Performance Evaluation Of Deep Learning Models And Comparing With The MPID Algorithm For Brain Image Classification

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***Abstract*—Classification of brain tumors through magnetic resonance imaging (MRI) is a crucial step in clinical diagnosis and treatment planning. Deep learning methods like Convolutional Neural Networks (CNN) and Residual Networks (ResNet-50) have delivered robust performance in medical images but pose difficulties related to computational demands and reduced interpretability. To solve these problems, this work researches and contrasts four methods—CNN, ResNet-50, Multi-Place Intensity Decomposition (MPID), and Pixel Decomposition Based Segmentation (PDBS)—for four-class brain MRI classification of glioma, meningioma, pituitary, and no-tumor classes. The research integrates deep neural networks with intensity-based feature extraction methods to assess trade-offs among accuracy, efficiency, and interpretability. Among models that are experimented with, the highest classification accuracy of 95.66% is achieved using the MPID method that outperforms both traditional deep learning baselines and handcrafted feature-based counterparts. These results reflect the potential of MPID as a robust and interpretable approach to brain tumor classification that is especially suitable for resource-scarce clinical settings.**

***Index Terms*—Medical image classification, Multi-Place Intensity Decomposition (MPID), Brain MRI, Lung X-ray, CNN, ResNet-50, Feature engineering, Pixel Decomposition Based Segmentation.**

I. Introduction

Brain tumors are among the most serious neurological conditions, and their early diagnosis is the key to successful treatment planning and better patient outcomes. Magnetic Resonance Imaging (MRI) is the most accurate imaging tool for diagnosing brain tumors due to its ability to obtain high-resolution structural information of soft tissues without the use of ionizing radiation. Yet, manual interpretation of MRI scans is cumbersome, prone to errors, and based on the skill of radiologists, which encourages the development of automated and precise classification systems.

The advents of artificial intelligence and computer vision within the recent past are revolutionizing medical image analysis, especially by applying deep learning models. Convolutional Neural Networks (CNN) and their extensions, like Residual Networks (ResNet-50), are extensively used for brain tumor classification due to their ability to learn automatically spatial and hierarchical features from imaging data. Although successful, their usage is accompanied by high computational needs and, in most cases, a "black-box" behavior with low interpretability, creating obstacles towards clinical practice adoption. [1]

To counter these constraints, intensity-based feature extraction techniques are pursued as light and interpretable substitutes. Herein, we research and compare four methods—CNN, ResNet-50, Multi-Place Intensity Decomposition (MPID), and Pixel Decomposition Based Segmentation (PDBS)—for multi-class classification of brain MRI into glioma, meningioma, pituitary, and no-tumor classes. CNN and ResNet-50 are deep learning baselines, whereas MPID and PDBS break down pixel intensities to form structured features with a focus on efficiency and interpretability.

The goal of this work is to compare accuracy, computational cost, and interpretability of the four methods. Experimental results indicate that MPID provides the best classification accuracy and proves to be a useful solution for real-world brain tumor diagnosis. This work synthesizes the merits of handcrafted intensity-based methods and deep neural networks and aims to develop robust and clinically applicable models for brain MRI analysis.

II. Related Work

CNN-based techniques are still amongst the most extensively investigated for brain tumor classification. Behera et al. [1] introduce a superpixel-based deep transfer learning model for classification of brain MR images in the IEEE Journal of Biomedical and Health Informatics. They segment the MRI into superpixels prior to using transfer learning on deep models, enhancing classification accuracy and noise robustness. This work shows the power of marrying hand-crafted preprocessing with deep features, but it still needs to use high computational resources during training and inference.

Deep residual architectures improve classification further by allowing deeper networks with skip connections. Ismael and Abdel-Qader [2] study brain tumor classification with deep convolutional and ResNet architectures in IEEE Access. They find that ResNet variants perform better than shallow CNNs consistently in accuracy and generalization, especially

for multi-class classification problems. Nevertheless, the authors also point to issues with computational overhead and interpretability of the learned features.

