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# Development of Advanced Deep Ensemble Model for Brain Tumor Detection

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**ABSTRACT:** Worldwide, brain tumors are growing extremely quickly. Brain tumors are the cause of a huge number of deaths each year, globally. As a result, precise identification, as well as diagnosis, are crucial for the handling of brain tumors. Brain tumor identification and segmentation utilizing conventional machine learning (ML) and deep learning (DL) algorithms, several experimental methodologies have been presented in recent years. Hence, to safeguard the lives of millions of individuals worldwide, prompt investigation and automated brain tumor diagnosis become necessary. Existing methods, yet, provide subpar results, as a consequence, a reliable method for making accurate diagnoses is required. In this research, an advanced deep ensemble model for brain tumor detection has been developed. This proposed ensemble model is a hybrid model that is based on multiple models namely Enhanced CNN, KNN, and VGG16 and ResNet50, SVM, and CapsNet. An open-access experimental database namely Kaggle was used to evaluate the ensemble framework, and the results were 98.04% accuracy, 98.08% precision, 98.11% sensitivity, and a 98.25% F1-score. By comparing the suggested framework to the various other mathematical models, researchers can conclude that the proposed framework is trusted for the prompt diagnosis of many different kinds of brain tumors. The future of AI as well as DL models for identifying as well as categorising brain tumours is quite promising. This involves investigating DL architectures, engaging in transfer learning (TL), and using generative adversarial network (GAN) models to enhance imaging data.

**KEYWORDS:** Brain Tumor, ML, DL, Deep Ensemble, Tumour Diagnosis.

## I. INTRODUCTION

The brain of a person serves as both the primary nervous system's administrative hub also is in charge of carrying out everyday functions. The central nervous system takes in inputs or data from the human body's sense parts, processes them, and then transmits ultimate choices as well as final data to the musculature [1], [2]. A cerebral tumor develops when an aberrant population of cells throughout the central nervous system is produced by unregulated tissue proliferation or abnormalities. Among the most frequent indications of brain tumors are migraines, memory problems, nausea, shifts in personality, and visual problems, including difficulties with speaking [3]–[5]. The progression of a cerebral tumor has an impact on an individual's personality traits, manner of pondering, and numerous types of vital processes. Brain tumors often fall into two different groups: benign (also known as non-cancerous) as well as malignant (also known as cancerous) [6], [7]. Brain-originating benign tumors remain non-progressive. It is unable to spread across the body of a human and isn't as aggressive as other tumor types. Carcinoma tumors, on the other hand, constitute cancerous tumors that quickly invade different parts of the human anatomy [8], [9]. The cerebral cortex is a crucial tissue that regulates all body processes as well as is an integral component of the neurological network. One of the worst skull disorders that may be damaged is known as a brain tumor, which is brought on by an unexpected development of the population of cells inside the cerebral cortex [10], [11].

These tumors harm and eventually malfunction the nervous system, which may be fatal if ignored over an extended amount of period. Brain tumors are expected to rise by 7.8% each year, according to the World Health Organisation (WHO) [12], [13]. According to a different study, brain tumors comprise the tenth most common reason for human death. A dangerous cerebral or central nervous system (CNS) tumor is predicted to claim the lives of around 25,600 people this year [12]. Therefore, early and correct tumor identification may improve the individual's prognosis. Since the degree, as well as the nature of the tumor, affects the process of therapy, a timely as well as accurate assessment of

a cerebral tumor is essential for the individual's well-being [13]. Tumors vary in dimensions, position, and even form, making it difficult to distinguish between them. The probability of an individual recovering from a cerebral tumor can be decreased by an incorrect or delayed treatment [14], [15]. To identify cerebral tumors in the past, clinical practitioners have employed accurate tumor position tracking and subjective interpretation of imaging studies.

## II. RELATED WORK

Throughout the following section, researchers reviewed earlier studies that looked at ML algorithms for detecting brain tumors. Many models involve the DL [16], ML [2], ANN [17], SVM [18], KNN [19], Decision Tree [20], LSTM [21], GAN [22], and many more. C. Malik et al. [23] discussed deep learning methods for brain tumor analysis. A skull tumor is a collection of strange cells discovered inside the central nervous system which might develop into carcinoma. An MRI scan remains the greatest method for finding a head tumor among the many simple approaches to identifying skull tumors. The proposed model is rooted in the convolutional neural network (CNN) concept for the determination of the kind of tumor in the human skull using the scanned MRI images. Nevertheless, this CNN model has limits involving the class imbalance or high overfitting.

