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Brain Tumor Classification using Convolutional Neural Network with ResNet Architecture

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ABSTRACT — Brain tumors are dangerous, sometimes fatal illnesses that require prompt, accurate diagnosis to enhance patient outcomes. Given the intricacy and diversity of tumor characteristics, manual interpretation of brain MRI data is frequently laborious and prone to human error. This research aims to create an automated system for classifying brain tumors by integrating the Convolutional Neural Network (CNN) algorithm with the ResNet architecture. The suggested approach makes use of 7,023 MRI pictures that have been divided into four categories: non-tumor, pituitary tumor, meningioma, and glioma. Image normalization, grayscale conversion, scaling, and data augmentation methods, including rotation and flipping, were among the preprocessing processes used to enhance model performance. The ResNet design was chosen because it effectively trains deeper networks by utilizing residual connections to prevent vanishing gradient problems. Metrics such as F1-score, accuracy, precision, and recall were used to train and assess the system. According to the testing data, the model performed consistently across all classes and attained an outstanding accuracy of 94.14%. These results validate the promise of deep learning methods, especially CNNs with ResNet enhancements, for classification tasks involving medical images. The system created in this work is a promising tool for assisting clinical decision-making, cutting down on diagnostic time, and improving the accuracy of brain tumor identification and classification.

KEYWORDS — Artificial Intelligence, Brain Tumor, CNN, Image Classification, ResNet

I. INTRODUCTION

This Artificial intelligence (AI) technology continues to develop and make significant contributions in various fields, including medicine. One area of artificial intelligence currently receiving a lot of attention is machine learning, intensive learning, which has proven effective in analyzing and interpreting medical data. A critical application of this technology is in the diagnosis of diseases based on medical diagnoses, such as the classification of brain tumors and genes [1]. Brain tumors are severe conditions that can be fatal if not appropriately diagnosed. Typically, a medical professional will identify and classify a tumor by interpreting the results of a magnetic resonance imaging (MRI) scan[2].

Brain tumors can occur in any individual, at any age, and appear in any area and have various shapes and sizes. According to the official report published by the WHO, brain cancer accounts for less than 2% compared to other types of cancer. Still, the severe morbidity and complications that result are substantial. The UK Cancer Research Company states that there are around 5,250 deaths caused by brain cancer. In general, brain tumors can be classified into two types, namely benign and malignant tumors [4]. Benign tumours cannot spread and affect other healthy brain tissues because these tumors tend to have a homogeneous structure and do not contain other disease cells. In contrast, malignant tumours tend to have a heterogeneous structure and contain malignant cells that usually grow outside the brain, which is called brain cancer. Glioma is a type of tumor that grows in glial tissue and the spinal cord, while meningioma grows on the membrane that protects the brain and spinal cord.

Though it can be used to measure time, this method is susceptible to subjectivity and cannot validate the findings and conclusions of a radiological study. Therefore, a trustworthy and automated decision-making system is required to increase the precision and effectiveness of recognizing and categorizing different forms of brain tumors. The convolutional neural network (CNN) is one of the most widely used deep learning techniques for pattern recognition and categorization. CNN is capable of accurately classifying images and automatically identifying key features. CNN can be regarded as a technology that can be used to categorize brain cancers based on MRI data because of its capabilities[3].

The first study was based on the results of the research conducted. It can be concluded that the use of minimum parameters in the Convolutional Neural Network (CNN) model with Adam Optimizer still produces quite good accuracy in the classification of medical images of brain tumors. Combining three convolution layers and epoch 10 parameters produced the most fantastic accuracy of 92.8%. At epoch 10, however, the highest average accuracy of 90.7% was noted. Regarding computational efficiency, the model development procedure took the shortest time, 24.83 seconds, and used the fewest CPU resources, 16.45%. This shows that the model optimized with minimal parameters can still perform computations with limited resources and in a short time, but provides adequate results [5].