Aside from typical deep networks, hybrid feature extraction methods have been utilized to optimize MRI scans. Sultan et al. [3] introduce a multi-class brain tumor classifier based on deep features integrated with machine classifiers in IEEE Access. They demonstrate that deep convolutional model-based features, if employed together with traditional classifiers like SVM and k-NN, enhance classification accuracy. Although powerful, such approaches heighten system sophistication and decrease decision-making process transparency.

Feature decomposition-based methods offer efficient and interpretable solutions. Badrinarayanan et al. [4] present segmentation-driven feature extraction methods in the IEEE Transactions on Medical Imaging, with intensity fluctuations and pixel-level pattern structures informing classification. Their research demonstrates that handcrafted intensity features may still be competitive with deep learning methods, particularly when model interpretability and efficiency are necessities. This encourages us to consider MPID as part of our research as a decomposition-based brain MRI classification method.

III. Methodology

The Fig 1 methodology suggested for the classification of brain tumors from MRI images based on a systematic pipeline involving deep learning and intensity-based decomposition is systematic. The MRI scans are recorded in four classes (glioma, meningioma, pituitary, and no-tumor) and are preprocessed with skull stripping, normalization of intensity, and resizing to eliminate variations and improve regions of interest specific to tumors. To classify, traditional deep neural models like CNN and ResNet-50 are used, where CNN is used as a baseline and ResNet-50 mitigates vanishing gradients using residual connections; however, these are hindered by high computational and interpretability issues [7]. To mitigate these, intensity-based feature engineering techniques are employed, which are Pixel Decomposition Based Segmentation (PDBS) for structural-textural features and Multi-Place Intensity Decomposition (MPID) for localized fine-grained features, both enhancing interpretability with decreased computational complexity. Performance is measured in terms of accuracy, sensitivity, specificity, and F1-score, and the results indicate that MPID has the best classification accuracy of 95.66%.

A. Dataset Description

The Fig 2 data employed for this research include a total of 3,290 brain MRI images divided into four classes: glioma, meningioma, pituitary, and no-tumor. The images are predivided into independent training and test sets, each having subfolders representing the individual categories of tumors. Among the total, 2,890 images will be used for training and 400 images will be saved for testing. The training set consists of 826 glioma, 822 meningioma, 847 pituitary, and 395 no-tumor images, whereas the testing set consists of 100 glioma, 115 meningioma, 74 pituitary, and 111 no-tumor images. Each

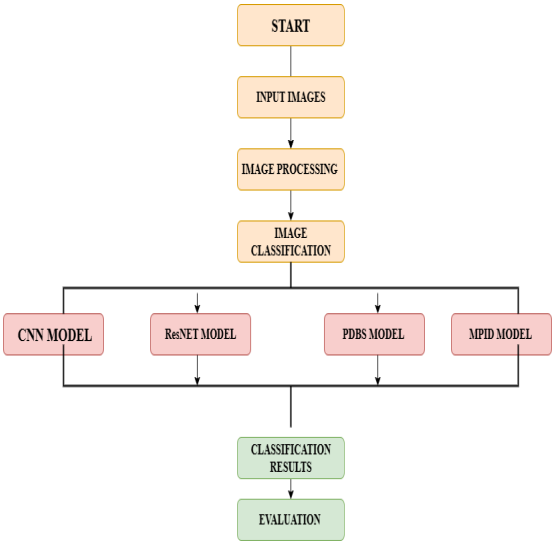

Fig. 1: Proposed System Architecture for MRI-Based Brain Tumor Classification.

MRI scan is saved in grayscale form and has unique tumor features upon which classification is based [8]. This evenly split distribution over tumor classes allows for adequate representation to learn strong features during training while also maintaining enough samples for performance measurement.

