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Convolutional Neural Network based Brain Tumor Detection

Shruti Karmarkar[1*], Preeti Karmarkar[1], Shruti Bagesar[1], Kalyani Chahare[1], Nitin Janwe[1]
Department of Computer Science and Engineering[1]
Rajiv Gandhi College of Engineering, Research & Technology, Chandrapur, Maharashtra, India.
* Corresponding author E-mail: shrutikarmarkar06@gmail.com

Abstract: *Our objective towards working on this project was to train a deep learning model that would be able to accurately predict the presence of tumor in a human brain by examining the MRI images of a person using a Convolutional Neural Network. In our quest for achieving the highest accuracy in our project, we employed a multi-faceted approach to network selection. We began by developing our own CNN architecture with four convolutional layers, which delivered a promising accuracy of 97%. However, to further improve our results, we delved into the realm of transfer learning and explored pre-trained models like Inception, ResNet, VGG16, and VGG19. After rigorous evaluation, we found that combining VGG16 with our novel architecture yielded the most remarkable outcomes. This fusion of VGG16's advanced feature extraction capabilities with our tailored architecture allowed us to achieve the highest accuracy of 99.17% for our specific dataset. This network selection process exemplifies our commitment to maximizing performance and showcasing the power of combining state-of-the-art models with innovative architectural designs*

Keywords*:* Tumor

I. INTRODUCTION

The timely and accurate detection of brain tumor is crucial in medical imaging to ensure optimal patient outcomes. However, traditional methods of brain tumor detection that rely on manual inspection of MRI images by radiologists can be prone to human error and time-consuming. To address this issue, automated detection of brain tumors using machine learning techniques has gained significant attention in recent years.

Our objective in developing a CNN-based brain tumor detection system is to surpass the accuracy and efficiency of past models and research. By leveraging advanced techniques. We aim to improve the model's ability to accurately identify brain tumors from medical images. Additionally, we strive to optimize the computational efficiency of the system for real-time clinical applications. Our goal is to make significant contributions to the field of brain tumor detection, benefiting both patients and healthcare professionals.

We worked on a Dataset extracted from Kaggle. The Dataset consists of 400 images, including 200 images of patients with Brain Tumor and 200 images of patients without Brain Tumor. Prior to training our model we performed several Image pre-processing steps including data augmentation, resizing, cropping, etc to prepare the dataset before using it to enhance the quality of the images and improve the performance of the model.

II. METHODOLOGY

Data Collection: We collected our dataset, named "Br35H :: Brain Tumor Detection 2020," from Kaggle. It consists of 400 MRI brain images, with 200 images containing brain tumors and 200 images representing normal brain MRI scans. Additionally, we applied data augmentation techniques to increase the diversity and size of the dataset.

70% of the data for training. 15% of the data for validation. 15% of the data for testing
number of training examples = 1679
number of development examples = 360
number of test examples = 360

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Image Pre-processing: Image preprocessing plays a crucial role in enhancing the quality of images and improving the performance of machine learning models by applying various techniques to prepare the data before analysis.

We used the "ImageDataGenerator" provided by Keras among other technique for data augmentation. It replaces the original batch with the new, randomly transformed batch of images. For augmentation the following operations were applied: rotation_range=10width_shift, height_shift, shear, brightness, horizontal_flip, vertical_flip, fill_mode=nearest