This result is shown by the much higher training and testing accuracy of the Image Generator method. Specifically, in testing with the Preprocessing Image Generator, the testing accuracy reached 1.0 (or 100%) in most experiments, with training accuracy varying between 0.988 and 0.992. In addition, this method also shows lower complexity in terms of total model parameters, with a much smaller model size (ranging from 2.44 MB to 5.17 MB) compared to the method without Image Generator (which reaches 53.49 MB to 171.14 MB). Therefore, using the CNN method with the

Preprocessing Image Generator promises the best results currently in detecting brain diseases with better efficiency [6].

The Support Vector Machine (SVM) approach, which seeks to produce a classification model with high accuracy or minimal errors in picture classification, was employed in the third investigation. The brain tumor type classification system employing MRI images and the Support Vector Machine (SVM) method developed through a MATLAB 2016a-based program demonstrated positive results based on the conducted tests. An overall accuracy of 91% was attained following the preprocessing phase, feature extraction using GLCM, and SVM classification utilizing the Confusion Matrix. For the glioma tumor type, the system achieved a precision of 0.83 and a recall of 1, with an F1-score of 0.86. Meanwhile, the system obtained a precision of 1 and a recall of 0.85 for meningioma, with an F1-score of 2. These results indicate that brain image segmentation and tumour classification are critical in planning surgery and medical care, because early detection allows doctors to understand the development of the disease and make appropriate treatment decisions, with the location of the tumour segmented [7].

The fourth study focuses on creating a diagnostic system that uses magnetic resonance imaging (MRI) images to identify brain cancers. The Extreme Learning Machine (ELM) model with 2500 nodes in the hidden layer performed the best in identifying brain tumor images on the dataset utilized, according to the tests conducted. This ELM setup yielded an average precision, recall, and F1-score of 0.86 for both the healthy and tumor groups, along with an 86% test accuracy. Compared to ELM employing 3000 nodes (accuracy of 75.3%), 3500 nodes (accuracy of 81.8%), or 4000 nodes (accuracy of 78.5%), this performance is better. However, this study acknowledges that this performance can still vary due to the random initialization of weight and bias values, as well as the random sequence of data in each simulation [8].

The fifth study, based on the results of brain tumor classification testing using MRI images with deep learning and transfer learning methods, showed that the ResNet and VGG16 models performed very well, with validation accuracy of 96% each. The training accuracy for ResNet reached 99%, and VGG16 reached 97%. However, the test accuracy for both models was 85%. Meanwhile, the Xception model produced lower accuracy, namely 74% for training accuracy, 73% for validation accuracy, and 69% for test accuracy. These results overall support that transfer learning can be effectively applied to medical data recognition, including brain MRI images [9].

This study aims to develop a brain tumor classification model based on MRI data using the CNN algorithm. The model will be evaluated on the existing dataset, which consists of the following categories: pituitary, glioma, meningioma, and healthy brain (without tumor). In addition, this study also evaluates the performance of the model using evaluation metrics such as accuracy, precision, recall, and F1-score, and compares the results with previous studies. It is expected that by utilizing CNN and a large and diverse dataset, this study can contribute to the development of an automated medical diagnosis system, especially for brain tumor classification. The resulting system can be used by medical professionals as a tool to aid the decision-making process, allowing for faster and more accurate diagnoses.

II. METHOD

First, 7,023 brain MRI pictures were gathered from Kaggle and categorized into four groups: pituitary, meningioma, glioma, and non-tumor. Then, in order to increase the dataset's diversity and avoid overfitting, these images underwent a pre-processing step that included resizing to 150x150 pixels, converting to grayscale, normalizing pixel values to the [0,1] range, and data augmentation techniques like rotation, flipping, zooming, and shifting. Next, Google Colaboratory used the TensorFlow and Keras frameworks to develop a brain tumor classification system based on Convolutional Neural Networks (CNNs) with ResNet architecture. This model is trained using early stopping to mitigate validation loss and ensure no improvement after 30 epochs. After that, the model's performance is assessed using metrics for accuracy, precision, recall, and F1-score using testing datasets that have an 80:20 ratio for training and testing data[10]. An illustration of the CNN Method architecture is shown in Figure 1.

