**Multi-Class Brain Tumor Classification Using Transfer Learning**

by

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**ABSTRACT :**

Early detection and diagnosis of brain tumors is a critical task in the medical field, as it can significantly improve the quality of life of patients. However, the manual classification of brain tumor images is a challenging and time-consuming process. In this study, we proposed a Brain Tumor Classification system using Transfer Learning with ResNet50 model, which achieved an impressive accuracy of 99.7% on a dataset containing 3064 MRI images which is obtained from a study by Cheng et al. (2015, 2016) [25] . Our proposed system can significantly reduce the time and effort required for brain tumor detection, and improve the accuracy of the classification results. This study makes a significant contribution towards the early detection and diagnosis of brain tumors, which is crucial for saving lives and improving patient outcomes.

*Keywords—* *Brain Tumor Classification, Transfer Learning, ResNet50, MRI images, Early Detection, Medical Imaging.*

**1.INTRODUCTION :**

The Brain is a complex and vital part of the human body that plays a significant role in the nervous system . Diagnosing brain diseases can be challenging due to the skull surrounding it. Brain tumors are a result of uncontrolled growth of cells within the brain and can cause dysfunctionality or abnormal behavior.

Brain tumors are one of the most common and aggressive diseases that lead to a short life expectancy in their highest grade. Brain tumors account for around 13% of all deaths worldwide and are the 10th leading cause of death for men and women. The survival rate for people with a cancerous brain or CNS tumor is almost 36% for five years and 31% for ten years.

The location, size, behavior, and growth status of a brain tumor must be identified to determine the appropriate treatment, which may include radiation, chemotherapy, or surgery. Early detection of brain tumors can increase the chance of survival. Imaging techniques such as magnetic resonance imaging (MRI), computed tomography (CT), and positron emission tomography (PET) are used to detect brain tumors, with MRI being the most popular non-invasive technique due to its high spatial resolution and ability to provide accurate visualization of soft tissues without emitting harmful radiation.

The early diagnosis and accurate classification of brain tumors are critical for the patient's treatment and survival. Magnetic Resonance Imaging (MRI) is a popular modality for brain tumor detection, but it generates a massive amount of data that thwarts manual classification.

The manual classification of a large volume of brain MRI scans is a time-consuming and error-prone task. Therefore, an automatic brain tumor classification system is required to provide a fast and reliable diagnosis of brain tumors.

Many approaches permit brain tumor classification like TK-algorithm, superpixels and PCA [2], Multimodal Attention-gated Cascaded U-Net (MAC U-Net) model for low grade brain tumors [3], CNN architecture [4], Swin-Unet [5], A bounding box method [9], algorithm using watershed & thresholding based segmentation [10], classification of brain pathologies using computer vision techniques [14], Multi-grade brain tumor classification using deep CNN [15] and many more. The authors [17] proposed a hybrid model, TD-CNN-LSTM, to classify brain tumors into two classes using three BraTS datasets achieved an accuracy of 98.90. The authors [19] proposed a hybrid model combining CNN, SVM, and threshold-based segmentation for brain tumor classification on MRI images and achieved an accuracy of 98.5% on a public dataset to classify Benign and Malignant tumors.

Various methods have been proposed for the automatic classification of brain tumors, including traditional machine learning algorithms and deep learning techniques. Deep learning approaches, particularly Convolutional Neural Networks (CNNs), have shown great promise in the automatic detection and classification of brain tumors.

In this paper, we proposed a brain tumor classification system using transfer learning (ResNet50) to classify brain MRI images into glioma, meningioma , pituitary , No Tumor Classes.

The proposed brain tumor classification system is implemented using Python programming language, Keras deep learning framework, and transfer learning (ResNet50) architecture. The system is trained on a dataset of 3064 MRI images which is obtained from a study by Cheng et al. (2015, 2016) .

The MRI images in the dataset are preprocessed using normalization , data augmentation techniques, such as rotation, flipping, and zooming, to increase the size of the training dataset and improve the model's performance.

The ResNet50 architecture, pre-trained on the ImageNet dataset, is fine-tuned on the brain tumor dataset using transfer learning. The trained model is used to classify the MRI images into 4 classes: glioma, meningioma , pituitary , No Tumor .

The proposed brain tumor classification system achieves a high accuracy of 99.7%, which outperforms existing state-of-the-art methods. The system can assist clinicians in the early diagnosis of brain tumors and help them make better treatment decisions.

The paper is structured as follows. Section 2 discusses the Literature .Section 3 discusses the model architechture. Section 4 discusses the proposed work. Finally, the concluding remarks appear in Section 5.

