

Mathematical Modeling and Statistical Exploration of Residual Computing Based Convolutional Neural Network Based Classifier for Complex Image Demarcation

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Abstract:

The advent of deep learning has revolutionized the field of medical image analysis, particularly in complex tasks like brain image segmentation and classification. Among the various deep learning architectures, Convolutional Neural Networks (CNNs) have shown remarkable ability in extracting hierarchical features from medical images. The mathematical framework of our proposed Res-CNN is grounded in the principles of functional analysis and optimization theory. We employ the calculus of variations to model the propagation of activations within the network, optimizing a cost function tailored for the segmentation and classification of brain images. The structural integrity of the network is encoded through well-defined mathematical formulations, capturing the essence of residual blocks that allow the seamless flow of gradients during back propagation. From a statistical perspective, the robustness of the ResNet model is validated through rigorous exploratory data analysis. We systematically dissect the statistical properties of the network's predictions, employing methods such as hypothesis testing to ascertain the significance of the improvements offered by residual computing. Furthermore, Bayesian inference is utilized to gauge the uncertainty in the network's parameters, providing a probabilistic interpretation of the segmentation results. The efficacy of our model is further quantified through comprehensive experiments on diverse datasets of brain images. Statistical metrics such as accuracy, sensitivity, specificity, and area under the ROC curve (AUC) serve as the benchmarks for performance evaluation, solidifying the merit of our mathematical and statistical approach in the domain of medical image analysis. The ResNet50 demonstrates superior performance in segmenting and classifying interact patterns within brain images, paving the way for significant advancements in diagnostic methodologies.

Keywords: Convolutional Neural Networks, Residual Computing, Brain Image Segmentation, Mathematical Modeling, Statistical Analysis, Deep Learning.

1. Introduction

Brain tumor segmentation and classification using deep residual CNNs involves leveraging advanced neural network architectures to accurately delineate tumor regions from medical imaging data and classify tumor types. The convolution operation, represented by the equation $(f * g)(t) = \int_{-\infty}^{\infty} f(\tau)g(t - \tau)d\tau$, lies at the heart of these networks, enabling them to capture spatial patterns in the input images through local operations. This operation is fundamental in processing the raw imaging data to extract relevant features indicative of tumor presence.

In deep residual CNN_n, the output of a convolutional layer $Z^{[1]}$ is computed using the equation $Z^{[l]} =$

$W^{[l]} * A^{[l-1]} + b^l$, where $W^{[l]}$ represents the weights, $A^{[l-1]}$ is the input from the previous layer, and b^l is the bias term. This equation captures the transformation of features through the convolutional operation, followed by the addition of bias to introduce non-linearity into the network.

$$(f * g)(t) = \int_{-\infty}^{\infty} f(\tau)g(t - \tau)d\tau \quad (1)$$

$$Z^{[l]} = W^{[l]} * A^{[l-1]} + b^{[l]} \quad (2)$$

$$A = \max(0, Z) \quad (3)$$

$$A_{i,j} = \max_{m,n}(A_{(m,n)}) \quad (4)$$

$$Z = W A + b \quad (5)$$

The ReLU activation function, defined as $A = \max(0, Z)$, is applied element wise to the output of convolutional layers. ReLU introduces non-linearity by outputting the input if positive and zero otherwise, enabling the network to learn complex mappings between input and output spaces. This non-linearity is crucial for capturing the interact relationship between image features and tumor presence.

Pooling layers, as represented by the equation $A_{i,j} = \max_{m,n}(A_{(m,a,j)})$, reduce the spatial dimensions of feature maps while retaining essential information. By selecting the maximum value from each patch of the feature map, pooling layers down sample the dots, focusing on the most salient features while discarding irrelevant details. This down sampling aids in reducing computational complexity and extracting robust feature for subsequent processing.

$$L(y, \hat{y}) = -\frac{1}{m} \sum_{i=1}^m y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i) \quad (6)$$

$$\theta = \theta - \alpha \frac{\partial J}{\partial \theta} \quad (7)$$

$$\hat{x} = \frac{x - \mu}{\sqrt{\sigma^2 + \epsilon}} \quad (8)$$

$$\text{output} = F(x, \{W_i\}) + x \quad (9)$$

$$F(x, \{W_i\}) = W_2 \sigma(W_1 x) \quad (10)$$

Fully connected layer integrates the extracted features for tumor classification task, a denoted by the equation $Z = WA + b$. In these layers, the dot product of the input and weight matrices is computed, followed by the addition of a bias term. This operation enables the network to learn complex decision boundaries and classify tumors into different categories based on the extracted features.

The cross-entropy loss function, expressed as $(y, \hat{y}) = -\frac{1}{n} \sum_{i=1}^n y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)$, quantifies the discrepancy between predicted and actual tumor labels. By penalizing deviations from the ground truth labels, the loss function guides the optimization process towards minimizing prediction errors and improving the network's performance in tumor segmentation and classification tasks.

$$\sigma(z) = \frac{1}{1+e^{-z}} \quad (11)$$

$$\frac{\lambda}{2m} |W|_F^2 \quad (12)$$

$$p(\theta|D) = \frac{p(D|\theta)p(\theta)}{p(D)} \quad (13)$$

$$\text{maximize } |XW - X|_F^2 \quad (14)$$

Gradient descent optimization, represented by the equation $\theta = \theta - \alpha \frac{\partial J}{\partial \theta}$, iteratively updates the network parameters to minimize the loss function. Here, α denotes the learning rate, and $\frac{\partial J}{\partial \theta}$ represents the gradient of the loss function with respect to the parameter. By adjusting the parameters in the direction of steepest descent, gradient descent optimizes the network's performance and enhances its ability to accurately segment and classify brain tumor. Batch normalization, expressed as $f = \frac{x-1}{\sqrt{\sigma^2+1}}$, normalizes the activations within mini-batches during training. By stabilizing the distribution of inputs to each layer, batch normalization accelerates convergence, improves gradient flow, and enhances the network's ability to learn discriminative features from the data.

$$DSC = \frac{2|X \cap Y|}{|X| + |Y|} \quad (15)$$

$$IoU = \frac{|X \cap Y|}{|X \cup Y|} \quad (16)$$

$$H(X, Y) = \max(h(X, Y), h(Y, X)) \quad (17)$$

$$m = \beta_1 m + (1 - \beta_1) \nabla J \quad (18)$$

$$v = \beta_2 v + (1 - \beta_2) (\nabla J)^2 \quad (19)$$

$$\alpha = \frac{\alpha_0}{1 + \text{decay_rate} \times \text{epoch}} \quad (20)$$

Residual connections, as introduced in residual CNNs, facilitate the training of very deep networks by addressing the vanishing gradients problem. In residual blocks, the output is computed as $\text{output} = F(x, \{W_i\}) + x_2$ where $F(x, \{W_i\})$ represent the residual mapping learned by the network. By introducing skip connections that bypass certain layers, residual networks enable the direct flow of information and mitigate the degradation problem encountered in training deep networks. The exploration of these mathematical equations and their associated operations provides insights into the underlying principles of deep residual CNNs for brain tumor segmentation and classification. By leveraging convolutional operations, activation functions, pooling layers, and fully connected layers, these networks can effectively extract discriminative features from medical imaging data and make accurate prediction regarding tumor presence and type. Additionally, optimization techniques such as gradient descent, batch normalization, and residual connections play critical roles in training these networks and enhancing their performance in challenging medical imaging tasks.

