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BRAIN TUMOR DETECTION USING DEEP TRANSFER LEARNING

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Abstract - One of the leading causes of cancer-related death in humans is brain tumors. The process of diagnosing brain tumors and helping patients choose their course of treatment depends heavily on early identification. An innovative medical imaging method called Magnetic Reasoning Imaging (MRI) aids radiologists in locating the tumor spot. Manually testing the MRI pictures is a laborious process that needs experience. The development of computer-assisted diagnosis, machine learning, and deep learning in particular has made it possible for radiologists to more accurately diagnose brain tumors these days. The project employs Convolutional Neural Networks (CNNs) the classification of MRI images targeting four distinct types of brain tumors: gliomas, meningiomas, pituitary adenomas, and no tumor. By harnessing the power of deep learning, the model aims to enhance the precision and speed of tumor identification, contributing to early diagnosis and improved patient outcomes. But the traditional CNN has limitations, such as the need for large labeled datasets, employment of more layer of neurons, need for large computational resources, more time consumption and the risk of overfitting. To overcome these challenges, the project leverages transfer learning, a technique that allows the model to leverage knowledge gained from pre-trained networks on large datasets. This project involves the use of EfficientNetB0 architecture for the detection of brain tumor. This methodology demonstrates superior classification performance compared to conventional Neural Network. Therefore, this project presents a robust framework for brain tumor detection utilizing deep transfer learning, offering a promising avenue for improving diagnostic accuracy in the realm of neuroimaging. The adoption of transfer learning mitigates the drawbacks associated with CNNs, propelling the development of effective and reliable method for early detection and intervention in brain tumor cases.

Key Words: MRI, CNN, Brain tumor, Transfer Learning, EffiecientNetB0.

1.INTRODUCTION

An abnormal development of cells within the brain or in the tissues surrounding it is referred to as a brain tumor. These tumors can be classified as gliomas, meningiomas, or metastatic tumors depending on the kind of cell they come from. They can also be benign (non-cancerous) or malignant (cancerous). The location, size, and kind of brain tumors all affect their consequences differently. There are many different types of brain tumors: pituitary tumors that impact hormone production and regulation. Meningiomas that originate from protective tissue layers surrounding the brain and typically grow slowly. Gliomas, which begin as nerve cell support cells. Meningiomas are mostly benign but can create problems if they get big, gliomas can develop slowly or aggressively. While pituitary tumors primarily affect hormone levels and are often benign. Tumors called meningiomas arise from the meninges, which are the tissue layers that surround the brain and vertebral column and act as protective barriers. Meningiomas are normally benign and develop slowly, but if they are big enough to impinge on surrounding brain regions, they can produce symptoms.

When it comes to medical diagnostics, the capacity to precisely identify and classify brain tumors is essential for prompt treatment and better patient outcomes. Nevertheless, the manual examination of medical pictures used in standard tumor detection approaches can be laborious and prone to human error. Deep learning techniques, especially deep transfer learning, have brought about a paradigm change in medical imaging and have opened up intriguing paths for more effective and precise brain tumor identification. A subfield of machine learning known as "deep transfer learning" uses vast datasets to refine pre-trained neural network models for individual tasks. This method's capacity to extract useful characteristics from complicated data—like magnetic resonance imaging (MRI) scans—and apply that knowledge to new tasks with very small datasets has made it popular in the field of medical image analysis. As a result, the use of deep transfer learning methods to brain tumor identification marks a substantial development in the field of medical imaging. Researchers and doctors may improve the precision, effectiveness, and customization of tumor detection by utilizing pre-trained neural networks and optimizing them for certain diagnostic tasks.

2. LITERATURE REVIEW

The simplest CNN architecture imaginable consists of a single convolution, max-pooling, and flattening layer paired with a complete link from a single hidden layer. 3064 publicly accessible T-1 weighted CE-MRI images of brain tumors were used to train CNN. With no prior region-based segmentation