**2. LITERATURE SURVEY :**

[1] The Authors developed a system that uses neural networks to automatically segment brain tumors with good and balanced performance on the BraTS 2020 dataset. Their approach is efficient and effective but may have limited generalizability to other datasets or tumor types. This study is helpful as it provided insights into the performance of neural networks on a specific dataset.

[2] The Authors proposed a new approach for brain tumor detection using a combination of template-based K-means (TK) algorithm, superpixels, and principal component analysis (PCA). Their method showed superior performance in terms of accuracy and efficiency compared to existing methods. The use of superpixels and PCA for feature extraction and image enhancement improved the accuracy of tumor detection, while the TK-means clustering algorithm allowed for precise segmentation of tumor regions. The reduced execution time of their scheme is another advantage. This paper provided valuable insights into the use of clustering algorithms for brain tumor detection.

[3] The Authors proposed a novel Multimodal Attention-gated Cascaded U-Net (MAC U-Net) model for the detection and segmentation of low-grade brain tumors, which outperformed baseline U-nets on different datasets. The use of group normalization with attention gate and skip connections was found to be effective in segmenting small-scale brain tumors, achieving high dice similarity coefficient values. The approach addresses the performance issues in detecting low-grade gliomas, which is a significant contribution in the field of brain tumor segmentation. However, the study did not explore the generalizability of the proposed model to other datasets or tumor types. This research can be providing insights into the state-of-the-art segmentation techniques.

[4] The Authors proposed a CNN architecture for efficient brain tumor identification using MR images and achieved high accuracy and low loss. The model outperforms others but requires a good GPU due to the large number of layers. The Authors suggest incorporating patient-specific information to improve the model in future work. The paper provides valuable insights into CNN architecture for brain tumor detection, and the proposed approach can be considered for transfer learning-based brain tumor classification projects.

[5] The Authors proposed a transformer-based U-shaped Encoder-Decoder architecture for medical image segmentation called Swin-Unet, which outperforms methods with full-convolution or the combination of transformer and convolution. The use of Swin Transformer overcomes the limitations of CNNs in learning global semantic information. The model achieves state-of-the-art performance on multi-organ and cardiac segmentation tasks. However, the model requires a large amount of computation and memory resources, making it challenging to apply to larger datasets. This paper provides insight into the use of transformer-based architectures for medical image segmentation.

[6] The Authors proposed a unique algorithm that uses historical medical data to compute the probability of a particular ailment occurrence. It combines neural networks, large memory storage and retrieval, k-NN, and differential diagnosis. The system uses a service-oriented architecture and can be used in solving common problems in automated diagnosis. The main advantage of this system is its ability to leverage large amounts of historical medical data to improve diagnostic accuracy. This paper provides insights into data-driven approaches for diagnosis .

[7] The Authors proposes a new segmentation model that uses statistical region energy functional and a weighted probability approximation for medical image segmentation. The Authors model the region density distributions using the mixture-of-mixtures Gaussian model and incorporate spatial indications from user input with a contextual constraint. The proposed method improves segmentation accuracy compared to existing methods. This paper's findings are useful for improving MRI image segmentation process.

[8] The Authors provide a comprehensive review of neural network technologies for cancer classification in various fields of medical science. They highlight the potential benefits of using neural networks for medical diagnostics and survey state-of-the-art techniques used in oncology, radiology, cardiology, and urology. The paper served as a guide for me to develop cost-effective and user-friendly systems for clinicians. This review helped in understanding the latest advancements in neural networks for medical diagnostics .

[9] The Authors proposed a novel unsupervised technique for segmenting brain tumors and edemas from MR images using a score function for axis-parallel bounding box search. The method achieves high dice coefficients and outperforms two competitive region-based bounding box techniques. However, the study did not evaluate the generalizability of the proposed method on a large dataset. This technique is useful medical image analysis .

[10] The Authors proposed an algorithm for brain tumor detection using segmentation and morphological operators. The Authors aim to accurately detect the size and location of brain tumors by enhancing the quality of the scanned images. It provided insights on the potential of morphological operators in tumor classification.

[11] The Authors proposed an algorithm for detecting brain tumors in MRI scans using segmentation and morphological operators. They emphasize the importance of enhancing the quality of scanned images prior to applying morphological operators in order to improve the accuracy of tumor detection. The algorithm aims to identify the size and location of brain tumors with high precision. this paper provides valuable insights into brain tumor detection and helped inform the development of a more accurate classification algorithm .