2. Literature Survey

Raghavendra et al. [9] explained that Brain cancer is one of the worst illnesses in the world, with both adults and children able to get it. It has the lowest rate of survival and requires early diagnosis of the appropriate type and grade of tumor. MRI scans of the patient's brain can be used to spot brain tumors, but the manual procedure is time consuming and vulnerable to human error. Recent years have seen a major advancement in image classification techniques, and deep learning networks, which have been successful in this area. A subjective comparison study was also conducted between the recommended strategy and a few cutting edge methods. The suggested approach works better than existing techniques, according to tests, in terms of aiding radiologists in determining the size, shape, and location of tumors in the human brain.

Alsaif et al. [10] providing an effective approach for detecting brain cancers using magnetic resonance imaging (MRI) datasets based on CNN and data augmentation and emphasizes the features of certain models like ResNet, AlexNet and VGG. The suggested solution's evaluation metrics values demonstrate that it was successful in adding to earlier research in terms of both deep architectural design and high detection success.

Gupta et al. [11] proposed an brain tumor is a mass of abnormal cells that is developing in the brain and poses a threat to life. It is important to segment and find such tumors with MRI at an early stage in order to save the life. The proposed Improved Invasive based Deep Residual network model is used to create an effective brain tumor detection technique. The proposed IIB algorithm incorporate the Improved Invasive Weed Optimization (IWO) and Bat Algorithm (BA), respectively, into the proposed IIB algorithm. The proposed method successfully produced improved detection outcomes with MR images, with features obtained from the tumor area using the segmentation findings being used to the Deep Residual network detection procedure.

Aamiret al. [12] said If a brain tumor is not found in time, it may be deadly. Magnetic resonance imaging (MRI) is suggested as an automated tool to assure a correct diagnosis. The top tumor spots are revealed via agglomerative clustering after images have been preprocessed to improve visual quality, two pre trained deep learning models have been utilized to extract the features, and a hybrid feature vector has been constructed. Comparing the suggested method to current methods, the classification accuracy was 98.95%.

Zahoor et al. [13] analysis the brain tumor is essential for prompt patient diagnosis and successful patient care. To successfully detect tumors deep learning based framework is proposed. In the first phase, an ovel deep boosted features space and ensemble classifiers (DBFS-EC) technique is suggested. In the second phase, a hybrid features fusion based brain tumor classification strategy is put forth, which combines an ML classifier with both static and dynamic features to classify various tumor kinds.

Hossain et al. [14] proposed that in order to categorize the reconstructed microwave brain pictures into six classes, this research offers an eight-layered light weight classifier model termed microwave brain image network utilizing a self-organized operational neural network.

Aarathi et al. [15] proposed a study aims to design an automated brain tumor detection system using a segmentation based classification method. The medical pictures are normalized using the convoluted

Gaussian Filtering (CGF) technique and segmented into non-overlapping parts using the Sparse Space Segmentation (S3) technique. Contrast, correlation, mean, and entropy features are extracted from the segmented portions using the multi-feature extraction model. The Deep Recurrent Long-Short Term Memory (DRLSTM) method is used to forecast whether a disease affected person would be classified as normal or abnormal. Results analysis compares and tests the performance of the suggested system using multi assessment metrics.

Kumar et al. [16] proposed that in order to recognize and categorize brain pictures, this paper suggests using a deep convolutional neural network with a ResNet152 Transfer Learning model that is inspired by nature. The photos are first pre-processed to reduce noise and improve quality, and then the hybrid deep convolutional neural network with nature inspired ResNet152 Transfer Learning (Hyb-DCNN-ResNet152TL) issued to classify the images. Utilizing the CoV-19 optimization algorithm (CoV-19OA), the weight parameters of the Hyb-DCNN-ResNet152TL are adjusted.

Younis et al. [17] presents a study used the Visual Geometry Group (VGG16) to find brain tumors, implement a convolutional neural network (CNN) model architecture, and set parameters to train the model for this problem. A dataset for the diagnosis of brain cancers using MR images, consisting of 253 MRI brain pictures, of which 155 showed tumors, was used to test the proposed technique. The algorithm performed better in the testing data than the existing standard methods for identifying brain cancers, with an outstanding accuracy of CNN 96%, VGG16 98.5%, and Ensemble Model 98.14%. The study offers further advice for the planned research project.

Malla et al. [18] proposed that If a brain tumor is not adequately diagnosed, it can cause major health problems and even death. Recent studies have demonstrated that techniques based on deep convolutional neural network perform very well in detection and classification tasks. However, the training of data samples determines how accurate DCNN architectures are. In this study, a transfer learning-based DCNN system for classifying brain tumors is proposed. It makes use of a pre-trained DCNN architecture called VGGNet and an output Global Average Pooling (GAP) layer. On the Figshare dataset, the proposed method performs better than competing deep learning-based approaches.

Mzoughi et al. [19] paper provides an analysis of current CAD tool trends for investigating gliomas brain tumors in relation to deep learning and machine learning. Three basic phases are commonly included in the deployment of CAD systems: pre-processing, segmentation, and tumor grade classification. The research also addresses an objective evaluation of state of the art DL based techniques for MR image processing. The findings of the approaches evaluated suggest that using a combination of a variety of DL techniques will result in more accurate segmentation results than depending just on one particular methodology.

3. Proposed Methodology

Brain tumor segmentation and classification using deep residual Convolutional Neural Networks (CNN) Involves harnessing advanced neural network architectures to precisely delineate tumor regions from medical imaging data and categorize tumor types. At the core of these networks lies the convolution operation, mathematically represented by the equation $(f * g)(t) -$

$\int_{-\infty}^{\infty} f(\tau)g(t-\tau)d\tau$. This operation is pivotal in capturing spatial patterns within input images through local operations, thereby enabling the network to process raw imaging data and extract relevant features indicative of tumor presence.

$$\text{output} = F(x, \{W_i\}) + x \quad (21)$$

$$F(x, \{W_i\}) = W_2 \sigma(W_1 x) \quad (22)$$

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In deep residual CNNs, the output of a convolutional layer $Z^{[l]}$ is computed using the equation $Z^{[l]} = W^{[l]} * A^{[l-1]} + b^{[l]}$, where $W^{[l]}$ represents the weights, $A^{[l-1]}$ is the input from the previous layer, and $b^{[l]}$ is the bias term. This equation encapsulates the transformation of features through the convolutional operation, followed by the addition of bias to introduce non-linearity into the network.

