3,266 brain MRI scans depict tumors and are categorized in the positive folder, while 2,000 MRI images without tumors are placed in the negative folder. This distribution indicates that 38% (2,000 images) of the dataset consists of negative examples, while 62% (3,266 images) are positive examples [22]. The dataset initially included 3,266 brain tumor and 2,000 non-brain tumor MRI images. Through augmentation, the non-brain tumor images were increased to 3,266, matching the brain tumor images. As a consequence, 6,532 photos made up the entire dataset. Next, the dataset was split into two groups: 80% (5,226 photos) for training and 20% (1,306 images) for testing, with the goal of maintaining equal representation of brain tumor and non-brain tumor images in both sets. For the purpose of training and assessing machine learning models on MRI image classification tasks, this approach guarantees a representative and balanced dataset. The model is ready to reliably and accurately discriminate between images of brain tumors and those without them by utilizing augmentation and strategic splitting.

C Metrics Evaluation

Accuracy: In brain tumor detection, accuracy measures how effectively a machine learning model identifies tumors across diverse MRI images. It compares correct predictions to total predictions, providing a reliable measure of the model's overall effectiveness.

Precision: Precision evaluates a model's ability to minimize false positives in brain tumor detection. This metric is critical in medical diagnostics to ensure that identified tumors are genuine, influencing patient treatment decisions with confidence and reducing unnecessary interventions.

Recall (Sensitivity): Recall assesses a model's capacity to detect true positive tumors out of all actual positive cases. It's crucial in healthcare settings where missing a tumor (false negatives) could have severe consequences, emphasizing the model's accuracy in identifying tumors promptly and accurately.

F1 Score: The F1 score in brain tumor detection harmonizes precision and recall, essential for ensuring accurate tumor identification and comprehensive coverage. It balances the model's performance by minimizing false positives while

maximizing true positive detections, vital for reliable healthcare diagnostics.

D. Result and Discussion

The dataset experimentation has shown considerable improvements in brain tumor diagnosis with Convolutional Neural Networks (CNNs). The comparison of VGG16's training and validation measures is shown in Figure 3, highlighting the model's performance throughout the training process. Another potent CNN design, DenseNet121, has been tested and shows excellent performance metrics. Specifically, DenseNet121 shows a precision of 0.88 for class 0 (non-tumor) and an impressive 0.99 for class 1 (tumor), indicating a high percentage of correctly identified positive cases. Class 1's recall, at 0.92, is noticeably strong compared to class 0's 0.98, indicating that the model is able to accurately identify the majority of genuine positive tumour instances. The summation of these metrics results in an F1-score of 0.95 for class 1 and 0.93 for class 0. This illustrates how well the model balances recall and precision, hence reducing false positives and false negatives. Consequently, the DenseNet121 model can accurately categorize patients as either having tumors or not, achieving an overall accuracy of 0.94. This high level of accuracy underscores the model's potential for practical application in medical diagnostics, offering a reliable tool for brain tumor detection and classification.

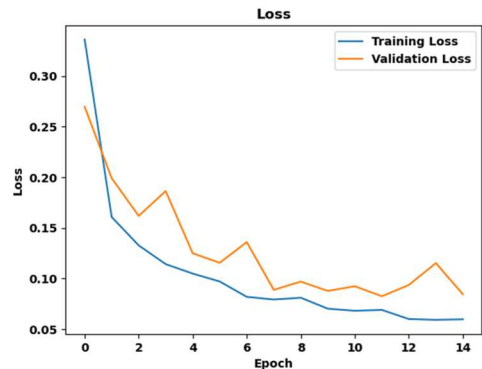


Fig. 3. Training and Validation Metrics graph of VGG16.

The precision scores for DenseNet121 are impressive; class 0 scored 0.987 and class 1 scored 0.922, respectively, showing that both classes had a high percentage of properly classified occasions. The recall values for both classes are also strong, with class 0 at 0.987 and class 1 at 0.922. Consequently, the F1-scores for both classes are impressive, standing at 0.987 for class 0 and 0.922 for class 1. Overall, the model achieves an accuracy of 0.943, demonstrating its effectiveness in accurately classifying tumor and non-tumor instances.

The precision scores for MobileNetV2 are high; class 0 scored 0.91 and class 1 scored 0.98, respectively, showing a high percentage of accurately detected instances for both classes. The recall values are also strong, with class 0 at 0.96 and class 1 at 0.95. Consequently, the F1 scores for both classes are impressive, standing at 0.93 for class 0 and 0.96 for class 1. Overall, the model achieves an accuracy of 0.95, underscoring its robust performance in accurately classifying tumor and non-tumor instances.

For EfficientNetB0, with class 0 obtaining 0.970 and class 1 earning 0.988, the precision scores are noticeably high, indicating a high percentage of correctly detected examples for both classes. The recall values for both classes are also strong, with class 0 at 0.964 and class 1 at 0.976. Consequently, the F1-scores for both classes are impressive, standing at 0.967 for class 0 and 0.976 for class 1. Overall, the model achieves an accuracy of 0.976, underscoring its robust performance in accurately classifying tumor and non-tumor instances.

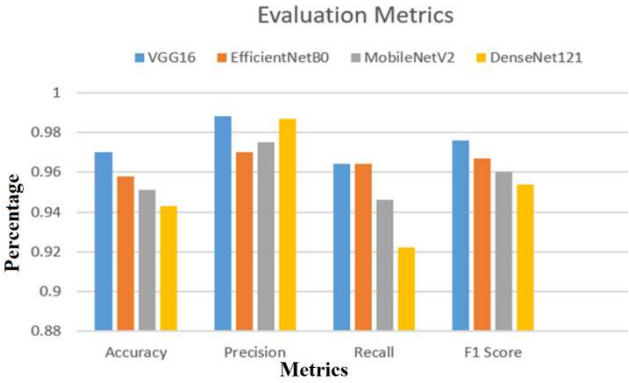


Fig. 4. Evaluation Metrics Graph.