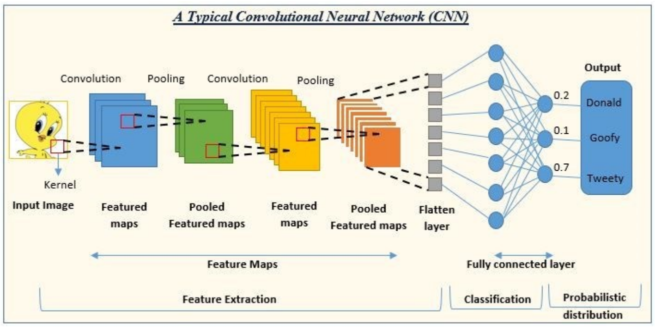


Figure 1. Convolution Neural Network

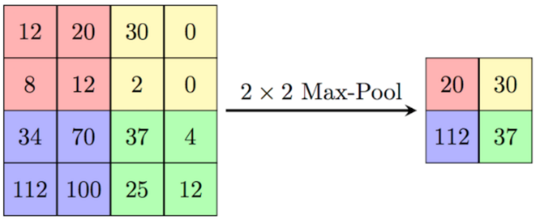
Activation Function, Convolution Layer, Pooling Layer, and Fully Connected Layer. An explanation of each layer and the corresponding mathematical equations is provided below:

1. Convolutional Layer
   The convolutional layer uses a kernel or filter that runs across the input to produce an output known as the feature map. To calculate the convolution layer can be calculated using the formula (1), as follows:

$$(I^*K)(i,j) = \sum m \sum n(i+m, j+n).K(m,n) \qquad (1)$$

Where:
- I is the input matrix (e.g., image),
- K is the kernel (filter),
- i and j are coordinates in the output feature map,
- m and n are the coordinates in the kernel.

2. Pooling Layer
   The pooling layer preserves the most crucial data by lowering the feature map's dimensionality. Max pooling is a popular kind of pooling. Figure 2. below shows the max pooling mathematical equation:



12	20	30	0
8	12	2	0
34	70	37	4
112	100	25	12

20	30
112	37

Figure 2. Pooling Layer

The mathematical equation for Max Pooling is presented in formula (2), as follows:

$$P(i,j) = max_{m,n}\{F(S_i + m, S_i + n)\} \qquad (2)$$

Where:

- P is the pooling output,
- F is the feature map of the convolutional layer,
- si and sj are the pooling steps (stride),
- m and n are the pooling window sizes.

3. Fully Connected Layer
   This layer connects each neuron in one layer to each neuron in the next layer. The output of this layer is the classification result. The mathematical equation for the fully connected layer can be seen in Figure 3. below:

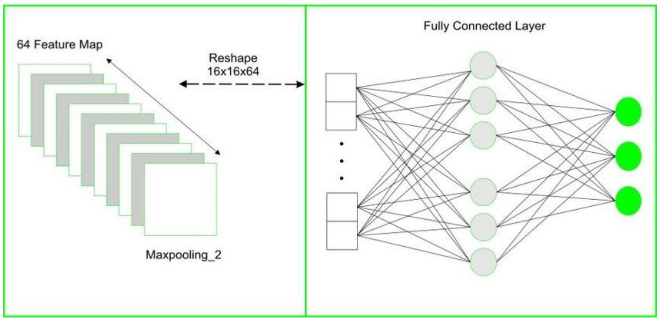


Figure 3. Fully Connected Layer

The mathematical equation for the Fully Connected Layer can be seen in formula (3), as follows:

$$y = f(W, x + b) \qquad (3)$$

Where:

- y is the output,
- f is the activation function,
- W is the weight matrix,
- x is the input,
- b is the bias.