In [24], S. Kothari et al. conducted an examination of brain tumors through a hybrid model based on DL. DL-based mathematical models feature many stages of processing that interpret information at various degrees of generality. Recently, DL has become very popular, especially in the fields of medicine, processing medicinal images, especially clinical picture assessment. DL was used in the present research to suggest a method for identifying as well as classifying malignant brain tumors. The underlying causes of head tumors, and different types of imaging for cerebral tumors, including autonomous computer-assisted approaches for cerebral tumor characterization are all summarised in this work using a variety of soft computing methodologies including a DL architecture.

K. R. Pedada et al. [25] proposed a DL-based approach for tumor analysis. Effective therapy for cerebral tumours as well as accurately quantifying their thickness are both hampered by the difficulty of determining the spread of the cancer. For the diagnosis of cerebral tumors, MRI has become the standard procedure. It takes a lot of information and depends greatly on the practitioner's experience to physically separate the size of a cerebral malignancy using 3D MRI. This model has some limits such as ethical as well as privacy concerns and interpretable features etc. In [26], R. Asad et al. explored a framework for brain tumor characterization through DL. Brain tumors impair the brain's regular operation, and when they are not handled promptly, the neighboring organs, veins, including synapses may also be affected by the malignant tumors. The dangerous ailment known as a brain tumor now affects a sizable portion of the global populace. This model is very complex to implement and receives low accuracy.

## III. PROPOSED ALGORITHM

The suggested study methods for classifying brain tumors at a finer level are explained in this part of the article. Researchers provide a full explanation of the suggested DL-based technique, its architecture, as well as the several pre-trained DL algorithms used to identify as well as categories of meningioma, pituitary tumor, as well as glioma tumor class within cerebral MR pictures.

### 3.1. Proposed Model Architecture:

Figure 1 illustrates the suggested study technique and provides a conceptual perspective of the suggested DL-based procedure for classifying brain tumors from the MR dataset. The subsequent phases make up the suggested DL-based categorization of brain tumors. initially inserted the data in our training subdirectory after downloading the open-access Kaggle MR picture collection, which includes glioma tumor, meningioma tumor, as well as pituitary MR pictures. These MR pictures of the data were accessed using the training subdirectory through Picture DataStore, which we also used. To assess the adaptability and accuracy of our DL frameworks, there has been used a data enhancement strategy in the subsequent stage. To increase the quantity of data that is already accessible while obtaining additional information, a technique known as dataset augmentation is used in picture categorization. The authors used the dataset augmentation strategy in this investigation since the data only included a certain number of MR pictures. After the data augmentation, MR imaging data preprocessing is required to perform multiple operations namely cleaning, transformation, resizing as well as optimal normalization of entire MR images. In the next step, the DL model is applied which contains multiple models simultaneously. There is used enhanced CNN, KNN (K-Nearest Neighbors), and VGG16. Also, a framework based on ResNet-50, SVM (Support Vector Machine), and CapsNet is used in this advanced deep ensemble model for brain tumor detection. The entire picture data is split into multiple classes i.e., 80% in the training group and 20% in the test group. The data split operation is accomplished utilizing the K-fold cross-validation. The value of K has been taken as 5 in this study. The influence of variability during the division of the MR dataset is lessened as a result of this approach, leading to a higher consistent as well as trustworthy assessment of the predictive model's ability to execute. Additionally, this aids in determining how well the prediction

model generalizes to other subgroups of the MR dataset. Figure 2 shows the architecture of the Convolutional Neural Network (CNN).