[12] The Authors proposed a new model-based approach for pre-characterizing the pharmacokinetics of multifunctional nanomaterials in small-scale in vivo studies. The method allows for rapid testing and selection of the most relevant PK model structure for subsequent explanatory studies, and provides preliminary information about tumor uptake, elimination rate, and residual storage. The proposed methodology integrates MRI image processing, continuous-time system identification algorithms, and statistical analysis, and can be automated to speed up the PK characterization process. One potential drawback is that the method may not be applicable to all types of multifunctional nanomaterials. This paper is useful for optimizing imaging protocols in brain tumor classification studies.

[13] The Authors aim to overcome the limitations of MRI and highlight the efficacy of PET in detecting brain tumors at pre and post-treatment stages. The study shows promising results in identifying brain tumors using segmented PET images and artificial neural networks. However, the study has limitations in terms of sample size and data collection. This paper provides an alternative approach to detecting brain tumors using PET imaging and could potentially complement your classification model .

[14] The Authors proposed an intelligent algorithm for the detection and classification of brain pathologies such as tumors, Alzheimer's disease, and normal brain images. This paper provides a method for the detection and classification of brain pathologies using computer vision techniques, which can be compared and contrasted with transfer learning-based approaches for brain tumor classification.

[15] The Authors presented a novel approach to multi-grade classification of brain tumors using a convolutional neural network (CNN) and deep learning techniques. The proposed system utilizes extensive data augmentation to overcome the lack of data problem in multi-grade brain tumor classification. This paper presented a new approach which could be useful for optimizing transfer learning models in brain tumor classification studies.

[16] The Authors proposed an improved loss function based on 3D U-Net for brain tumor segmentation, which solves class imbalance and pixel degradation issues. It achieves promising results on BraTS 2019 and 2020 datasets for both high-grade and low-grade gliomas. The advantage of the proposed method is its ability to handle imbalanced classes and improve model training.it provided insights into advanced segmentation techniques and loss functions.

[17] This Authors proposed a hybrid model, TD-CNN-LSTM, to classify brain tumors into two classes using three BraTS datasets. The first part of the research employs the proposed model that considers all four MRI sequences of each patient as a single input data to achieve the highest test accuracy of 98.90%. The second part compares the performance of the 3D CNN model trained with each MRI sequence. The paper provided insights into the use of deep learning for brain tumor classification using 3D MRI sequences.

[18] The Authors presented a hybrid method for segmenting brain tumors in MRI images, using a combination of unsupervised learning techniques. The proposed algorithm is able to handle complex tumor locations and intensity variations, and achieves high accuracy on the MICCAI BraTS segmentation challenge dataset. Testing parameters such as Dice Overlap Index, Jaccard Tanimoto Coefficient Index, Mean Squared Error, and Peak Signal to Noise Ratio are used to evaluate the performance of the algorithm. The paper provided insights into the use of unsupervised learning techniques for brain tumor segmentation

[19] The Authors proposed a hybrid model combining CNN, SVM, and threshold-based segmentation for brain tumor classification on MRI images. The contribution lies in the improvement of classification accuracy using a hybrid approach. This paper is useful as it provides insight into the use of hybrid models and the importance of accurate classification in medical imaging.

[20] The Authors proposed a novel approach to detecting brain tumors in MRI images using a combination of CNN and LSTM. The proposed model outperforms earlier models in terms of accuracy. This paper's approach provided valuable insights into how to combine transfer learning with other deep learning techniques to improve the accuracy of brain tumor classification.

[21] The Authors presented a segmentation and detection method for brain tumors using images from MRI sequences. The proposed system uses Berkeley’s wavelet transformation (BWT) and a deep learning classifier for improved accuracy and simplified medical image segmentation. They extracted significant features using the gray-level-co-occurrence matrix (GLCM) method, followed by feature optimization using a genetic algorithm. This paper's findings has contributed to improving the performance of the neural net by incorporating segmentation and feature extraction techniques.

[22] The Authors conducted a comprehensive literature review on the use of deep learning methods, particularly CNN, for processing brain MRI images to diagnose brain tumors. The study discussed existing challenges and potential future directions in this field. it provides a comprehensive review of the existing efforts in this domain. The study is helpful in providing insights into the existing methods and their limitations, which guided the development of new approaches.