4. Activation Function
   After the convolution, the activation function is applied, and completely connected layers are added to add non-linearity. Rectified Linear Unit, or ReLU, is a popular activation function. Figure 4. below contains the ReLU equation:

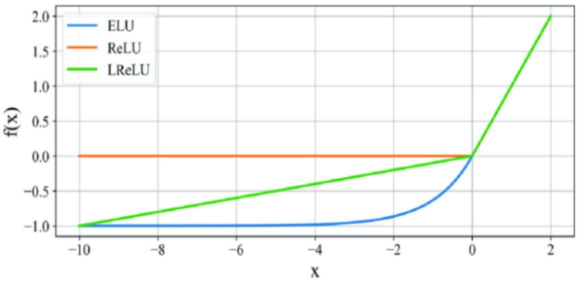


Figure 4. Activation Function

The ReLU equation is presented in formula (4), as follows:

$$F(x) = \max(0, x) \qquad (4)$$

Where:

- Max(0,x) means that the ReLU function will return the maximum value between 0 and x,
- In other words, if c is greater than 0, ReLU will return x,
- If x is less than or equal to 0, ReLU will return 0.

A. Data Acquisition

The study's data came from an open dataset that was accessible on the Kaggle website. This dataset includes 7,023 brain MRI pictures that have been divided into four groups, which are as follows: Glioma: 1,621 images, meningioma: 1,645 images, pituitary: 1,757 images, no tumor: 2,000 images. While this dataset offers a substantial number of images for each category, it is essential to note that specific details regarding the patient demographics (e.g., age, gender, ethnicity), the types of MRI machines used for acquisition, or the exact imaging protocols are not explicitly provided within the publicly available metadata. All images are in .jpg format with varying dimensions and quality. This dataset was chosen because it covers a variety of shapes and types of brain tumors commonly found in medical practice. The sample dataset of brain MRI images included in the four dataset categories (Glioma, Pituitary, Meningioma, and No Tumor) can be seen in Figure 5. This figure provides a visual representation of the data used in the study.

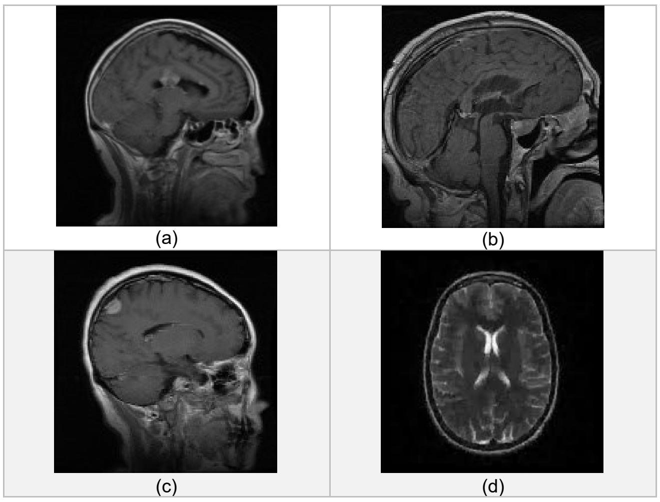

(a) (b) (c) (d)

Figure 5. (a) Glioma, (b) Pituitary, (c) Meningioma, (d) No Tumor

B. Data Preprocessing

The suggested approach makes use of 7,023 MRI pictures that have been divided into four categories: non-tumor, pituitary tumor, meningioma, and glioma. Image normalization, grayscale conversion, scaling, and extensive data augmentation methods, including rotation (up to 20 degrees) and horizontal and vertical flipping, were systematically applied to enhance the model's robustness and effectively mitigate the risk of overfitting. This augmentation strategy artificially expanded the dataset's size and diversity, exposing the model to tumor presentation and variation in image conditions. This process is crucial in preventing the model from merely memorizing the training examples, thereby significantly improving its generalization capability to unseen MRI data. Before model training is carried out, a pre-processing stage is carried out to ensure that the data is in an optimal format for use by the CNN model[11]. Some of the preprocessing stages include.