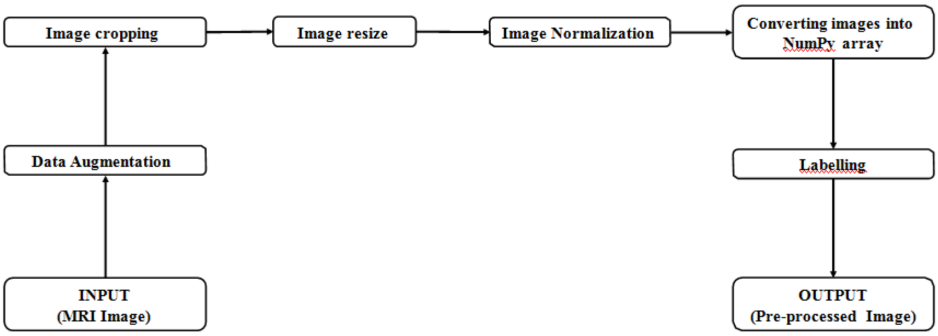


Image pre-processing

Pre-processing result

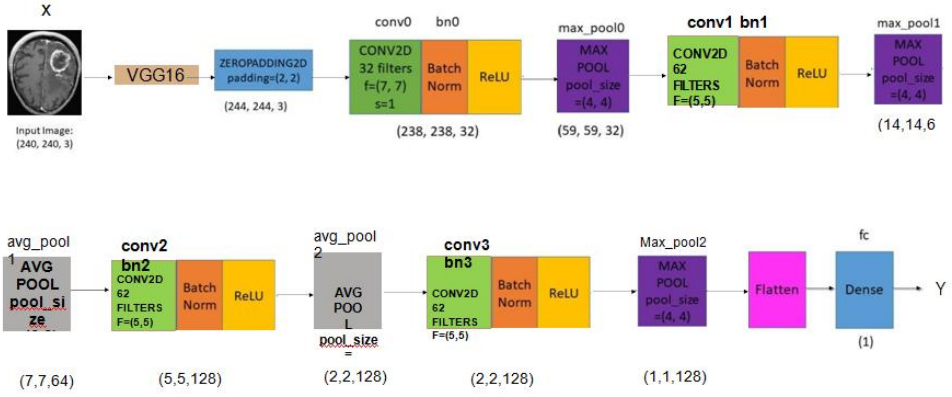
Feature Extraction: In the feature extraction stage, we aimed to extract meaningful and representative features from the brain MRI images. This process involved transforming the raw image data into a set of numerical features that capture relevant information for brain tumor detection. We have used pre-trained Convolutional Neural Network, specifically VGG-16 to extract high-level features from the input data. By leveraging on the knowledge learned by VGG-16, we were able to capture distinctive patterns and structures from the data.

Network Selection:

- We started with a baseline or novel CNN architecture and achieved an impressive accuracy of 97%.
- To further enhance our model's performance, we explored transfer learning using popular pre-trained models such as Inception, ResNet, VGG16, and VGG19.
- Through extensive experimentation, we discovered that combining our novel architecture with the VGG16 pre-trained model yielded the highest accuracy for our specific dataset.
- This combination capitalized on the deep representation learning capabilities of VGG16 and the adaptability of our custom architecture, resulting in a model that outperformed the baseline architecture in terms of accuracy

II. MODEL ARCHITECTURE

Covnet_Architecture



Output:
1 represents **tumorous** class
0 represents the **non-tumorous** class

The proposed model architecture is designed for brain tumor detection and incorporates a combination of pre-trained VGG16 layers and additional convolutional and pooling layers.

The model begins with the input layer, which takes in the brain MRI images with a shape of (240,240,3). The VGG16 model is loaded with pre-trained weights, excluding the top layers, to leverage its learned representations of image features. The layers of the VGG16 model are frozen to prevent them from being trained during transfer learning.

We have seamlessly merged the VGG16 model with our novel architecture, combining the strengths of both to improve the effectiveness of brain tumor detection.

The model architecture incorporates batch normalization, which normalizes the activations to stabilize training and accelerate convergence. Zero-padding is applied to maintain spatial dimensions during convolutional operations and preserve border-related features.

In addition to the normalization techniques, we fine-tuned certain parameters during training. This includes adjusting the momentum and learning rate, which optimize the model's performance and convergence. Furthermore, we explored two optimization algorithms, such as Adam, RMSprop, to find the most effective approach for training our model. These parameter adjustments and optimization algorithm variations contribute to the improved accuracy and robustness of our brain tumor detection model.

Here's a table showcasing the hyperparameters used in our brain tumor detection model and their corresponding values:

Hyperparameter	Value
Learning Rate	0.01
Momentum	0.9
Dropout Rate	0.3
Batch Size	32
Number of Epochs	25
Optimizer	RMSprop
Loss Function	Binary Cross entropy

Total params: 115,137
Trainable params: 114,433
Non-trainable params: 704

A fully connected layer with a sigmoid activation function is employed to generate the output. This binary classification layer predicts the presence or absence of a brain tumor based on the learned features.

The model is optimized using the RMSprop optimizer with a learning rate of 0.01. It is compiled and returned as a Keras model instance named "BrainDetectionModel", ready for training and evaluation.