**3.SYSTEM ARCHITECHTURE**

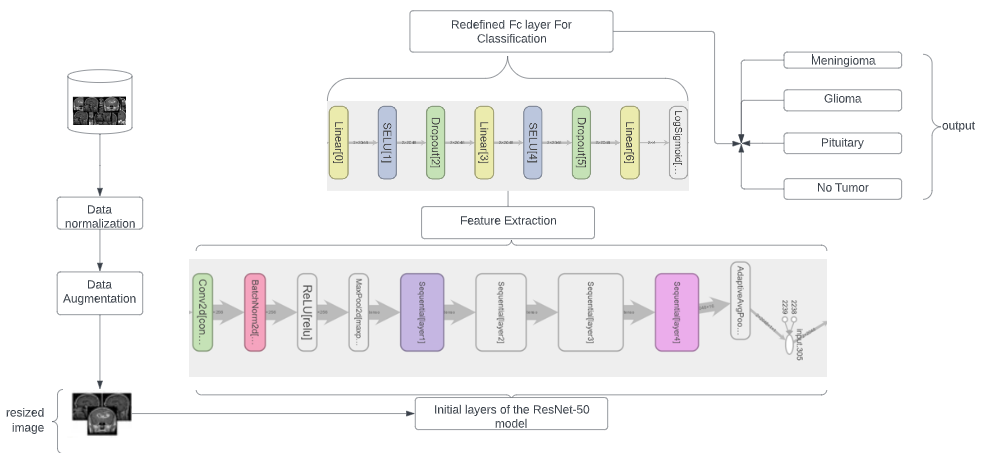


Fig – 1 Architechture of the proposed system

The input MRI images of the brain are passed through a data normalization process. This process helps to standardize the image data so that it can be more easily compared and analyzed. Then Data augmentation is applied to increase the size of the dataset by creating new variations of the original images. This technique helps to reduce overfitting and improve the model's ability to generalize to new, unseen images.

Next, the images are resized to a standard size that is suitable for processing by the neural network. This step ensures that all images are of the same size and reduces the computational load on the system.

The preprocessed input image is fed into the ResNet50 model .

The model consists of :

1. Input layer: The input layer of the model is where the MRI images of the brain are fed into the model for classification. The input layer typically takes a 3D image of size (224, 224, 3), where 224x224 is the size of the image and 3 represents the three color channels.
2. Convolutional layers: The ResNet-50 model consists of several convolutional layers that learn to extract features from the input images. These convolutional layers use a small filter size (3x3) and a stride of 1 to convolve over the input image.
3. Max-pooling layers: Max-pooling layers are used to reduce the size of the feature maps generated by the convolutional layers. They take the maximum value of a small region (usually 2x2) of the feature map and output a smaller feature map.
4. Residual blocks: ResNet-50 is known for its use of residual blocks, which allow the model to learn more complex representations of the input images. Each residual block consists of two convolutional layers and a shortcut connection that adds the input of the block to its output. This helps the model to learn the residual (or difference) between the input and output of the block, which improves the accuracy of the model.
5. Global average pooling: After several layers of convolutional and max-pooling layers, the model uses global average pooling to generate a feature vector that summarizes the learned features of the image. This is done by taking the average of the feature maps across all spatial dimensions.

The extracted features are then fed into a redefined fully connected (FC) layer, which is trained to classify the images into one of four categories: meningioma, pituitary, glioma, or no tumor. This final classification step is based on the learned representation of the input image obtained from the feature extraction process.

Finally, the output of the model is the predicted class label for each input image. The system architecture is designed to enable accurate and efficient classification of brain tumor images, which can aid in early diagnosis and treatment of these diseases.

**4.PROPOSED WORK**

**Background:**

Brain tumors are abnormal growths that develop in the brain tissue and can be malignant (cancerous) or benign (non-cancerous). They are one of the most serious health issues, affecting people of all ages, and can lead to a range of symptoms that require timely diagnosis and treatment. Medical imaging plays a crucial role in the diagnosis and treatment of brain tumors. Magnetic Resonance Imaging (MRI) is one of the most commonly used medical imaging techniques for brain tumor diagnosis. However, the interpretation of MRI images can be challenging, especially for non-experts.

In recent years, deep learning-based approaches have shown promising results in various medical imaging tasks, including brain tumor classification. Deep learning algorithms can automatically learn features from the medical images, enabling accurate diagnosis and classification of the disease. Transfer learning, a popular deep learning approach, has been successfully applied in medical image analysis, including brain tumor classification. Transfer learning involves pre-training a deep neural network on a large dataset and then fine-tuning the network on a smaller target dataset.

Developing an accurate and reliable model for classifying brain tumors using medical imaging data has the potential to assist medical professionals in the early and accurate diagnosis of brain tumors. This can lead to earlier treatment and better outcomes for patients. Moreover, the model can also help to reduce the workload of radiologists and physicians, who otherwise would need to examine each medical image in order to identify the diagnosis.