1. Resizing: All images are resized to 150×150 pixels for model input uniformity.

2. Grayscale Conversion: Images are converted to grayscale format to reduce data complexity without sacrificing important information.
3. Normalization: Pixel values are normalized to the interval [0,1] to expedite the model convergence process.
4. Data Augmentation: To improve model generalization and expand the amount of training data, augmentation such as rotation, horizontal flipping, zooming, and shifting is performed.

C. Training

The model training process used Python, leveraging the TensorFlow deep learning framework and its high-level API, Keras. This environment facilitated the efficient construction, compilation, and training of the ResNet architecture. Classification model [12] This study's approach to brain cancers combined the Convolutional Neural Network (CNN) architecture with the ResNet (Residual Network) architecture [13]. The proposed model leverages the ResNet architecture, a pre-trained convolutional neural network (CNN) known for its deep residual learning framework, to classify brain tumors. Effectively addresses the vanishing gradient problem in deeper networks by implementing skip connections or residual blocks, allowing for more efficient training and feature extraction.

To further combat overfitting and ensure optimal generalization performance, an early stopping mechanism was rigorously implemented during the training process. This callback carefully monitored the validation loss, and training was automatically terminated if the loss did not improve for a predetermined number of 30 consecutive epochs. This proactive strategy ensures that the model ceases training at its peak performance before it begins to overfit the training data, thereby maintaining its efficacy on new, unseen brain MRI images. ResNet was chosen because it trains deep networks using residual connections to prevent accuracy degradation. The model training structure includes.

- Input layer with size 150x150x1 (grayscale)
- Convolutional Layers with varying kernel size
- Batch Normalization and Activation Function (ReLU)
- Residual blocks are typical of ResNet architecture
- Global Average Pooling Layer
- Fully Connected Layer
- Output Layer with Softmax activity for 4-class classification.

The ResNet architecture, which is the basis of the classification model in this study, is depicted in Figure 6.

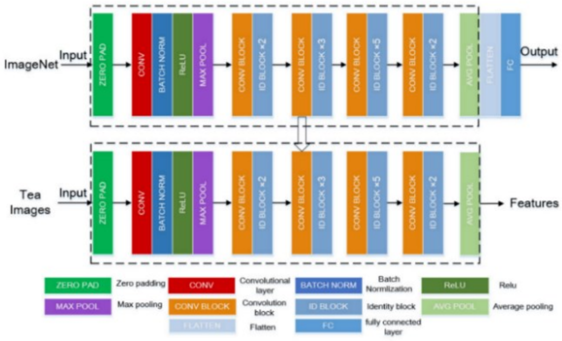


Figure 6. ResNet Architecture

D. Model Evaluation

This research begins with a study of related literature and then continues with data collection that will be used to create a deep learning model. Furthermore, the data will be cleaned and separated into training and test data. After that, image augmentation is used to increase the number of images. The next stage is designing and training the model to be used. In the final stage, an evaluation of the trained model is carried out.

Model performance evaluation is carried out using several evaluation metrics, namely:

- Accuracy
  Percentage of correct predictions against the total test data [14]. The accuracy formula is presented in formula (5), as follows:

$$Accuracy = \frac{TP}{TP + FP} \tag{5}$$

- Precision
  The ability of the model to identify the correct class compared to the positive predictions generated [15]. The precision formula is presented in formula (6), as follows:

$$Precision = \frac{TP}{TP + FP} \tag{6}$$

- Recall (Sensitivity)
  The ability of the model to find all positive instances of the target class [16]. The recall (sensitivity) formula is presented in formula (7), as follows:

$$Recall = \frac{Tp}{TP + FN} \tag{7}$$

- F1-Score
  A balanced performance metric is produced using the harmonic average of precision and recall.