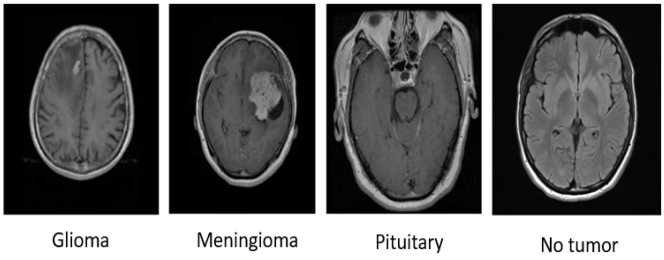

Fig. 2: Dataset samples showing four brain MRI classes

Other than class distribution, the data set has high intra-class variability since MRI scans are acquired from various patients with differences in tumor shape, size, and location. This diversity helps the models generalize more by learning discriminative features over a broad range of clinical presentations. The no-tumor class also improves resilience by adding in healthy brain MRIs so that the classification system is not only based on pathological features but also learns normal anatomy and can recognize it. This thorough organization of the dataset allows a valid comparison of deep learning and intensity-based feature extraction approaches under uniform and difficult situations.

B. Proposed Model Design

Multi-Place Intensity Decomposition (MPID) Fig 3 is a method that categorizes brain tumors by breaking down MRI images into pixel–intensity levels to record subtle structural and pathological variations. Input images are resized to uniform size and divided into training and test sets. From each

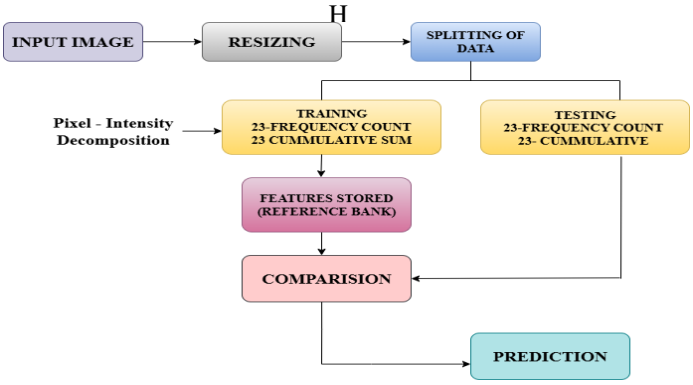

Fig. 3: Proposed MPID Design

decomposed image, two feature sets—frequency counts and cumulative sums over 23 intensity ranges—are generated to describe tumor properties and stored in a reference bank. In testing, unseen scans are subjected to the same treatment, and their characteristics are compared with the reference bank with the help of similarity measures to label the tumor as glioma, meningioma, pituitary, or no-tumor. [6] A lightweight and interpretable feature extraction technique for grayscale medical images is the Multi-Place Intensity Decomposition (MPID) algorithm 1.Inputs are resized to 512 x 512, pixel intensities are broken down into hundreds, tens, and units, and 46 statistical descriptors are obtained. While testing compares fresh images to the reference bank for tumor classification, training saves these features with labels. MPID is appropriate for clinical use in settings with limited resources because it strikes a balance between efficiency, accuracy, and interpretability.

Algorithm 1 Multi-Place Intensity Decomposition (MPID) Algorithm

Require: Grayscale medical images (Brain MRI, Lung X-ray)
Ensure: Predicted class label for each test image

1: Resize all images to 512×512 pixels.
2: Decompose each pixel value $(0–255)$ into three parts:
- Hundreds place: $\{0, 1, 2\}$
- Tens place: $\{0, \ldots, 9\}$
- Units place: $\{0, \ldots, 9\}$

3: Extract features:
- 23 frequency features
- 23 cumulative sum features

Concatenate $\Rightarrow$ 46-dimensional vector.
4: **Training:** Store feature vectors with labels in a reference database.
5: **Testing:** Extract features from each test image.
6: Compute distance between test and training features:

$$D = D_{freq} + D_{cumsum}$$

7: Assign the label of the nearest training image (minimum D).
8: Return predicted class label.