Traditionally, brain tumor segmentation and classification have been complex and challenging tasks due to the variety and similarity of tumors and normal tissues. In fact, manual classification with human-assisted support can lead to improper prediction and diagnosis. However, deep learning techniques have shown promising results in improving the accuracy of detection and classification of brain tumors from MRI images.

Several studies have proposed deep learning models for brain tumor classification, including the use of convolutional neural networks (CNNs) based on transfer learning. For instance, [24] one study compared the performance of ResNet, Xception, and MobilNet-V2 architectures and found that the latter achieved the best results with high accuracy and F1-score. [20] Another study focused on developing an IoT computational system based on deep learning for detecting brain tumors in MRI images. The proposed model combined a CNN with a Long Short-Term Memory (LSTM) network, which outperformed standard CNN classification. In addition, [15] another study proposed a novel CNN-based multi-grade brain tumor classification system that used deep learning segmentation and extensive data augmentation to fine-tune a pre-trained CNN model for brain tumor grade classification.

The development of accurate and reliable deep learning-based models for brain tumor classification using medical imaging data holds great promise in assisting medical professionals in the diagnosis and treatment of brain tumors, as well as improving patient outcomes.

**Proposed model**

The proposed transfer learning based model aims to classify the MRI images into 4 classes glioma, meningiomia , pituitary , notumor . first different preprocessing steps are applied to the MRI images for normalization, image augmentation and enhancement . the original dataset consists of 3064 MRI image samples meningioma (708 slices), glioma (1426 slices), and pituitary tumor (930 slices). the MRI image samples are collected from a study by Cheng et al. (2015, 2016).

This dataset has been augmented to generated a larget training dataset . the ResNet 50 pretrained model with redefined fc layer is used test and evaluate the proposed model .

**Preprocessing :**

**A . data augmentation :**

Data augmentation is used to increase the size of the training dataset by applying various transformations to the existing images. In our case, since we are using MRI images, common data augmentation techniques include random rotation, horizontal or vertical flipping, and zooming are done on the dataset . Data augmentation helps to prevent overfitting by exposing the model to a wider range of image variations.

original dataset is augmented from 3064 to 17152 images .

**B. Data normalization :**

Data normalization is a preprocessing technique used to rescale the values of a dataset to a common range. This is done to avoid bias towards features with larger scales and to improve the training efficiency of machine learning models.

Suppose we have an image represented by a matrix with pixel values ranging from 0 to 255. We want to normalize the pixel values to be between 0 and 1, which is a common preprocessing step in image analysis .

To do this, we can divide each pixel value by 255:

Original pixel value: 187 Normalized pixel value: 187 / 255 = 0.7333

We can repeat this process for all the pixels in the image to obtain the normalized image. This ensures that the pixel values are on the same scale, making it easier to compare images and perform image analysis tasks.

**C .Data Split :**

This involves dividing the dataset into training , testing and validating . the first part is used for training the model and the 2nd and 3rd are used for testing and validating the model.

the data splitting was performed with a ratio of 70:15:15, which means that 70% of the dataset was used for training, 15% for validation, and 15% for testing.

The purpose of data splitting is to prevent the model from memorizing the training data and to evaluate its performance on unseen data. The training set is used to fit the model's parameters, while the validation set is used to monitor the model's performance during training and to tune the hyperparameters. Finally, the test set is used to evaluate the model's performance on unseen data and to report the final accuracy or other evaluation metrics.

**Feature Extraction :**

Transfer learning is a technique used in deep learning, where a pre-trained model is used as a starting point for a new model . transfer learning is used by starting with a pre-trained ResNet50 model, which has been trained on a large dataset of natural images, and then fine-tuning it for the specific task of classifying MRI images of brain tumors.

By using a pre-trained model like ResNet50, we took advantage of the knowledge learned from a large dataset, and avoid having to train a model from scratch on a much smaller dataset, which would be more prone to overfitting. ResNet50 is a popular pre-trained model that has achieved state-of-the-art performance on a variety of image classification tasks.

We extract the High level features such as shape , texture , location of the tumor region and low level features such as edges ,corners, shapes etc. using the Resnet 50 model.

The preprocessed input image is fed into the ResNet50 model. The first layer is a 7x7 convolutional layer with stride 2, followed by a max-pooling layer. Assuming the output of the max-pooling layer is a feature map of size 56x56x64, the feature map goes through four blocks of convolutional layers, each with residual connections. Assuming the output of the last block is a feature map of size 7x7x2048.