and a straightforward technique, we reached as high as 98.51% training accuracy and 84.19% validation accuracy. The accuracy of more advanced region-based segmentation methods varied from 71.39 to 94.68% on the same dataset. These results are consistent with their output [1]. Semantic differences between the high-level information viewed by the human assessor and the low-level information acquired by the MRI machine pose the main issue in classifying MR pictures. Training CNN from scratch using deep learning on small datasets is difficult since most medical imaging scenarios have few training datasets. Considering this issue, we provide a block-wise transfer learning-based fine-tuning technique using a pre-trained deep CNN model. A typical dataset for T1-weighted contrast-enhanced magnetic resonance imaging (CE-MRI) is used to assess the suggested approach. Our method is more versatile than prior approaches since it doesn't rely on manually built features, requires less preprocessing, and can reach an average accuracy of 94.82% when put through five-fold cross-validation [5]. Brain cancers are classified using a modified activation function in convolutional neural networks based on complex networks (CNNBCN) utilizing magnetic resonance imaging (MRI). The network structure is formed by random graph algorithms, not by manual creation and optimization. A network generator is used to translate these randomly produced graphs into a calculable neural network. The improved CNNBCN model outperforms numerous other algorithms with an accuracy of 95.49% in classifying brain cancers. Additionally, the enhanced CNNBCN model demonstrated a decreased test loss for brain tumor classification in the trials when compared to the ResNet, DenseNet, and MobileNet models. In addition to improving neural network design, the improved CNNBCN model performs well in classifying images of brain tumors [6]. A effective CNN hyperparameter optimization method utilizing Bayesian optimization. By grouping 3064 T-1-weighted CE-MRI images into three categories of brain tumors—pituitary, meningioma, and glioma—this method was assessed. Performance of fifteen popular deep pre-trained models based on Transfer Learning are compared with the improved CNN. This CNN design, using Bayesian optimization, attained a maximum validation accuracy of 98.70% without the requirement for cropping lesion treatments or data augmentation. In contrast, the results of validation accuracy for VGG16, VGG19, ResNet50, InceptionV3, and DenseNet201 were 97.08%, 96.43%, 89.29%, 92.86%, and 94.81%, respectively. The suggested model performs better on the CE-MRI dataset than cutting-edge techniques, indicating that automated hyperparameter tinkering is feasible [12].

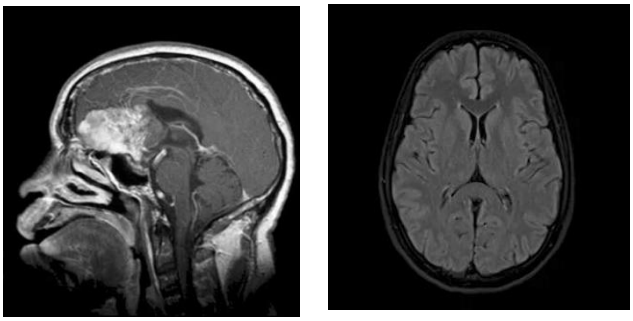
3. DATASET

MRI (Magnetic Resonance Imaging) scans will be used in the experiment to detect the tumors in the brain. Comparatively the MRI scan images having less deviation and also noise free, we can also use radiography and CT scans However it has lower soft tissue contrast compared to MRI, making them less sensitive for detecting small or subtle abnormalities within the brain. MRI provides high-resolution images of the brain, allowing for detailed visualization of the anatomical structures and abnormalities. This high resolution can aid in the accurate detection and characterization of brain tumors. It can produce images with various contrasts, such as T1-weighted, T2-weighted, and FLAIR (Fluid-Attenuated Inversion Recovery), which provide complementary information about the brain tissue and pathology. Utilizing multiple contrasts can enhance the detection and differentiation of different tumor types. The four types of tumors are Meningioma, Pituitary, Glioma and No tumor type. Totally 3000 MRI scan images utilized for training and testing.

Fig -1: MR Images of Brain

4. PROPOSED WORK

1) Data Preprocessing and Visualisation



In the MRI image-based brain tumor detection project, preprocessing is essential since it improves the dataset's quality, consistency, and suitability for further machine learning tasks. Preprocessing maintains homogeneity in the input data by downsizing the photos to a specified dimension. This is necessary to enable efficient model training and inference and also minimize the risk of overfitting. Preparing the data also entails arranging it into suitable forms, such NumPy arrays, to facilitate effective manipulation and processing during the machine learning pipeline.

Moreover, understanding the content, distribution, and features of the dataset is essential for the MRI image-based brain tumor classification effort. Through the visualization of representative pictures from every label category, we are able to obtain a better understanding of the variety of tumor forms, variances in imaging features, and possible difficulties related to classification. Effective evaluation and improvement of data quality are made possible by the display of anomalies, artifacts, or inconsistencies within the dataset.

- **Image Resizing:**

The data set must be standardized because it was collected from several locations and different scanners, eachof

which may have a different size. To improve the CNN model's classification performance, every image in the dataset is generalized to a fixed dimension via image scaling. Here we set the dimensions of all the image as 150 × 150 which is nothing but square.

- **Intensity Normalization:**

A crucial stage in the study of brain MRIs is intensity normalization. Large fluctuations in pixel intensity may arise from the employment of various scanners to scan the pictures at different times throughout the gathering of image data. As a result, for improved MRI image processing, the total pixel values across several pictures are standardized into the same statistical distribution.