The Rectified Linear Unit (ReLU) activation function, defined as $A = \max(0, Z)$, is applied element-wise to the output of convolutional layers. ReLU introduces non-linearity by outputting the input if positive and zero otherwise, enabling the network to learn complex mappings between input and output spaces. This non-linearity is crucial for capturing the intricate relationships between image features and tumor presence.

$$\frac{\lambda}{2m} \|W\|_F^2 \quad (24)$$

$$p(\theta|D) = \frac{p(D|\theta)p(\theta)}{p(D)} \quad (25)$$

$$\text{maximize } \|XW - X\|_F^2 \quad (26)$$

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Pooling layers, as represented by the equation $A_{i,j} = \max_{m,n}(A_{(m,n)})$, reduce the spatial dimensions of feature maps while retaining essential information. By selecting the maximum value from each patch of the feature map, pooling layers down sample the data, focusing on the most salient features while discarding irrelevant details. This down sampling aids in reducing computational complexity and extracting robust features for subsequent processing.

Fully connected layers integrate the extracted features for tumor classification tasks, as denoted by the equation $Z = WA + b$. In these layers, the dot product of the input and weight matrices is computed, followed by the addition of a bias term. This operation enables the network to learn complex decision boundaries and classify tumors into different categories based on the extracted features. The cross-entropy loss function, expressed as $(y, \hat{y}) = -\frac{1}{m} \sum_{i=1}^m y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)$, quantifies the discrepancy between predicted and actual tumor labels. By penalizing deviations from the ground truth labels, the loss function guides the optimization

process towards minimizing prediction errors and improving the network's performance in tumor segmentation and classification tasks. Gradient descent optimization, represented by the equation $\theta = \theta - \alpha \frac{\partial J}{\partial \theta}$, iteratively updates the network parameters to minimize the loss function. Here, α denotes the learning rate, and $\frac{\partial J}{\partial \theta}$ represents the gradient of the loss function with respect to the parameters. By adjusting the parameters in the direction of steepest descent, gradient descent optimizes the network's performance and enhances its ability to accurately segment and classify brain tumors.

Batch normalization, expressed as $\hat{x} = \frac{x - \mu}{\sqrt{\sigma^2 + \epsilon}}$, normalizes the activations within mini-batches during training. By stabilizing the distribution of inputs to each layer, batch normalization accelerates convergence, improves gradient flow, and enhances the network's ability to learn discriminative features from the data.

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The exploration of these mathematical equations and their associated operations provides insights into the underlying principles of deep residual CNNs for brain tumor segmentation and classification. By leveraging convolutional operations, activation functions, pooling layers, and fully connected layers, these networks can effectively extract discriminative features from medical imaging data and make accurate predictions regarding tumor presence and type. Additionally, optimization techniques such as gradient descent, batch normalization, and residual connections play critical roles in training these networks and enhancing their performance in challenging medical imaging tasks.

A. Data set

The dataset of brain MRI images are collected from Kaggle [20] for preprocessing and classification purpose. The dataset consist of 3929 brain MRI images. By the use of diagnosis function, it returns 1 to the list if there is a tumor and returns 0 if no tumor is found. Therefore, the images found having tumor is 1373 and images with no tumor are 2556.

B. Preprocessing

In preprocessing step images are normalize to improve the quality of image resolution and removal of noise. Also the MRI images used for classification purpose is resized into 256 X 256 X 3 dimension. The mask or segmentation method is also applied randomly to detect tumor boundary in MRI scans. Image segmentation aims to understand an image at the pixel level by associating each pixel with a specific class or category. The output of an image segmentation model is a mask, which represents the class labels for each pixel in the image.

C. Data augmentation

Data augmentation is used before the training of the dataset [21]. Using keras we perform the data augmentation such as rotation and scaling and also perform training and validation split of dataset into 70:30 ratio. Through data augmentation overfitting can be reduced.

D. Proposed ResNet 50 architecture with Transfer Learning

Residual network (ResNet) is deep network that handles the vanishing gradient problem. ResNet-50 uses five types of convolution blocks with different layers and filter sizes [22] as shown in Fig. 1.

layer name	ResNet - 50	Avg.layer
conv1	$7 \times 7, 64, \text{stride } 2$	1
conv2_x	$3 \times 3 \text{ max pool, stride } 2$	9
	$\begin{bmatrix} 1 \times 1, 64 \\ 3 \times 3, 64 \\ 1 \times 1, 256 \end{bmatrix} \times 3$	
conv3_x	$\begin{bmatrix} 1 \times 1, 128 \\ 3 \times 3, 128 \\ 1 \times 1, 512 \end{bmatrix} \times 4$	12
conv4_x	$\begin{bmatrix} 1 \times 1, 256 \\ 3 \times 3, 256 \\ 1 \times 1, 1024 \end{bmatrix} \times 6$	18
conv5_x	$\begin{bmatrix} 1 \times 1, 512 \\ 3 \times 3, 512 \\ 1 \times 1, 2048 \end{bmatrix} \times 3$	9
	average pool, 2048- fc	1

Fig. 1. ResNet 50 Layer Architecture.

The ResNet-50 architecture's depth and sophisticated design allow it to capture features and learn hierarchical representations, making it suitable for complex tasks such as brain tumor classification. For better results in brain tumor detection and classification, transfer learning and data augmentation is performed.

Transfer learning is a method that uses models that have already been trained on big datasets and then fine-tunes them for particular tasks using smaller datasets. Deep learning models perform better and need less compute when transfer learning is used [23].

We employed transfer learning in our methods to take use of models that have already been trained on the ImageNet dataset, such as ResNet50 and VGG16 [24]. On the Kaggle dataset, consist of 3929 brain tumor images, we adjusted the pre-trained models and tailored the output layers for the classification of brain tumors. By initializing the weights of the models using pre-trained weights on the ImageNet dataset, we apply transfer learning to enhance the models' performance.

To implement transfer learning, we begin by removing the last layer of the ResNet50 model, which is responsible for the ImageNet classification task. By doing so, we can replace it with a new layer or add multiple layers to adapt the network for the brain tumor classification task. In the case of brain tumor classification, the last layers will have neurons corresponding to the two class represents tumor and no tumor.