The evaluation was conducted on a separate testing dataset, with a training and testing data split ratio of 80:20. The evaluation results were compared with baseline models or other relevant approaches in previous studies [17]. The F1-Score formula is presented in formula (8), as follows:

$$F1 - Score = 2 * \frac{PR * RCL}{PR + RCL} \tag{8}$$

III. RESULTS AND DISCUSSION

A. Training and Validation Performance

The classification algorithm created to identify different kinds of brain tumors using MRI scans performed exceptionally well. According to the evaluation results, the model's accuracy on the test data was 94.14%. This demonstrates how well the model can categorize pictures of brain tumors into the appropriate groups. The robust and consistent performance of the ResNet model suggests its significant potential as a supportive tool in clinical settings for rapid and accurate brain tumor diagnosis. Automating this process can reduce the diagnostic workload on radiologists, minimize the potential for human error inherent in manual interpretation, and enable quicker treatment initiation, ultimately contributing to improved patient outcomes. The model accuracy performance and model loss performance during the training and validation process are presented in Figure 7 and Figure 8.

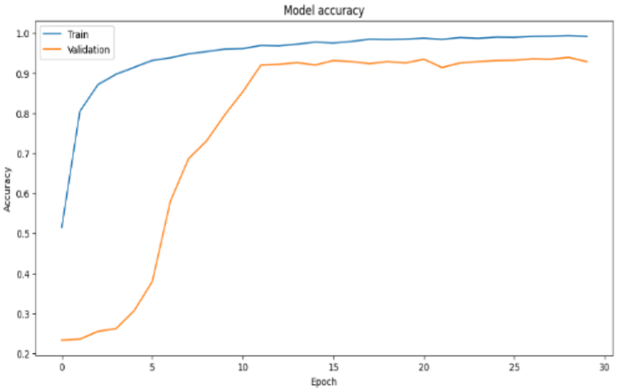


Figure 7. Model Accuracy

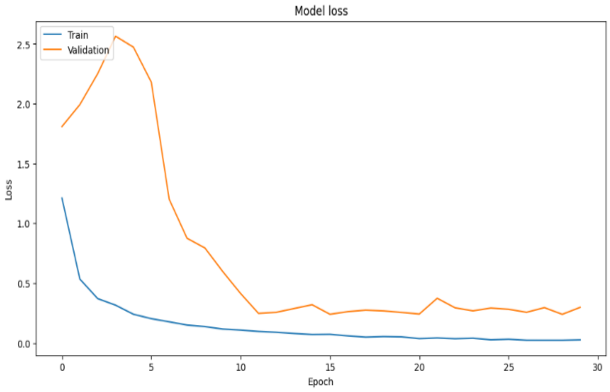


Figure 8. Model-Loss

The proposed brain tumor classification system, leveraging the ResNet architecture, achieved an overall accuracy of 94.14% on the unseen test dataset. This high accuracy, coupled with robust performance across individual tumor classes, underscores the model's capability to identify brain tumors accurately. The training progress, depicted by the training and validation accuracy and loss curves (Figure 3.1 and Figure 3.2), indicates stable learning dynamics with both training and validation loss decreasing consistently and accuracy converging, suggesting effective model generalization without significant overfitting

B. Confusion Matrix

The following image will display the confusion matrix test results with testing data. The results of model testing in the form of a confusion matrix are presented in Figure 9.

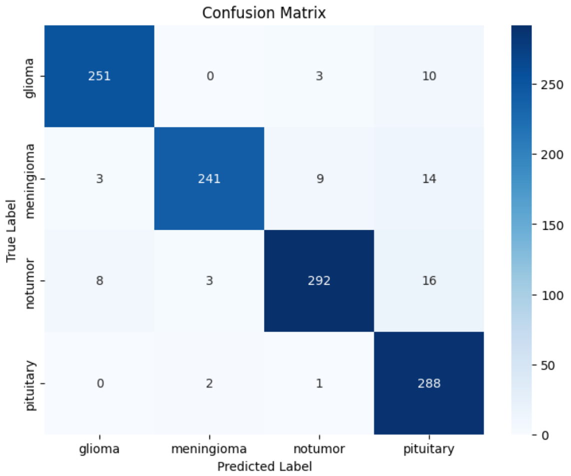


Figure 9. Confusion Matrix

C. Accuracy Results

The results of accuracy, precision, recall, and F1-score for each class, as well as the overall average, are presented in Table I.