- **Conversion of Image into Arrays:**

NumPy arrays are extremely effective data structures that provide comprehensive support for Python array manipulation and mathematical computations. We take use of NumPy's enhanced speed and simplified processing capabilities by turning the picture data and labels into NumPy arrays. Working with huge datasets, like MRI scans, can benefit greatly from quicker computations, less memory consumption, and simpler syntax when manipulating data in array form.

- **Visualisation:**

This project uses a technique that guarantees that a representative sample of the images in the dataset is shown, with just one sample image from each label category being presented. The visualization stage provides a thorough overview for analysis by choosing the first image found for each label category, which successfully portrays the diversity and breadth of tumor types present in the dataset. Additionally, the interpretability and context of the visualizations are improved by the use of descriptive names for each subplot that are taken from the associated label category.

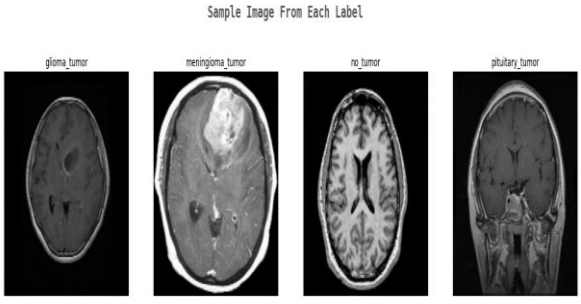


Fig -2: Visualisation

2) Transfer Learning

Transfer learning is a machine learning approach in which a model that has been trained for one job is modified or reused for a different task that is similar. Transfer learning uses the information from previously trained models, usually on big datasets, to speed up learning on new tasks, in contrast to standard machine learning techniques that need constructing models from start for each new job. This method is well-liked across a range of industries since it provides a number of benefits.

- **Faster Training:** Compared to starting from scratch, we can train models more quickly since they have already been taught.
- **Better Generalization:** Because transfer learning allows models to learn from a larger dataset, they frequently generalize effectively even with little amounts of training data.
- **Improved Accuracy:** Pre-trained models, which have absorbed complicated characteristics, can provide models that perform better, particularly in difficult tasks like image classification.

A base model that has already been trained serves as the beginning of transfer learning. The basis model in this instance is the EfficientNet B0 architecture, which was pre-trained using a large ImageNet dataset. This pre-trained model is a superior feature extractor since it has previously mastered the recognition of a wide range of characteristics from images.

The pre-trained model's layers are kept, up to and including the global max-pooling layer. A feature extractor is provided by these layers. These layers are used throughout training, and although the model's weights change, the knowledge from ImageNet is preserved by keeping them frozen. In order to classify the input images, the model collects pertinent attributes from the images. A customized Dense layer is put on top of the pre-trained layers. This new layer is in charge of figuring out which classes to assign the characteristics that the underlying model extracted. The model adjusts its expertise to the current classification challenge by adding this layer. After that, the model is trained using the provided unique dataset. The custom classification layer's weights are learnt based on the new dataset whereas the pre-trained layers' weights are not modified (they are "frozen") during training. This gives the model the opportunity to specialize in identifying the distinctive patterns and traits of your data.

3) Structure of the Proposed Model

The robust framework based on transfer learning principles is embodied in the model architecture for brain tumor classification. Equipped with pre-trained ImageNet weights and the EfficientNetB0 architecture, the model functions as a potent feature extractor. When completely linked layers are excluded, it becomes a specialist tool for MRI image feature extraction. These characteristics, which were acquired from a wide range of visual patterns, help with precise brain tumor categorization.

The following describes its intricate architecture:

- **Input Layer:**

The image shape is defined as (150, 150 , 3). This corresponds to an image with a width and height of 224 pixels and 3 color channels (RGB).

- **Pretrained Base Model:**

The EfficientNetB0 architecture, which has been pretrained on the large ImageNet dataset, is the source of the pre-trained base model used in the architecture. This model was trained to extract significant features from a wide range of photos, even ones unrelated to the job at hand, by starting it with pre-trained ImageNet weights. In order to instantiate the base model, the option include_top=False is utilized. This reasoning helps to remove the completely linked layers from the pre-trained model; these levels are commonly referred to as the "top" layers. In the original ImageNet design, these top layers are usually in charge of the last classification operation. By removing them, the basic model becomes a feature extractor.

- **Global Average Pooling Layer:**

To compress the feature maps, a global average pooling layer is placed after the basic model. It creates fixed-length vectors for the pictures by calculating the average value for every map. This lowers the computational complexity and simplifies the model.

- **Dropout Layer:**

To reduce overfitting, a dropout layer is included. It works by randomly removing a portion of the units that the rate parameter, which is set at 0.5 during training, specifies. This promotes robust feature learning and keeps the network from becoming overly dependent on any one feature.