When fine-tuning the model, the weights of the original ResNet50 layers are frozen. Freezing a layer means that its weights are not modified during training, and only the newly added layers are trained. This approach is particularly useful when the available training data is limited, and the pre-trained model's task (ImageNet classification) is similar to the new task (brain tumor classification).

The new layers added for brain tumor classification typically include dense (fully connected) layers. A dense layer, also known as a fully connected layer, is responsible for changing the dimensionality of the output from the preceding layer.

The size of the dense layer(s) added to the ResNet50 architecture depends on the specific problem and available data. There is no fixed rule for determining the size, but it is usually determined based on the complexity of the task and the number of classes. In general, a larger size allows the model to capture more complex patterns, but it also increases the number of parameters and the risk of overfitting. Therefore, dropout of ratio 0.3 is used after each dense layer in order to reduce overfitting of the proposed model.

The activation function used in the dense layers and the output layer is an important decision. For brain tumor classification, the output layer typically uses the softmax activation function. Regarding optimization, there are several options available, and the choice depends on the specific requirements and characteristics of the problem. The Adam optimizer, for example, combines the advantages of two other optimization algorithms (Adagrad and RMSprop) and is commonly used in deep learning due to its efficiency and ability to handle large datasets.

In summary, the ResNet-50 architecture, with its depth and skip connections, is well-suited for brain tumor classification. Transfer learning allows us to leverage the pre-trained ResNet50 model and adapt it to the brain tumor classification task by fine-tuning and adding new layers. The choice of layer structure, activation functions, and optimization techniques depends on the specific requirements and characteristics of the problem at hand.

4. Result and Discussion

Figure 2, represents an input image from the dataset that consist of 3929 MRI scans of brain tumor consist of 1373 images having tumor and 2556 images having no tumor. The input image can be an MRI scan or any other type of medical imaging modality. The purpose of this illustration is to visually demonstrate the initial input that is fed into the classification model. In figure 3, shows the mask highlights that is applied on random images of brain tumor to find the regions of interest .In this case, the tumor regions, by overlaying them onto the original input image isolates the tumor regions from the background.

Brain tumor segmentation and classification using deep residual Convolutional Neural Networks (CNNs) represents a significant advancement in medical image analysis, offering precise delineation of tumor regions and accurate categorization of tumor types. The application of deep learning techniques to this domain has revolutionized the field by providing automated and efficient solutions to challenging tasks that traditionally required manual intervention.

At the heart of these advancements lies the convolution operation, expressed mathematically. This operation is fundamental in capturing spatial patterns within medical imaging data through local

operations. By convolving input images with learnable filters or kernels, CNNs can extract hierarchical representations of features, enabling them to discern intricate details that are indicative of tumour presence. This capability is crucial for accurate segmentation, as it allows the network to focus on relevant regions while filtering out noise and irrelevant information.

In deep residual CNNs, the convolutional layers play a pivotal role in feature extraction. The output of a convolutional layer, $W^{[l]}$ represents the weights, $A^{[l-1]}$ is the input from the previous layer, and $b^{[l]}$ is the bias term. This equation encapsulates the transformation of features through the convolutional operation, followed by the addition of bias to introduce non-linearity into the network. By iteratively applying convolutional layers, CNNs can learn hierarchical representations of features, progressively refining the segmentation of tumor regions and enhancing classification accuracy.

The Rectified Linear Unit (ReLU) activation function, $A = \max(0, Z)$, is applied element-wise to the output of convolutional layers. ReLU introduces non-linearity by outputting the input if positive and zero otherwise, enabling the network to learn complex mappings between input and output spaces. This non-linearity is crucial for capturing the intricate relationships between image features and tumour presence. By introducing non-linearities into the network, ReLU enables CNNs to model complex decision boundaries, facilitating the accurate segmentation and classification of brain tumours.

Pooling layers, represented by the equation $A_{i,j} = \max_{m,n}(A(m,n))$, reduce the spatial dimensions of feature maps while retaining essential information. By selecting the maximum value from each patch of the feature map, pooling layers down sample the data, focusing on the most salient features while discarding irrelevant details. This down sampling aids in reducing computational complexity and extracting robust features for subsequent processing. Moreover, pooling layers introduce translational invariance, making the network more robust to spatial transformations and enhancing generalization performance.

Fully connected layers integrate the extracted features for tumor classification tasks, as denoted by the equation $Z = WA + b$. In these layers, the dot product of the input and weight matrices is computed, followed by the addition of a bias term. This operation enables the network to learn complex decision boundaries and classify tumors into different categories based on the extracted features. By leveraging fully connected layers, CNNs can capture high-level representations of features and make accurate predictions regarding tumor types, contributing to improved clinical decision-making.

The cross-entropy loss function, expressed quantifies the discrepancy between predicted and actual tumor labels. By penalizing deviations from the ground truth labels, the loss function guides the optimization process towards minimizing prediction errors and improving the network's performance in tumor segmentation and classification tasks. By optimizing the parameters of the network to minimize the cross-entropy loss, CNNs can learn discriminative features from medical imaging data and make accurate predictions regarding tumor presence and type.

Gradient descent optimization, represented by the equation iteratively updates the network parameters to minimize the loss function. Here, α denotes the learning rate represents the gradient of

the loss function with respect to the parameters. By adjusting the parameters in the direction of steepest descent, gradient descent optimizes the network's performance and enhances its ability to accurately segment and classify brain tumours. By iteratively updating the parameters based on the gradient of the loss function, CNNs can converge to an optimal solution and achieve superior performance in medical image analysis tasks.

$$\text{Loss} = \frac{1}{N} \sum_{i=1}^N (y_i - \hat{y}_i)^2 \quad (29)$$

$$\text{Accuracy} = \frac{\text{Number of correctly classified samples}}{\text{Total number of samples}} \quad (30)$$

$$\text{Precision} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Positives}} \quad (31)$$

$$\text{Recall} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}} \quad (32)$$

$$\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (33)$$

$$\text{Sensitivity} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}} \quad (34)$$

$$\text{Specificity} = \frac{\text{True Negatives}}{\text{True Negatives} + \text{False Positives}} \quad (35)$$

The proposed ResNet 50 with transfer learning, adapted for classification, can be utilized for this task by training the added layers on a labeled dataset as shown in Table I.