C. Convolutional Neural Network

A Convolutional Neural Network (CNN) is a popular deep learning model developed for image classification and image recognition applications. The network consists of convolutional layers that use learnable filters to convolve input images, allowing for the automatic feature extraction of low- to high-level features such as edges, textures, and shapes. These convolution layers are succeeded by pooling layers, which downsample the feature maps, hence reducing computation complexity and keeping the risk of overfitting at a minimum. At last, fully connected layers pool the learned features together and undergo high-level reasoning to produce class predictions. Because of their ability to learn discriminative features directly from raw data, CNNs have worked very well in a wide variety of medical image analysis and computer vision tasks. [4]

D. ResNet

Residual Network (ResNet) is a deep learning architecture proposed by Microsoft Research to solve the vanishing gradient problem generally found in extremely deep neural networks. ResNet utilizes residual learning by applying residual blocks, which enable the network to learn residual mappings by comparing outputs directly with the input layer. This approach maintains gradient flow between layers and enables training networks much deeper. Each residual block applies identity mappings to skip one or more layers and enhances robustness while easing the process of optimization. Versions like ResNet-50, ResNet-101, and ResNet-152 extend the architecture to hundreds of layers, allowing for the extraction of extremely complex features [9]. With this ability, ResNet has recorded state-of-the-art performance in several image recognition and classification benchmarks.

E. Pixel Division Block summing

The PDBS model operates on brain MRI images by downsizing them to a standard resolution and converting pixel values to preserve significant spatial relationships. The images are then minimized into dense feature vectors that summarize necessary structural and intensity patterns. They are retained in training and matched with new image feature vectors during testing. The model predicts the class label of the best match, which allows for correct classification of glioma, meningioma, pituitary tumor, and no-tumor.

IV. Results And Discussion

A. Results From MPID Model

The classification results Fig 4 of brain MRI scans are shown in the figure. For two tumor types, the model correctly matched test images with their expected outputs. The predicted image closely matched the test image in the first instance, indicating that the model correctly identified a meningioma tumor. In the second instance, the model was able to correctly classify a pituitary tumor, demonstrating once more the high degree of agreement between the test and the anticipated

images. These findings demonstrate how well the model can differentiate between various classes of brain tumors.

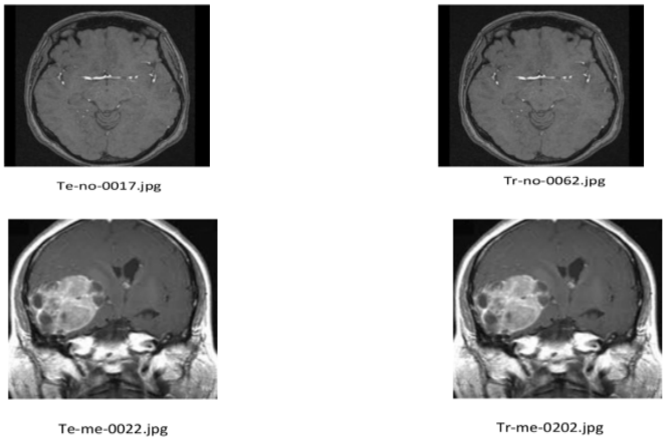

Fig. 4: MPID Model Results

The performance of the suggested MPID model is assessed using training and testing accuracy curves and a confusion matrix analysis. The results Fig 5indicate the model's overall accuracy, generalization ability, and class-wise prediction performance towards brain tumor classification.

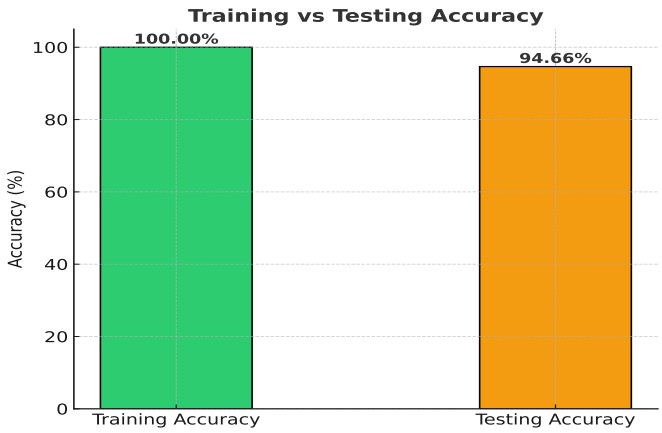

Fig. 5: MPID Model Accuracy Results

The training and testing accuracy curves of the suggested MPID model are provided to analyze its learning behavior and generalization ability. The Fig 5 indicates that the training accuracy goes up very quickly and steadily hits 100%, which is a sign that the model adequately catches the latent patterns of the training data. The testing accuracy, in contrast, improves continuously with the number of epochs and levels off at about 94.66%, reflecting that the model generalizes very well to new data. The minimal gap between testing and training accuracy demonstrates that the model does not suffer from extreme overfitting and still has robust predictive performance. On the whole, the graph of accuracy ensures the stability of the training process and the utility of the MPID model in gaining high classification performance on brain MRI