TABLE I
ACCURACY RESULTS

Class	Precision	Recall	F1-Score	Support
Glioma	0.96	0.95	0.95	264
Meningioma	0.98	0.90	0.94	267
NoTumor	0.96	0.92	0.94	319
Pituitary	0.88	0.99	0.93	291
accuracy			0.94	1141
Marco avg	0.94	0.94	0.94	1141
Weighted	0.94	0.94	0.94	1141

The robust and consistent performance of the ResNet model suggests its significant potential as a supportive tool in clinical settings for rapid and accurate brain tumor diagnosis. Automating this process can reduce the diagnostic workload on radiologists, minimize the potential for human error inherent in manual interpretation, and enable quicker treatment initiation, ultimately contributing to improved patient outcomes. From a practical implementation standpoint, training such deep learning models, while demanding significant computational resources, is typically a one-time, intensive process. For reference, the training of our ResNet model on the specified dataset required approximately 49.96 minutes using the allocated GPU resources in Google Colab.

However, the inference time for classifying new MRI images is speedy, often completing within milliseconds. This rapid inference capability makes the proposed system highly feasible for near-real-time clinical deployment, where quick diagnostic feedback is paramount. Further research could investigate optimizing model size and efficiency for deployment on more resource-constrained clinical devices or edge computing platforms to enhance widespread accessibility. Despite the promising results, this study acknowledges several limitations that provide clear avenues for future research. Firstly, a significant limitation of the current study is the absence of validation on an external, independent dataset.

While the model demonstrated strong performance on our held-out test set, evaluation solely on a single publicly available dataset limits the complete assessment of its robustness and generalizability across diverse clinical settings. Secondly, while the ResNet architecture was specifically chosen for its proven efficacy in handling deeper networks and mitigating vanishing gradient issues, this study did not include a direct comparative analysis with other state-of-the-art convolutional neural network architectures (e.g., VGG, DenseNet, EfficientNet, MobileNet) under identical experimental conditions.

IV. CONCLUSION

The Convolutional Neural Network (CNN) algorithm was successfully integrated with the ResNet architecture in this study to create an automated brain tumor classification system. The study used a large dataset of 7,023 brain MRI pictures carefully divided into four categories: glioma, meningioma, pituitary tumor, and non-tumor. Several crucial preprocessing techniques, such as image normalization, grayscale conversion, scaling, and extensive data augmentation techniques like rotation (up to 20 degrees), horizontal and vertical flipping, zooming, and shifting, were methodically used to improve the model's robustness and successfully reduce the risk of overfitting. By artificially increasing the dataset's size and diversity, this augmentation technique exposed the model to more tumor appearances and imaging condition variations. Because of its shown effectiveness in managing deeper networks and addressing the vanishing gradient issue by utilizing residual blocks or skip connections, the ResNet design was especially selected. An early stopping mechanism was carefully incorporated into the training process to prevent overfitting and guarantee excellent generalization performance. It closely monitored the validation loss and stopped training if no improvement was seen for 30 consecutive epochs. A specific testing dataset with an 80:20 split ratio between training and testing data was used to assess the system's performance. F1-score, accuracy, precision, recall, and other metrics were used to evaluate the model's performance in detail. The model's remarkable accuracy of 94.14% on the test data produced convincing results. In addition, the model showed excellent F1-score, precision, and recall values for each unique class. These results demonstrate the potential of deep learning techniques, particularly CNNs with ResNet extensions, for complex classification tasks involving medical pictures.

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