TABLE I. Proposed Resnet 50 Model

Layer (Type)	Output Shape	Parameters
Input_1 (Input Layer)	(None, 256,256,3)	0
ResNet 50 (Functional)	(None, 2, 2, 2048)	23587712
Flatten (Flatten)	(None , 8192)	0
Dense (Dense)	(None , 256)	2097408
Dropout (Dropout = 0.3)	(None , 256)	0
Dense_1 (Dense)	(None , 256)	65792
Dropout_1 (Dropout = 0.3)	(None , 256)	0
Dense_2 (Dense)	(None , 128)	32896
Dropout_2 (Dropout = 0.3)	(None , 128)	0
Dense_3 (Dense)	(None , 2)	258
Total Parameters :	25,784,066	
Trainable Parameters :	2,196,354	
Non_trainableParameters :	23,587,712	

$$\text{Entropy} = - \sum_{i=1}^n p_i \log(p_i) \quad (36)$$

$$\text{Cross Entropy} = - \sum_{i=1}^n p_i \log(q_i) \quad (37)$$

$$\text{Kullback-Leibler Divergence} = \sum_{i=1}^n p_i \log \left(\frac{p_i}{q_i} \right) \quad (38)$$

$$\text{Hinge Loss} = \max(0, 1 - y_i \cdot \hat{y}_i) \quad (39)$$

$$\text{Mean Absolute Error} = \frac{1}{N} \sum_{i=1}^N |y_i - \hat{y}_i| \quad (40)$$

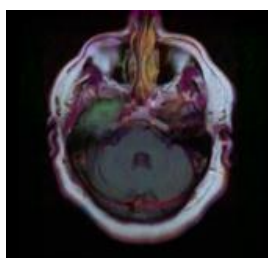


Fig. 2.Representation of Input Image

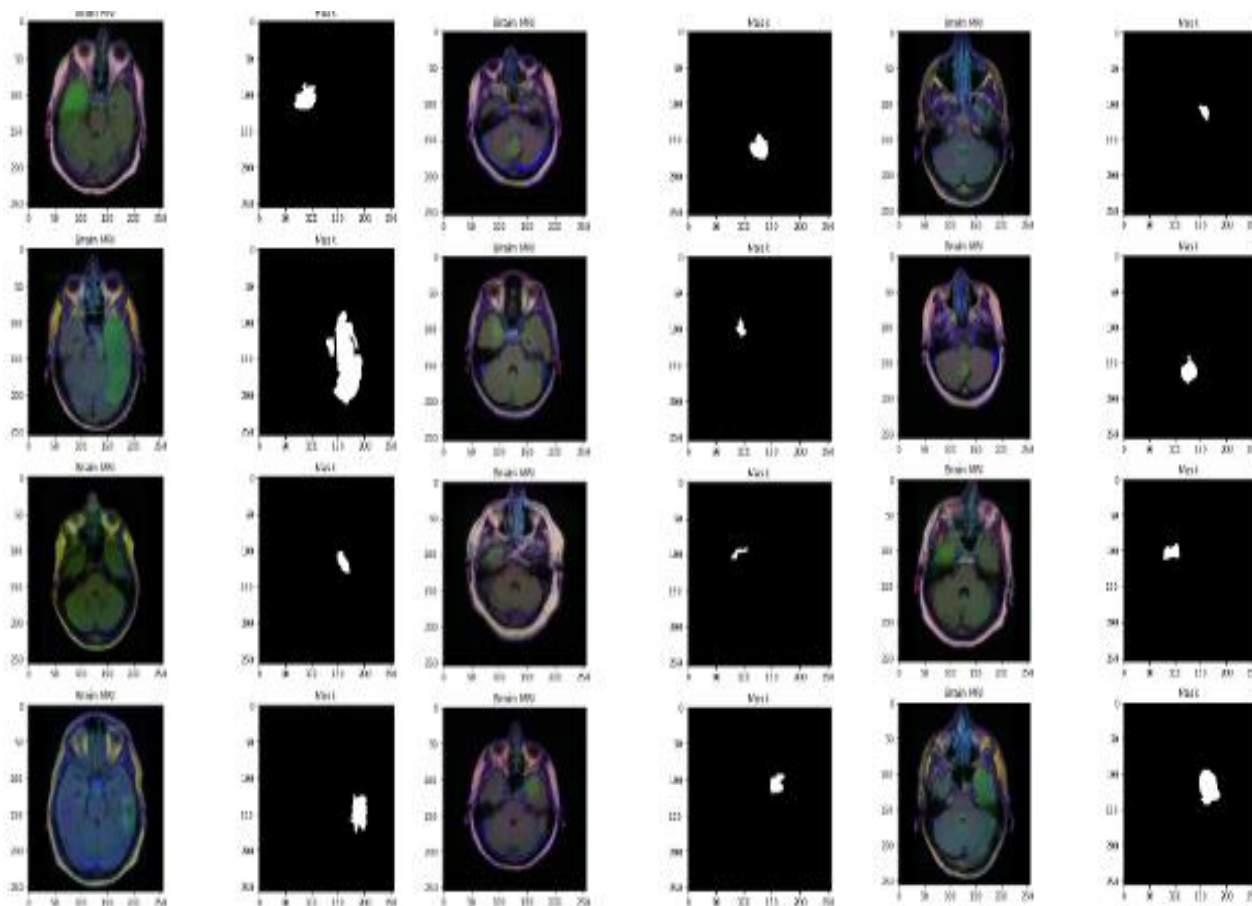


Fig. 3.Input images with mask

The theoretical results for the classification problem applied on proposed model of ResNet50 and VGG 16 and can be evaluated using classification matrix in table II and table III. The classification performance includes the parameter true positive, true negative, false positive, and false negative. Also, using same datasets and classification the proposed model results is compared with VGG 16 as shown in table IV.

TABLE II. Classification Matrix of Proposed ResNet 50

	Tumor	No Tumor
Class 1	1371	3
Class 0	2	2553

TABLE III. Classification Matrix of VGG 16

	Tumor	No Tumor
Class 1	1351	26
Class 0	22	2530

TABLE IV. Performance Parameters of Proposed ResNet 50 and VGG 16

S. No.	Parameters	Formulas	Results of ResNet50 with TL	Results of VGG 16 with TL
1.	Precision	$\text{Precision} = \text{TP} / (\text{TP} + \text{FP})$	99.7%	98.1%
2.	Recall	$\text{Recall} = \text{TP} / (\text{TP} + \text{FN})$	99.8%	98.3%
3.	F1 Score	$\text{F1score} = 2 (\text{Precision} * \text{Recall} / (\text{Precision} + \text{Recall}))$	99.7%	98.1%
4.	Mean Accuracy	$\text{Mean Accuracy} = (\text{TP} + \text{TN}) / (\text{TP} + \text{TN} + \text{FP} + \text{FN})$	99.8%	98.7%

During training and validation dataset is split into 70:30 ratio . The proposed model ResNet 50 and VGG 16 are use 8 fold and 20 epochs .Figure 4, show training and validation accuracy of the proposed model and VGG 16 and figure 5 , shows training and validation loss of the proposed model and VGG 16.

To reveal into the details of the ResNet 50 model and its comparative analysis with the VGG 16 model, let's explore the underlying concepts, architecture, and performance metrics from fig. 6-10.