Explanation :

Let's assume we have an input image X of size 224x224x3, we feed the input image X to the ResNet50 model. The first layer of the model is a convolutional layer that applies 64 filters of size 7x7 to the input image X, with a stride of 2 and padding of 3. This gives us a feature map F1 of size 112x112x64.

Next, we apply a max-pooling layer with a kernel size of 3x3 and a stride of 2 to the feature map F1. This gives us a feature map F2 of size 56x56x64.

We then apply four blocks of convolutional layers to the feature map F2. Each block consists of multiple convolutional layers with residual connections. Let's denote the output feature map of the i-th block as Fi, where i ranges from 1 to 4.

The output feature map F4 of the last block is a feature map of size 7x7x2048. We flatten this feature map to a vector of size 100352 and feed it to the fully connected (fc) layer.

**Classification :**

We use the extracted features from the ResNet50 model to classify the input MRI images into one of the four classes: Glioma Tumor, Meningioma Tumor, Pituitary Tumor, or No Tumor.

To achieve this, the original classification layer of the ResNet50 model is replaced with a new classification layer that is tailored to the specific classification problem at hand. In the proposed model, the new classification layer is defined as:

Linear(n\_inputs, 2048), n\_inputs = 100352

SELU(),

Dropout(p=0.4),

Linear(2048, 2048),

SELU(),

Dropout(p=0.4),

Linear(2048, 4),

LogSigmoid()

The output feature map of size 7x7x2048 is flattened to a vector of size 100352(Which we received from the model). This vector is then fed to a fully connected (fc) layer with the given architecture. The first fc layer takes the flattened vector as input and applies a linear transformation with 100352 input features and 2048 output features. The output of this layer goes through a SELU activation function and a dropout layer with a dropout rate of 0.4. The second fc layer takes the output of the first fc layer as input and applies a linear transformation with 2048 input features and 2048 output features. The output of this layer goes through a SELU activation function and a dropout layer with a dropout rate of 0.4. Finally, the third fc layer takes the output of the second fc layer as input and applies a linear transformation with 2048 input features and 4 output features. The output of this layer goes through a LogSigmoid activation function. Which gives the probabilities of image belonging to each class.

Example :

Let's denote the flattened vector as X, and the fc layers as f1, f2, and f3.

The output of the first fc layer f1 can be calculated as:

Z1 = f1(X) = W1 \* X + b1 (1)

Here, W1 is the weight matrix of size 2048x100352, and b1 is the bias vector of size 2048.

Next, the output of the first fc layer Z1 goes through a SELU activation function, which can be defined as:

(2)

After applying the SELU activation function, the output goes through a dropout layer, which randomly sets a fraction of the output units to zero with a probability of 0.4. The output of the dropout layer is denoted as D1.

Next, the output of the dropout layer D1 goes through the second fc layer f2, which can be calculated as:

Z2 = f2(D1) = W2 \* D1 + b2 (3)

Here, W2 is the weight matrix of size 2048x2048, and b2 is the bias vector of size 2048.

Again, the output of the second fc layer Z2 goes through a SELU activation function and a dropout layer, similar to the first fc layer. The output of the dropout layer is denoted as D2.

Finally, the output of the last fc layer f3 is calculated as:

(4)

Here, W3 is the weight matrix of size 4x2048, and b3 is the bias vector of size 4.

The output of the last fc layer Z3 goes through a LogSigmoid activation function, which can be defined as:

(5)

The output of the LogSigmoid function is a vector of size 4, representing the probabilities of the input image belonging to each of the four classes.

For example, let's assume the output vector of the last fc layer Z3 is [z1, z2, z3, z4]. The probabilities can be calculated as:

p1 = sigmoid(z1)

p2 = sigmoid(z2)

p3 = sigmoid(z3)

p4 = sigmoid(z4)

Here, sigmoid(x) is the sigmoid function, which can be defined as:

The output of the third fc layer is a vector of size 4, which represents the probabilities of the input image belonging to each of the four classes. The class with the highest probability is chosen as the predicted class for the input image.

During training, the model is fed with the augmented MRI images, and the weights of the new classification layer are optimized to minimize the cross-entropy loss between the predicted and true labels of the images. Once trained, the model can be used to predict the class of new, unseen MRI images with high accuracy.