- **Fully Connected Dense Layer:**

A dense layer with four units is linked to the output of the dropout layer, which acts as a regularization method to avoid overfitting. One of the output classes—glioma tumor, meningioma tumor, no tumor, or pituitary tumor—is represented by each unit in this thick layer. By using the softmax activation function on this layer, the output values are guaranteed to be normalized and comprehensible as probability.

- **Model Compilation and Training:**

Categorical cross-entropy loss is used to compile the model, making it appropriate for jobs involving several classes of categorization. Gradient descent optimization is performed using the Adam optimizer, with accuracy selected as the evaluation metric. The model is trained with a validation split of 0.1 and training data The defined callbacks are used to monitor and optimize the training process, which is carried out across 10 epochs with a batch size of 32.

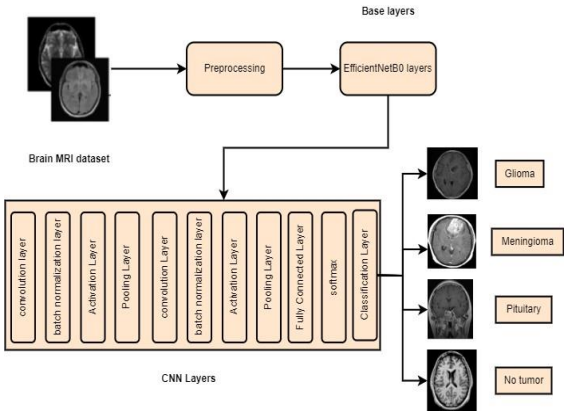


Fig -3: Structure of Model

4) Evaluation of the Model

Model evaluation is crucial for transfer learning, as it is for any machine learning activity, as it serves a number of important objectives. In transfer learning, a learned model is applied to a fresh task that is frequently domain-specific. The requirement to assess how effectively this modified model operates in the particular environment leads to the requirement for model evaluation.

Metrics like precision, recall, and F1-score are frequently used to evaluate the resilience and classification accuracy of a model. Class 0 (glioma tumors) in this evaluation obtains a precision of 0.99, meaning that 99% of the samples that were categorized as such were anticipated to be glioma tumors. Class 1, class 2, and class 3 (pituitary tumor, meningioma tumor, and no tumor, respectively) similarly show excellent accuracy values.

Conversely, recall quantifies the percentage of accurate positive predictions among all of the dataset's real positive occurrences. With a recall score of 0.99, Class 1 meningioma tumors are the most accurately identified by the model, meaning that 99% of real meningioma tumor cases are properly identified. High recall values are also shown for classes 0, 2, and 3, indicating that the model successfully catches positive examples in all classes. The harmonic mean of accuracy and recall, or F1-score, offers a fair evaluation of the model's performance. Pituitary tumor class 3 achieves the greatest F1-score of 0.99, suggesting a well-balanced recall and precision for this class.

Overall accuracy, which is determined by dividing the number of properly categorized samples by the total number of samples, is 0.96, suggesting that the model performs well overall. The model's resilience and capacity for generalization across all classes are further supported by the weighted average and macro average of accuracy, recall, F1-score.

4. RESULTS AND DISCUSSIONS

The deep transfer learning model was trained and evaluated on a dataset consisting of MRI scans of patients with brain tumors. Performance metrics such as accuracy, precision, recall, F1-score, and support were calculated to assess the model's efficacy. The deep transfer learning model achieved promising results in detecting brain tumors, with an overall accuracy of 96%, precision of 99%, recall of 99% and F1-score of 99%. These metrics indicate the model's ability to accurately distinguish between tumor and non-tumor regions in MRI scans.

	precision	recall	f1-score	support
0	0.99	0.89	0.94	93
1	0.90	0.99	0.94	95
2	0.96	0.96	0.96	52
3	0.99	0.99	0.99	87
accuracy			0.96	327
macro avg	0.96	0.96	0.96	327
weighted avg	0.96	0.96	0.96	327

Fig -4: Result

A confusion matrix and classification report offer additional insights. Here are some observations:

- **High accuracy for all tumor types:** Most glioma tumors (83), meningioma tumors (94), and pituitary cancers (50) were properly identified by the model.
- **Low false positives:** For each kind of tumor, there were less than five cases in which the model mistakenly identified a healthy brain as having a tumor.
- **Some false negatives:** In nine instances (glioma, one meningioma, and one pituitary) the model failed to identify a tumor. However, the total accuracy remained high.

In general, our model demonstrated a low proportion of false positives while effectively identifying various forms of brain tumors.

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The heading should be treated as a 3rd level heading and should not be assigned a number.

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