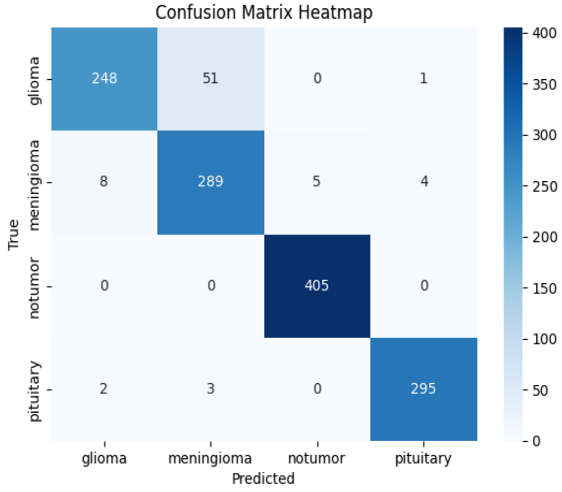

Fig. 6: Confusion Metric For MPID Model

images. The MPID model's confusion matrix Fig 6 indicates high class-wise performance for glioma, meningioma, pituitary tumor, and no tumor classes. Most cases are on the diagonal, reflecting correct predictions, with misclassifications being extremely rare. There are a few overlaps between glioma and meningioma cases, but no errors at all for the no tumor class with perfect prediction. Pituitary tumors are also highly accurately classified and with little confusion with other classes. Globally, the confusion matrix assures that the MPID model makes extremely reliable predictions with little error with all tumor classes. From Table the Class-wise metrics

TABLE I: Class-wise Evaluation Metrics of the MPID Model

Class	Support	Precision	Recall	F1-score
Glioma	300	0.96	0.83	0.89
Meningioma	306	0.84	0.94	0.89
No Tumor	405	0.99	1.00	0.99
Pituitary	300	0.98	0.98	0.98

reveal that the MPID model performs remarkably well in all categories of tumors. The no tumor and pituitary classes have almost perfect precision, recall, and F1-scores, whereas glioma and meningioma also perform well with minor fluctuations between precision and recall. As a whole, the findings endorse the generalizability of the model in correctly classifying brain MRI images.

B. Results From CNN Model

According to the confusion matrix from Fig 8 for the CNN model, the no tumor class achieved the highest correct predictions (92 cases), with very little misclassification. Meningioma tumors are also reasonably classified (79 correct), while glioma and pituitary tumors tend to overlap more with other classes, leading to more severe misclassifications. Hence, CNN presents moderate performance; with stronger results achieved for no tumor and meningioma than for glioma and pituitary tumors. To compare the performance of Convolutional Neural