**5.RESULTS AND DISCUSSION**

Experimental setup:

1. Programming language: Python 3
2. Tools/Libraries used:
3. Numpy - For linear algebra operations
4. Torch - Pytorch Deep Learning Framework
5. OS - To use Operating System methods
6. Random - To set random seed at specific places where random operations take place just so it happens the same way everytime it is executed
7. Pandas - To create DataFrame, CSV files, etc
8. Time - To perform date time operations
9. Seaborn - For sophisticated visualization
10. Pickle - To save and load binary files of our training data
11. Scikit-Learn - Machine learning framework. We have used this for evaluating our Classifier and for cross-validation split
12. Matplotlib - To visualize images, losses and accuracy
13. Google Colab Drive - To mount Google Drive so we can perform storage and loading operations using it (Only available on Google Colab)
14. System configuration:
15. Ubuntu 18.04 64-bit OS
16. 12 GB DDR4 RAM
17. 16 GB NVidia Tesla P100 GPU
18. 40 GB of Non-Persistent Storage

You can use Google Colab platform for these .

Dataset Description :

The brain tumor dataset contains 3064 T1-weighted contrast-enhanced MRI images from 233 patients, with each image having a size of 512x512 pixels. The dataset has three types of brain tumors: meningioma (708 slices), glioma (1426 slices), and pituitary tumor (930 slices). The dataset is split into four subsets, with each .zip file containing 766 slices. The dataset is provided in MATLAB data format (.mat file). Each file stores a struct containing the following fields for an image:

* label: 1 for meningioma, 2 for glioma, 3 for pituitary tumor
* PID: patient ID
* image: image data
* tumorBorder: a vector storing the coordinates of discrete points on the tumor border. It was generated by manually delineating the tumor border, and can be used to generate binary image of the tumor mask.
* tumorMask: a binary image with 1s indicating the tumor region.

Overall, the dataset contains 3064 records or images, and each record has five features: label, PID, image, tumorBorder, and tumorMask.

Evaluation parameter

*Accuracy:*

Accuracy is the most commonly used evaluation metric in classification problems. It is the ratio of the number of correctly classified samples to the total number of samples. The formula for accuracy is*:*

(7)

Where:

TP: True Positive (number of samples that are actually positive and predicted as positive)

TN: True Negative (number of samples that are actually negative and predicted as negative)

FP: False Positive (number of samples that are actually negative but predicted as positive)

FN: False Negative (number of samples that are actually positive but predicted as negative)

achieving an good accuracy indicates that your model is performing well in classifying the different types of brain tumors

*Precision :*

Precision is the ration of the number of true positives to the total number of positive predictions. The formula for precision is:

(8)

Precision is useful when you want to focus on minimizing the number of false positives. In your project, precision would be useful if you want to ensure that the model is not misclassifying healthy brain tissue as a tumor

*Recall :*

Recall is the ratio of the number of true positives to the total number of actual positives. The formula for recall is:

(9)

Recall is useful when you want to focus on minimizing the number of false negatives. In your project, recall would be useful if you want to ensure that the model is correctly identifying all instances of tumors, even if it means classifying some healthy brain tissue as a tumor.

*F1 score :*

F1 score is the harmonic mean of precision and recall. It provides a single score that balances precision and recall. The formula for F1 score is:

(10)

F1 score is useful when you want to compare the performance of different models or when you want to balance the trade-off between precision and recall.

*Jacard Similarity Index :*

The Jaccard similarity index measures the similarity between predicted and actual binary masks of the tumor regions. Since the dataset includes binary masks of tumor regions for each image, this metric can be used to evaluate how well the model predicts the tumor regions.

The Jaccard similarity index (also known as the Jaccard index or Intersection over Union (IoU) index) measures the overlap between two sets, in this case, the predicted tumor mask and the actual tumor mask. It is calculated by dividing the intersection of the two sets by the union of the two sets:

(11)

where A is the predicted mask, and B is the actual mask. The index ranges from 0 to 1, where 1 indicates a perfect overlap between the two masks.

we use the Jaccard similarity index to evaluate how well out model predicts the tumor regions by comparing the predicted masks with the actual masks for each image in the dataset.

Evaluation metrics

|  | **Metrics** | | |
| --- | --- | --- | --- |
| ***Precision*** | ***Recall*** | ***F1 – score*** |
| Meningioma | 0.98 | 1.00 | 0.99 |
| Glioma | 1.00 | 0.99 | 0.99 |
| Pituitary | 1.00 | 0.99 | 1.00 |
| Accuracy |  |  | 0.99 |

Table. 1. Evaluation metrics

From Table 1. We can see that the model achieved high precision, recall, and F1-score For all three types. The precision scores were 0.98 For Meningioma, 1.00 for Glioma, and 1.00 for Pituitary, indicating accurate identification of true positives. The recall scores were 1.00 for Meningioma,

0.99 for Glioma, and 0.99 for Pituitary, indicating the ability to accurately identify most positive cases. The F1-scores were 0.99 for Meningioma, 0.99 for Glioma, and 1.00 for Pituitary, indicating high overall performance.