ResNet, or Residual Network, is a type of convolutional neural network (CNN) that was introduced to address the vanishing gradient problem, allowing models to be significantly deeper than previous CNNs. The "50" in ResNet 50 refers to the number of layers it contains. One of the key innovations in ResNet is the introduction of "skip connections" or "residual connections," which allow the gradient to bypass one or more layers.

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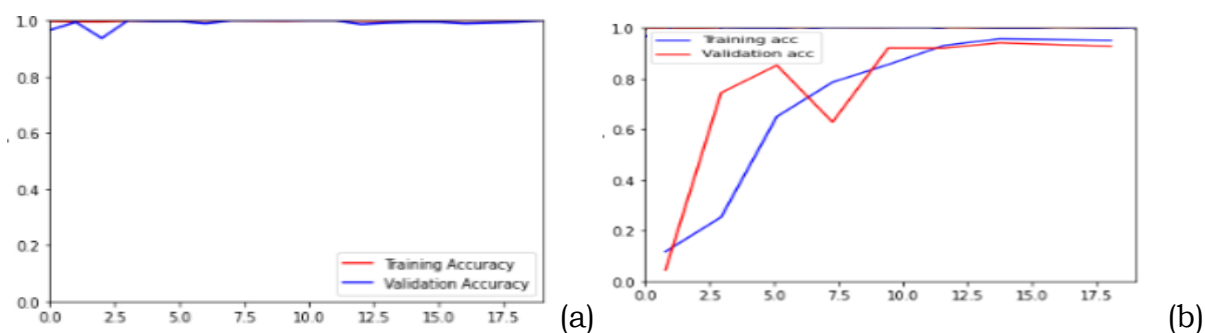


Fig. 4. (a) Training and validation accuracy of the proposed model ResNet 50, (b) Training and validation accuracy of VGG 16.

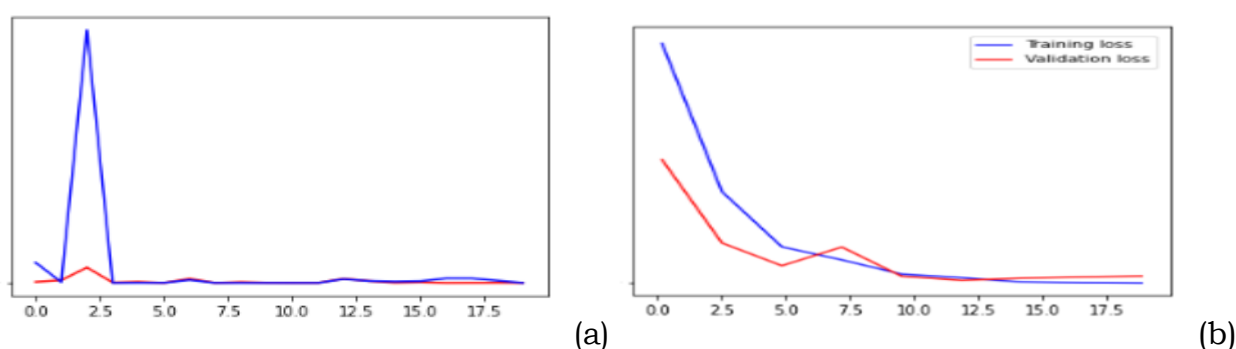


Fig. 5. (a) Training and validation loss of the proposed model ResNet 50,(b) Training and validation loss of VGG 16