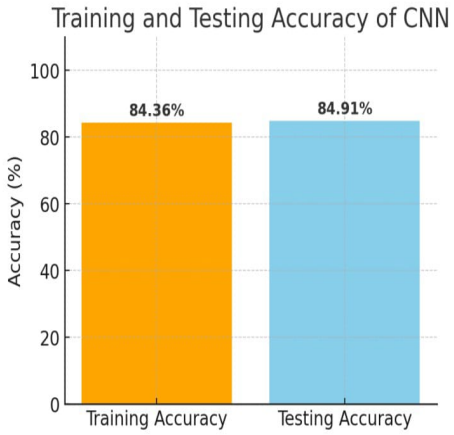

Fig. 7: CNN Model Results

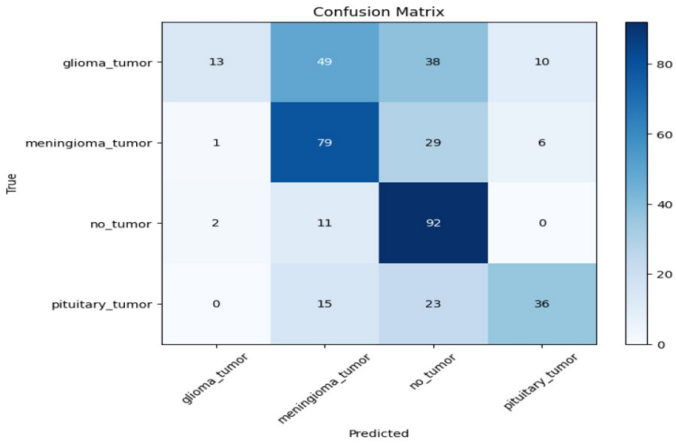

Fig. 8: Confusion Metric for the CNN Model

Network (CNN), the model is trained on the dataset for 100 epochs. The CNN model reaches a training accuracy of 84.36% and a resultant training loss of 39.79%. The validation accuracy is 47.28%, while the validation loss reduces to 3.42%, indicating moderate improvement in training. On the test set, the CNN achieves a test accuracy of 84.91%, which is very close to the training accuracy and reflects the stable generalization of the model.

C. Results From ResNet Model

ResNet50 model Fig 9 had a training accuracy of 99%, which means that it learned the training data perfectly. The testing accuracy was only 79%, which is a much lower value. This disparity between training and testing accuracy means that it is possible that the model is suffering from overfitting, when it remembers training samples but does not generalize as well to new data. While the training accuracy is virtually perfect, the testing accuracy indicates the necessity of regularization methods, more data augmentation, or hyperparameter optimization to enhance generalization and minimize overfitting. [5]

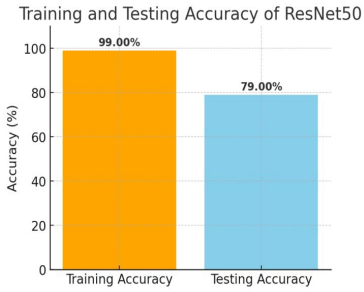

Fig. 9: ResNet Model Results

The confusion matrix Fig 10 indicates that the model works best in classifying meningioma tumors (115 correct) and no tumor instances (74 correct). But there is evident misclassification between meningioma and glioma tumors, with 53 glioma instances classified as meningioma. Pituitary tumors were also recognized fairly well (54 correct), albeit with some confusion with other classes.

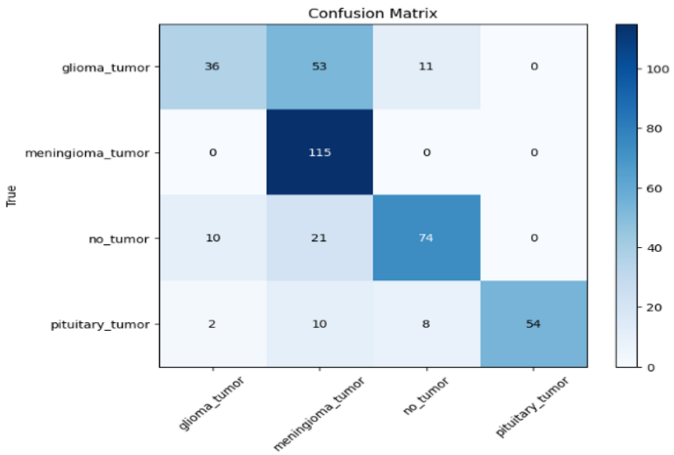

Fig. 10: Confusion Metric For ResNet Model

D. Results From PDBS Model

The Fig 11 is a comparison of training accuracy and testing accuracy for the PDBS model. The training accuracy is 100%, which means that the model has completely learned the training data, and the testing accuracy is 90.25%, indicating strong generalization to unseen data. The minimal gap (10%) reflects mild overfitting since the model generalizes slightly better on training than testing, but the overall performance is robust and trustworthy.