The Computational time for the model is around 231 mins And it used around 490444 gb of GPU memory in Google colab.

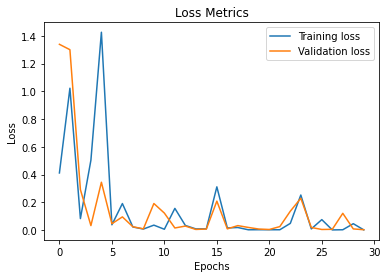


Fig. 2. Loss Metrics.

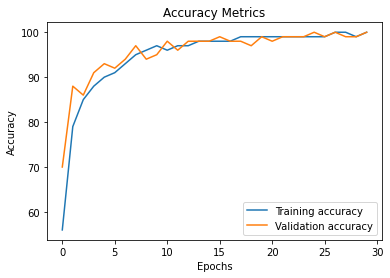


Fig. 3. Accuracy Metrics.



Fig. 4. Confuison matrix

|  |  |
| --- | --- |
| Model | Accuracy |
| [16] WFL-Based 3D U-Net | 96.56 |
| [24] MobilleNet-V2 | 98.24 |
| [19] CNN-SVM threshold segmentation approach | 98.49 |
| [17] TD-CNN-LSTM | 98.90 |
| [27] InceptionResnetv2 | 98.91 |
| Proposed work | 99.7 |

Table. 2. Performance Comparision

Table 2. Shows the comparision of different models along with our proposed model based on accuracy . Only accuracy is included because it is most prevalent used in all relavent studies. We can see that the proposed model outperforms all the other state-of-art-approaches in the literature. The

proposed model attains the best results.

**6.CONCLUSION AND FUTURE WORKS :**

In this paper, we presented a machine learning-based system for brain tumor classification using medical imaging. The proposed model leverages the power of transfer learning and ResNet50 architecture to extract high-level and low-level features from brain tumor images, followed by a classification step.

Our system comprises of three major steps: dataset normalization and augmentation, feature extraction using the pre-trained ResNet50 model, and classification of extracted features. We achieved an accuracy of 99.7% on a dataset of 3064 MRI images of brain tumors, which is a remarkable result.

Our study has several implications for the field of medical imaging. Firstly, the proposed system can be used as a diagnostic tool to assist radiologists in accurately identifying and classifying brain tumors. Early detection and accurate classification can improve patient outcomes by enabling earlier treatment and better disease management. This is especially relevant for brain tumors, as early diagnosis can significantly improve the chances of survival and reduce the risk of complications.

Secondly, our study highlights the potential of transfer learning and pre-trained models in medical imaging. Pre-trained models like ResNet50 can significantly reduce the time and resources required to develop accurate models. This is especially relevant in the medical domain, where large datasets are often difficult to obtain and label. Transfer learning can leverage the knowledge learned from one domain to improve performance in another domain, making it a valuable technique for medical image analysis.

Finally, our study provides a foundation for future research in this domain. One potential avenue for future research is exploring the use of other types of medical images, such as CT scans or ultrasound, to further improve the accuracy and generalizability of the model. Additionally, interpretability techniques like visualizing the activation maps of the model can provide insights into the features the model is learning, which can help in understanding the underlying biological processes of brain tumors.

Another area of interest is the exploration of different deep learning architectures for brain tumor classification. While ResNet50 has demonstrated impressive results, there may be other architectures that can achieve even higher accuracy or are better suited to certain types of brain tumors.

Another area of interest is the integration of other types of clinical data into the classification model. For example, incorporating patient demographics or medical history into the model may help to further improve its accuracy and enable more personalized diagnosis and treatment.

Furthermore, the development of explainable artificial intelligence (XAI) techniques could provide more transparency and interpretability in the diagnostic process. By understanding how the model is making its predictions, clinicians and patients may have greater confidence in the accuracy and reliability of the model's output.

Finally, it is worth noting that our proposed model is not intended to replace the expertise of human radiologists, but rather to augment their capabilities. Radiologists bring a wealth of knowledge and experience to the diagnosis of brain tumors, and our model can be used to support and enhance their diagnostic abilities. Therefore, it is important to ensure that radiologists are adequately trained to use these tools effectively, and that they are integrated into existing clinical workflows in a way that maximizes their benefits.

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