III. EXPERIMENTAL RESULTS

We evaluated several pre-trained models with our novel architecture during training, such as VGG16, inception, ResNet, VGG19, and VGG16. By comparing the training, validation, and test accuracies of these models, we aim to identify the most effective architecture for brain tumor detection. The training process involved optimizing the model’s weights using different optimizers, including RMSProp and adam. The validation accuracy was assessed to measure the generalization capability of the models. Finally, the test accuracy was evaluated to validate the performance of the models on previously unseen brain images

The below table covers results obtained for each network architecture we trained, Optimization was done keeping test accuracy on mind

Model	Training Accuracy	Validation Accuracy	Stable?	optimizer	Test Accuracy
Novel CNN	0.97	0.98	yes	RMSprop	0.97
Novel CNN	0.99	0.99	yes	Adam	0.97
VGG16 + (Novel CNN)	**0.9869**	**0.9833**	**yes**	**RMSprop**	**0.9917**
Inception + (Novel CNN)	0.9881	0.9889	no	RMSprop	0.9889
ResNet + (Novel CNN)	0.9744	0.9722	no	RMSprop	0.9833
VGG19 + (Novel CNN)	0.9917	0.9889	no	RMSprop	0.9778
VGG19 + (Novel CNN)	0.9911	0.9806	yes	Adam	0.9833
VGG16 (Novel CNN)	0.9917	0.9889	yes	Adam	0.9861

These findings demonstrate the potential of these CNN architectures in accurately detecting brain tumors, which can significantly impact early diagnosis and treatment planning. Further research can explore ensemble techniques or model fusion strategies to leverage the strengths of multiple architectures for improved performance.

IV. EVALUATION MATRIX

We have used various evaluation matrix to evaluate the model’s performance.

Accuracy: Measures the overall correctness of a model's predictions by calculating the ratio of correctly classified instances to the total number of instances. It provides a percentage of correct predictions made by the model.

Accuracy (all correct / all) = TP + TN / TP + TN + FP + FN

Precision: Quantifies the proportion of correctly predicted positive instances out of all instances predicted as positive. It focuses on the accuracy of positive predictions and helps minimize false positives

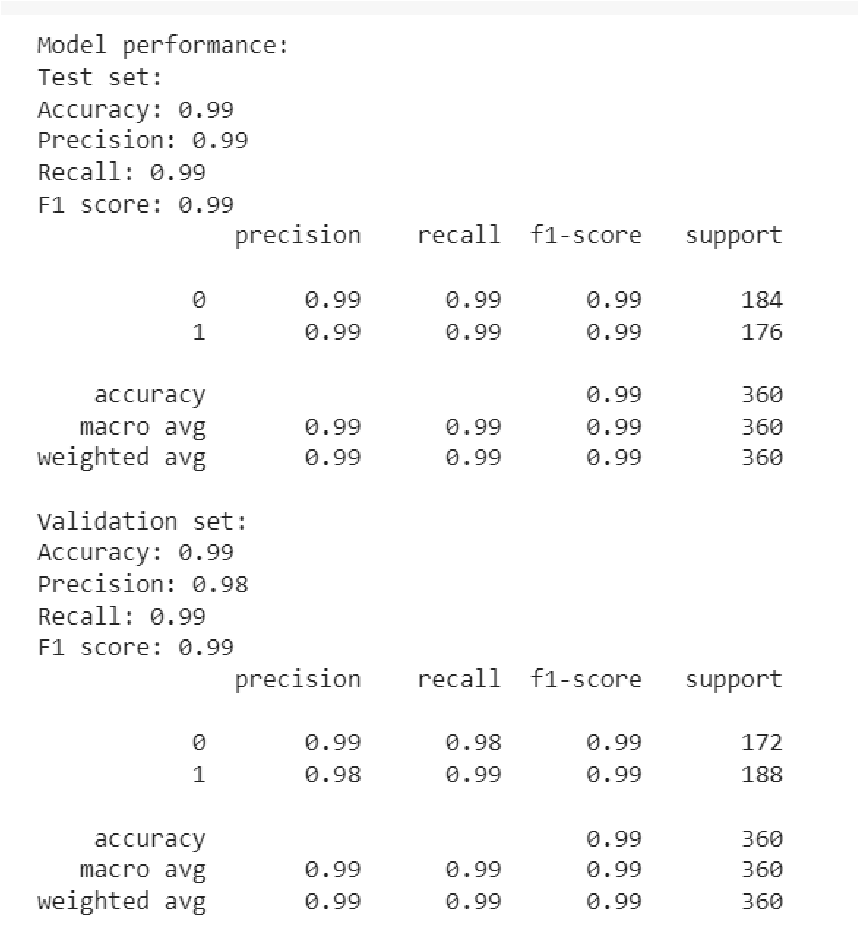
Precision (true positives / predicted positives) = TP / TP + FP