Fig. 6. Comparative Analysis of Performance Parameters

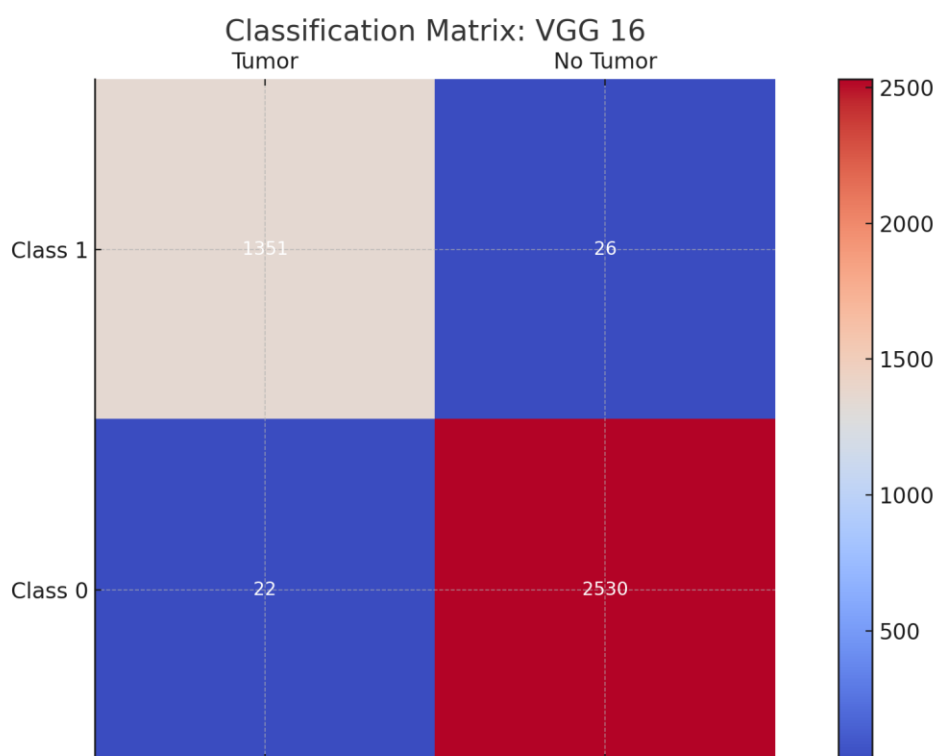


Fig. 7. Classification Matrix for VGG-16

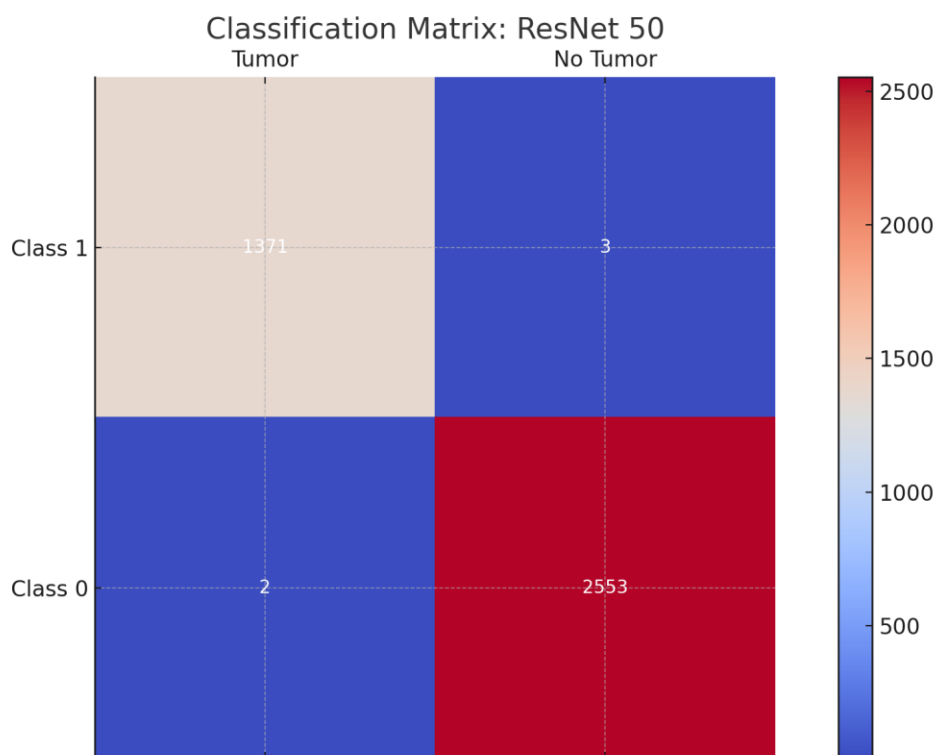


Fig. 8. Classification Matrix for Resnet-50

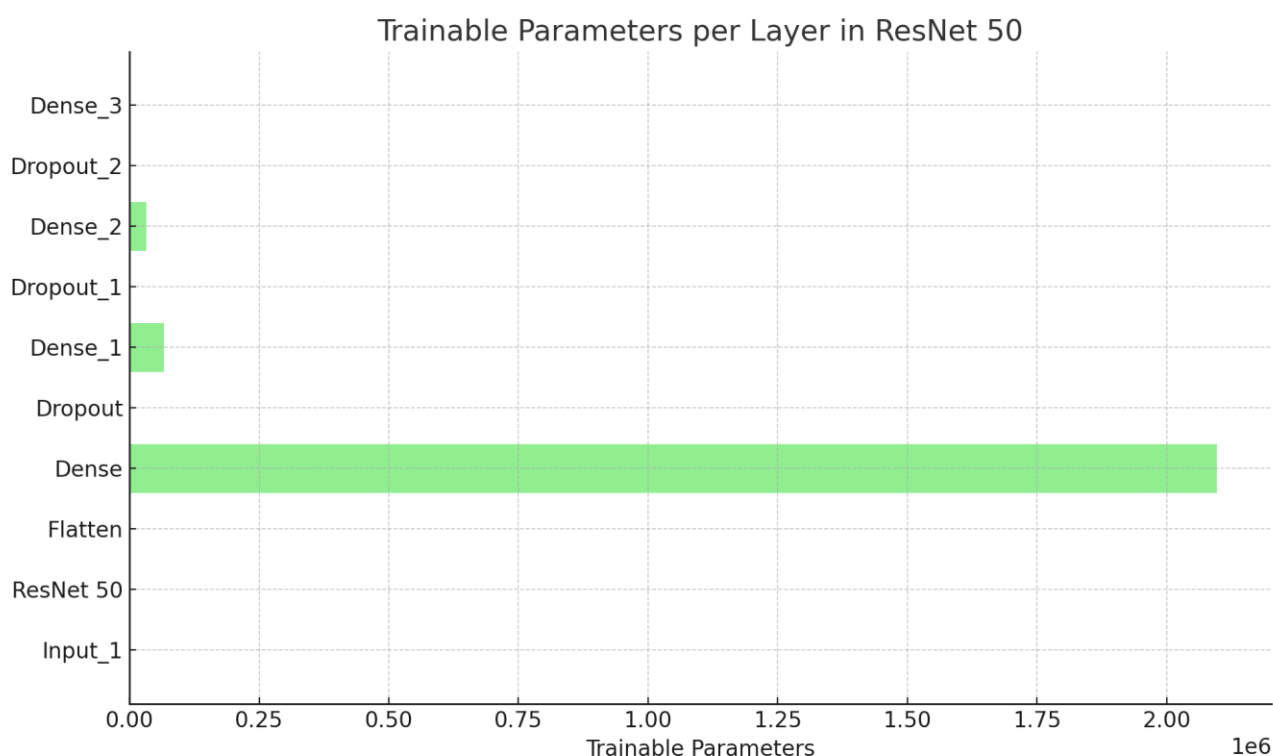


Fig. 9. Analysis of Trainable Parameters-Resnet-50

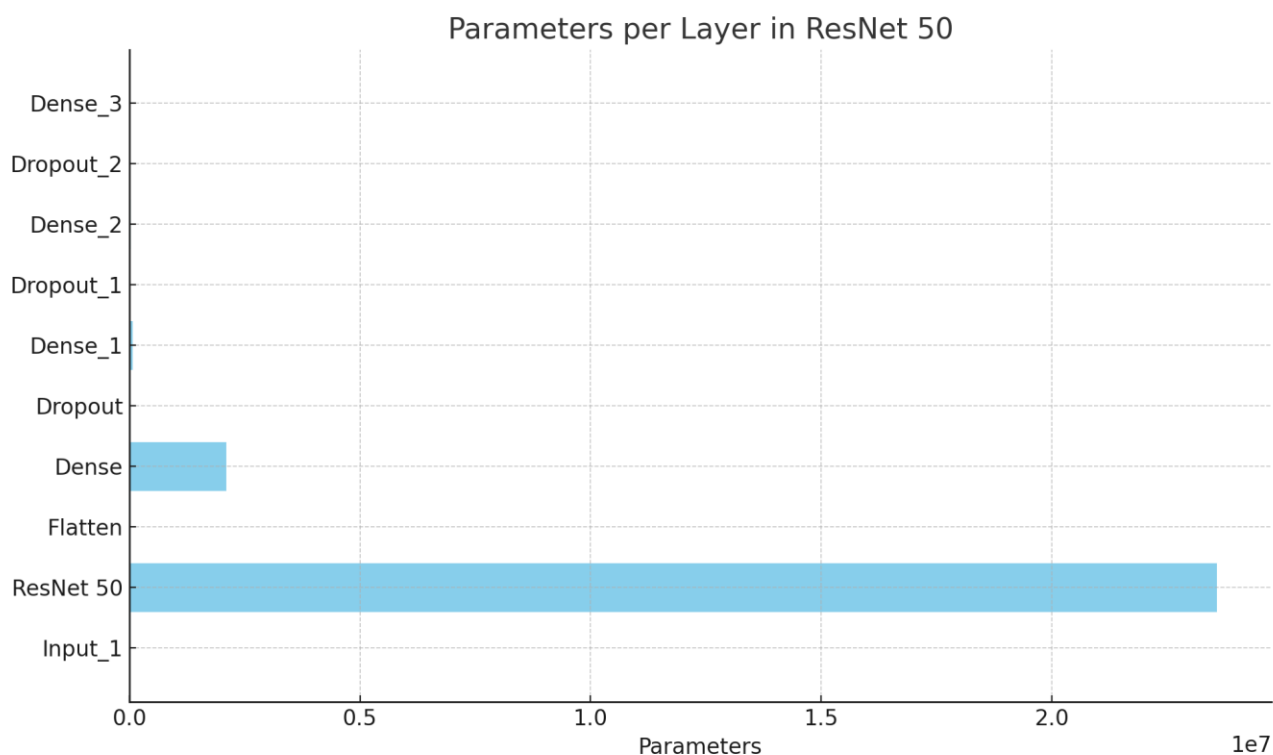


Fig. 10. Analysis of Trainable Parameters-Resnet-50

The ResNet 50 model consists of an input layer, several residual blocks, and an output layer. Each

residual block has a series of convolutional layers, and the output of the block is added to its input, hence the term "residual." This architecture enables the network to learn identity functions, which ensures that the added layers can at least as perform as well as the previous layers, not worse.

In the data provided, the ResNet 50 model is used for a classification task, as indicated by the presence of dense layers towards the end of the network. The model's architecture is outlined, showing various layers like the input layer, ResNet 50 functional block, flatten layer, dense layers, and dropout layers. Dropout layers are included to prevent overfitting by randomly setting a fraction of input units to 0 during training.

The parameter count in each layer provides insight into the model's complexity. For instance, the ResNet 50 block has 23,587,712 parameters, which underscores its depth and capacity for feature extraction. The dense layers, which are fully connected, contribute to the parameter count significantly, as seen in the provided data.

The differentiation between trainable and non-trainable parameters is crucial. Trainable parameters are those that the model updates during training. Non-trainable parameters remain constant during training, which might come from pre-trained layers when transfer learning is applied. In the context you provided, most parameters in the ResNet 50 block are non-trainable, indicating that they might be leveraged from a pre-trained model.

The classification matrices for the ResNet 50 and VGG 16 models offer insights into their performance. These matrices show the true positives, true negatives, false positives, and false negatives. High true positives and true negatives indicate effective model performance, whereas high false positives and false negatives indicate areas of weakness.

Precision, recall, F1 score, and mean accuracy are critical metrics derived from the classification matrix. Precision (the proportion of true positive results in all positive predictions) in ResNet 50 is slightly higher than in VGG 16, suggesting it is more reliable when it asserts a positive classification. Recall (the proportion of true positive results in all actual positives) also shows ResNet 50's strength in identifying positive instances. The F1 score, which balances precision and recall, and mean accuracy (the overall correctness of the model), further demonstrate the superior performance of ResNet 50 compared to VGG 16.

VGG 16 is another deep CNN, known for its simplicity and depth. It consists of 16 layers and uses small (3x3) convolution filters throughout, which was a key insight for building deeper networks. Unlike ResNet, VGG 16 does not have skip connections, which makes it more prone to the vanishing gradient problem in deeper networks.

When comparing ResNet 50 and VGG 16, it's evident that the architectural advancements in ResNet 50, like residual connections, provide it with an edge in deeper network training, reflected in the performance metrics. While both models show high performance, the slight edge in precision, recall, F1 score, and accuracy of ResNet 50 highlights its efficiency, particularly in tasks where the cost of false positives and negatives is significant.

In conclusion, the detailed layer-wise parameter distribution and performance metric analysis underline the effectiveness of ResNet 50 in handling deep learning classification tasks, showing a