For VGG16, with class 0 obtaining 0.970 and class 1 earning 0.988, the precision scores are noticeably high, indicating a high percentage of correctly detected examples for both classes [23]. The recall values for both classes are also strong, with class 0 at 0.964 and class 1 at 0.976. Consequently, the F1-scores for both classes are impressive, standing at 0.964 for class 0 and 0.976 for class 1. Overall, the model achieves an accuracy of 0.976, boasting its robust performance in accurately classifying tumor and non-tumor instances. In table 1 and figure 4, evaluation metrics are presented for the various deep neural architectures. This graph offers a visual summary of the performance metrics, facilitating a quick and intuitive comparison of the models' effectiveness in brain tumor detection tasks.

Model	Accuracy	Precision	Recall	F1 Score
DenseNet121	0.943	0.987	0.922	0.954
MobileNetV2	0.951	0.975	0.946	0.960
EfficientNetB0	0.958	0.970	0.964	0.967
VGG16	0.970	0.988	0.964	0.976

Table.1 Performance metrics comparison of all models for brain tumor prediction.

E. Comparative Analysis

The comparative analysis (Table 2) of various classification methods for brain tumor detection reveals a range of accuracy and methodological diversity. Chattopadhyay et al. (2022) used a deep learning technique achieving 92.13% accuracy, indicating strong performance but potentially limited by model complexity. Pashaei et al.

(2018) and Parvin & Mamun (2022) both used CNNs with deep feature fusion, achieving 93.68% accuracy, highlighting their effectiveness in feature extraction but possibly constrained by computational demands. Ali Işın, Cem Direkoğlu, and Melike Sah (2016) implemented FCNN with 94.00% accuracy, offering advantages in handling structured data but might be less effective with unstructured inputs. Deepak & Ameer (2019) applied deep CNN with transfer learning, reaching 95.00% accuracy, leveraging pre-trained models for improved performance but dependent on the quality of transfer learning data. Saeedi and Rezayi (2023) used CNN, achieving 96.47% accuracy, showcasing robust performance with high computational efficiency. Naveen V et al. (2023) employed DNN with 96.82% accuracy, excelling in complex pattern recognition but potentially limited by overfitting. Our method, using VGG16, achieved the highest accuracy of 97.00%, benefiting from a well-structured and deep architecture but requiring significant computational resources and large training datasets. Each method has its strengths in accuracy and computational efficiency, but trade-offs exist concerning model complexity and resource requirements.

S.No	Author (Year)	Method	Accuracy
1	Chattopadhyay et al. (2022) [25]	Deep Learning Technique	92.13%
2	Pashaei et al. (2018) [26]	CNN	93.68%
3	Parvin et al. (2022) [27]	CNN (Deep Feature Fusion)	93.68%
4	Ali Işın et al. (2016) [28]	FCNN	94.00%
5	Deepak et al. (2019) [29]	Deep CNN (Transfer Learning)	95.00%
6	Saeedi, S. et al. (2023) [30]	CNN	96.47%
7	Naveen V et al. (2023) [31]	DNN	96.82%
8	Our Method (2024)	VGG16	97.00%

Table. 2 Comparative analysis with baseline models.

F. Research Discussion

VGG16 offers superior accuracy but at a high computational cost, making it less scalable. EfficientNetB0 balances accuracy and efficiency, providing a versatile option suitable for various applications. MobileNetV2 [24] prioritizes computational efficiency, making it ideal for resource-constrained environments, though it may sacrifice some accuracy. DenseNet121 combines high accuracy with efficient feature reuse but can be memory-intensive. The choice of architecture depends on specific project requirements, including the need for high accuracy, available computational resources, and the intended deployment environment.

This paper emphasizes how well CNNs in particular, which use deep learning, can identify brain tumors from MRI data. Using data augmentation, it demonstrates the potential of CNN architectures like VGG16, EfficientNetB0, MobileNetV2, and DenseNet121. VGG16 stands out with a 97% accuracy rate. The proposed method accelerates brain tumor identification, offering a reliable alternative to manual MRI analysis. This research underscores deep learning's transformative impact on medical diagnostics, enhancing early detection and

treatment of brain tumors. By leveraging various CNN models and addressing dataset limitations, the approach improves diagnostic accuracy and patient outcomes, showcasing the potential of deep learning in healthcare.

V. CONCLUSION

In conclusion, this study thoroughly assessed four distinct convolutional neural networks (CNN) architectures: DenseNet121, EfficientNetB0, VGG16, and MobileNetV2. Key performance parameters, including accuracy, precision, recall, and F1 score, were used to evaluate each model. With a high F1 score of 0.976 and an accuracy of 0.970, VGG16 stood out as the most effective and efficient model among them, demonstrating a remarkable balance between precision and recall. Although both models performed admirably in correctly identifying cases with and without tumors, VGG16's higher performance highlights its potential as a reliable tool for practical use in medical image analysis.

V. FUTURE DIRECTIONS

Future research in brain tumor detection should focus on advanced CNN architectures like ResNet, Inception, EfficientNet, and Vision Transformers (ViTs). Integrating multimodal data from MRI, CT scans, PET scans, and clinical information can boost diagnostic accuracy. Enhancing model robustness with advanced data augmentation techniques such as GANs and domain-specific methods is crucial. Ensuring interpretability using methods like Grad-CAM, SHAP, and LIME is essential for clinical trust. Optimizing computational efficiency through model compression will enable deployment on edge devices, while conducting clinical trials and developing user-friendly tools are vital for real-world implementation.

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