Recall (Sensitivity or True Positive Rate): Measures the ability of a model to correctly identify positive instances out of all actual positive instances. It helps minimize false negatives and is particularly important when the detection of positive instances is crucial.

Sensitivity aka Recall (true positives / all actual positives) = TP / TP + FN

F1 Score: The harmonic mean of precision and recall, the F1 score provides a balanced measure of a model's performance by combining both metrics into a single value. It is commonly used when a balance between precision and recall is desired.

F1−measure=2×[Precision*Recall / Precision + Recall] Given below is our performance matrix on test set and validation set



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Model performance:
Test set:
Accuracy: 0.99
Precision: 0.99
Recall: 0.99
F1 score: 0.99
              precision    recall  f1-score   support

           0       0.99      0.99      0.99       184
           1       0.99      0.99      0.99       176

    accuracy                           0.99       360
   macro avg       0.99      0.99      0.99       360
weighted avg       0.99      0.99      0.99       360

Validation set:
Accuracy: 0.99
Precision: 0.98
Recall: 0.99
F1 score: 0.99
              precision    recall  f1-score   support

           0       0.99      0.98      0.99       172
           1       0.98      0.99      0.99       188

    accuracy                           0.99       360
   macro avg       0.99      0.99      0.99       360
weighted avg       0.99      0.99      0.99       360
```

V. DISCUSSION

Our research focused on developing a deep learning model for accurate brain tumor detection using MRI images. We employed a multi-faceted approach to network selection, starting with our own novel CNN architecture and later exploring transfer learning with pre-trained models such as Inception, ResNet, VGG16, and VGG19. Through rigorous evaluation, we found that combining VGG16 with our novel architecture yielded the most remarkable outcomes, achieving an impressive accuracy of 99.17% on our specific dataset. This network selection process exemplifies our commitment to maximizing performance and showcases the power of combining state-of-the-art models with innovative architectural designs.

The integration of VGG16, with its advanced feature extraction capabilities, and our tailored architecture allows for the extraction of high-level features and patterns crucial for accurate tumor detection. The fusion of these models demonstrates the potential for leveraging pre-trained models to enhance the performance of specific tasks.

Our research has practical implications in the medical field, where the timely and accurate detection of brain tumors is crucial for patient outcomes. By automating the detection process using deep learning techniques, our model can provide quick and accurate results, reducing the reliance on manual inspection by radiologists and potentially improving diagnostic accuracy. This can significantly impact early diagnosis and treatment planning, leading to improved patient care and outcomes.

However, there are some limitations to our study. Our research was conducted on a specific dataset extracted from Kaggle, which may not fully represent the variability and complexity of real-world clinical cases. Additionally, the generalization capability of our model should be further evaluated on diverse datasets to assess its performance across different populations and imaging conditions. Future research should focus on collecting larger and more diverse datasets to enhance the robustness and reliability of the model.

Moreover, while our model achieved high accuracy, it is essential to consider false positives and false negatives in the context of clinical applications. False positives can lead to unnecessary interventions, while false negatives may result in missed diagnoses. Balancing sensitivity and specificity are crucial to ensure the model's clinical utility. Further refinement and optimization of the model, along with thorough validation on independent datasets, are needed to address these concerns.

VI. CONCLUSION

In conclusion, our research presents a deep learning model for brain tumor detection with the goal of improving the accuracy and efficiency of previous models. By combining our novel architecture with pre-trained models, we achieved a remarkable accuracy of 99.17% on our specific dataset. Our findings highlight the potential of deep learning and transfer learning techniques in accurately identifying brain tumors from MRI images. The practical implications of our research in improving patient care and outcomes are significant. However, further research and validation are necessary to enhance the model's generalization capability, address potential limitations, and ensure its reliability in real-world clinical settings.

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