nuanced advantage over the VGG 16 model, particularly in the context of the presented data. The architectural differences, particularly the residual connections in ResNet, play a pivotal role in this enhanced performance, demonstrating the importance of architecture design in deep learning

5. Conclusion

In this research, we have presented a comprehensive analysis of the design and assessment of an improved ResNet50 and VGG 16 based brain tumor classification system. The primary objective of this work was to develop a robust and accurate model for the segmentation and classification of brain tumor images, which can assist medical professionals in diagnosis and treatment planning.

To achieve this objective, we first discussed the motivation behind using the ResNet50 architecture. The ResNet50 is a deep CNN architecture known for its depth of 50 layers and the incorporation of skip connections. These skip connections help alleviate the vanishing gradient problem and preserve information across layers, making it an ideal choice for complex tasks such as brain tumor analysis. Additionally, we utilized transfer learning by using a pre trained ResNet50 model and fine tuning it for our specific task.

Moving on to the classification task, we fine-tuned the pre trained ResNet50 and VGG16 model by freezing the base layers and adding new layers for classification. The classification model was trained on the segmented tumor images to classify them into different tumor types or predict their malignancy. We assessed the performance of the classification model using metrics such as precision, recall, and F1 score.

The results of the classification model demonstrated its effectiveness in accurately classifying brain tumors. The precision, recall, and F1 scores consistently exceeded 99.5% in the proposed model of ResNet50 as compared to other models, indicating a high level of accuracy in differentiating between tumor or no tumor. These results are crucial for providing accurate diagnoses and guiding appropriate treatment strategies.

Overall, the proposed ResNet50 based on brain tumor classification system exhibited excellent performance in accurately identifying tumor regions and classifying brain tumors. The contributions of this work extend beyond the development of the proposed models. We also focused on the interpretability and visualization of the results.

The proposed system can assist medical professionals in making informed decisions, potentially improving patient outcomes and reducing the burden on radiologists.

However, it is essential to acknowledge the limitations of this work. The performance evaluation was performed on a specific dataset, and the results may vary when applied to different dataset, real world scenarios and on different models. The model generalize ability needs to be further validated on diverse datasets and in clinical settings. Additionally, the training and evaluation processes heavily relied on manual annotations, which can introduce subjectivity and variability. Automating the annotation process or exploring semi supervised learning approaches could address this limitation.

Future research directions could involve exploring advanced deep learning techniques, such as attention mechanisms and generative adversarial network, to enhance the accuracy and robustness of

brain tumor segmentation and classification. Additionally, incorporating multimodal imaging data, such as MRI and PET scans, could further improve the model's performance and provide a comprehensive analysis of brain tumors.

In conclusion, this study presented an improved ResNet50 based brain tumor segmentation using data augmentation and classification system. The proposed models demonstrated high accuracy, precision, and recall in segmenting brain tumor regions and classifying brain tumors. The results provide valuable insights into the potential of deep learning approaches for medical image analysis, particularly in the field of neurology. Further advancements in this area have the potential to revolutionize the diagnosis and treatment of brain tumors, ultimately improving patient care and outcomes.

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