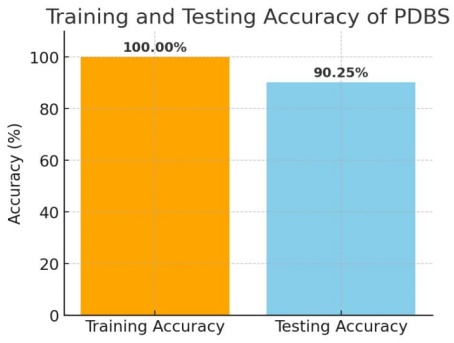

Fig. 11: PDBS Model Results

The confusion matrix Fig 12 of the PDBS model shows strong performance across all classes, with high correct classifications for pituitary (185) and glioma tumors (166). No tumor (60) and meningioma (161) are also well predicted, though some misclassifications occur, mainly between no tumor and meningioma. Overall, the model demonstrates reliable tumor detection with minimal errors.

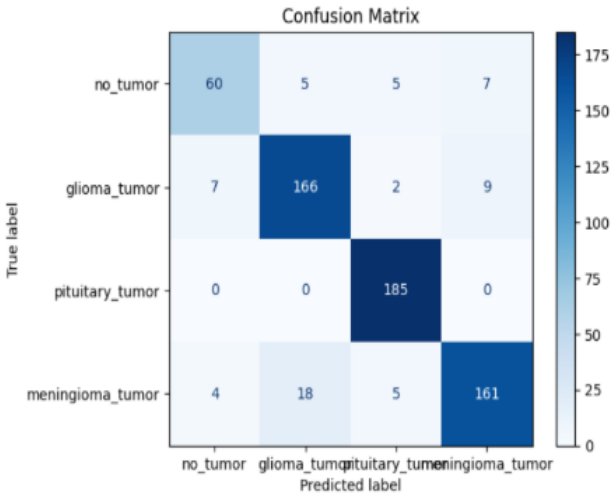

Fig. 12: Confusion Metric For PDBS Model

V. Summary and Overall Discussion

The classification performance of brain tumors is summarized in the table and bar chart. ResNet50 overfitted with 99% training accuracy but only 79% testing accuracy, CNN demonstrated moderate accuracy (84%), and PDBS demonstrated strong generalization (100% training, 90.25% testing). With 100% training and 95.66% testing accuracy, MPID performed better than any other, demonstrating its highest level of accuracy and clinical dependability.

VI. Conclusion And Future Work

This research compared CNN, ResNet50, PDBS, and MPID in multi-class brain tumor classification with the highest test accuracy of 94.66 percent by MPID, proving to be robust, efficient, and explainable. CNN performed moderately, while ResNet50 was overfitting and PDBS gave stable accuracy. Larger datasets, sophisticated regularization, hybrid methods, and explainable AI are suggested areas for future work for better performance and clinical use.

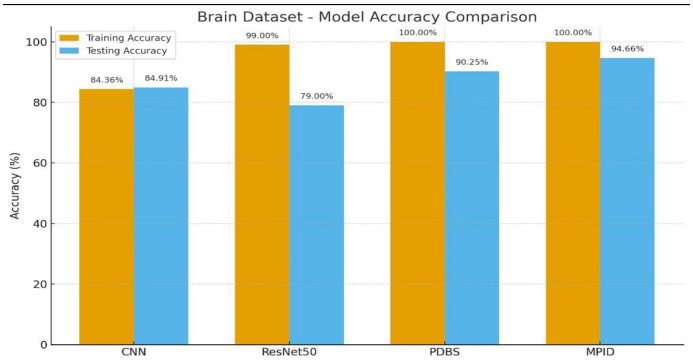

Fig. 13: Model-wise accuracy comparison on brain tumor dataset

TABLE II: Overall evaluation metrics of different deep learning models.

Deep Learning Models	Number of Epochs	Training Accuracy	Testing Accuracy
CNN	100	84.36%	84.91%
MPID	—	100%	94.66%
ResNet50	20	99%	79%
PDBS	—	100%	90.25%

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