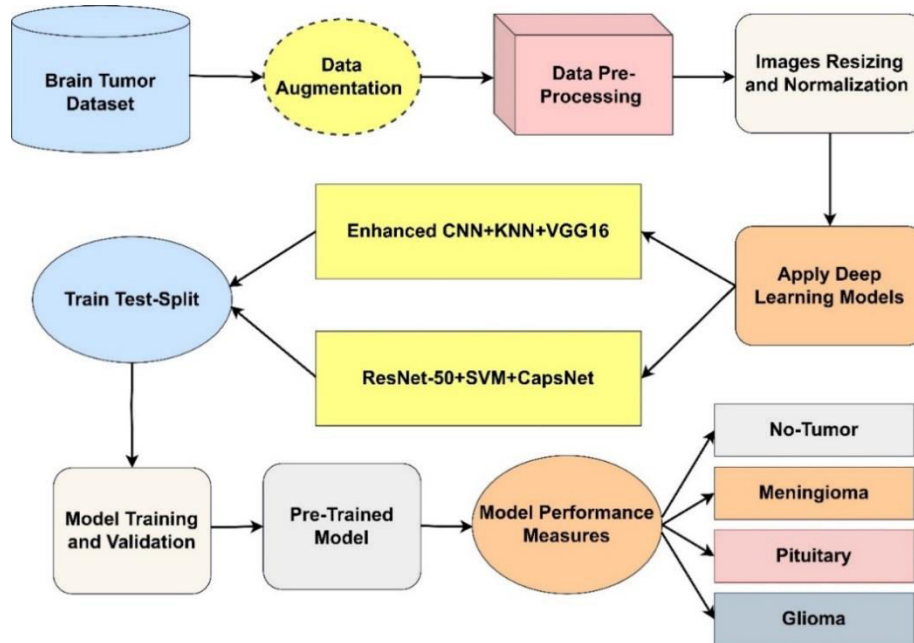


Figure 1: Shows the proposed ensemble model for brain tumor detection and classification.

### 3.2. Training and Validation Procedure:

The training procedure of the proposed model is summarized as follows:

**Step 1:** Provide the framework with the training datasets (features along with multiple labels).

**Step 2:** Throughout the training procedure, the simulator repeatedly modifies its parameters such as weights as well as biases to minimize specified losses or expenditure functions.

**Step 3:** To modify the framework's settings, optimization methods like Adam, as well as RMSprop are frequently utilized.

**Step 4:** To update the hyperparameters i.e., learning rate, hidden layers, and batch size in real-time.

**Step 5:** To utilize validation set for experiments with the aid of multifarious hyperparameters settings to receive the optimal configuration which improves the performance of the proposed DL-based model.

**Step 6:** After certain epochs regularly evaluate the performance of the proposed model on the train set for computing the progress of the model as well as identify the threats such as overfitting etc.

**Step 7:** Once the training process is done, the final framework progress has been assessed utilizing the test data sets i.e., not observed in the hyperparameter setting or training process.

**Step 8:** To apply dropout, regularization L1 and L2, batch normalization has been applied for minimization of overfitting as well as enhancement of the model generalization in real-time.

**Step 9:** To observe the metrics such as accuracy, F1-score, or other metrics.

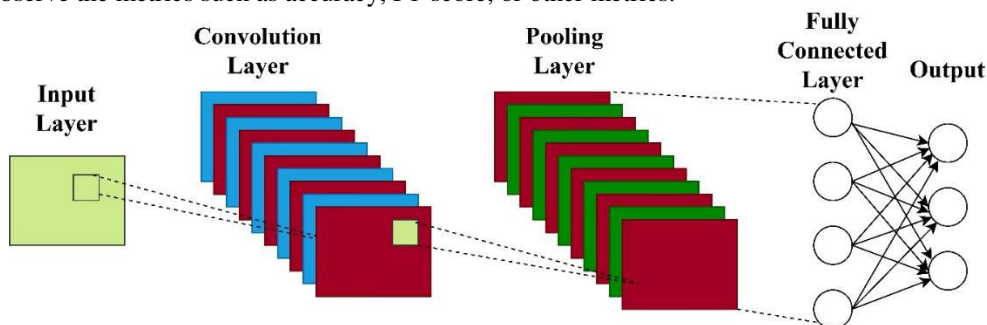


Figure 2: Shows the architecture of the Convolutional Neural Network (CNN).

### 3.3. Experimental Setup:

This DL model has been implemented on a computer system platform. This system platform has the following settings: AMD Ryzen 5 CPU, Memory of 16GB, Storage of 512 SSD, Windows 11, and IPS panel for better color accuracy. Further, the Google Colab has been used as a main experimental setup to execute multiple experiments. The coding part is done using the Python programming language.

### 3.4. Dataset information:

Table 1 shows the dataset settings for the proposed model implementation. There has been taken the images of from the Kaggle dataset for suggested model implementation. Several image classes are considered such as 340 images of Meningioma Tumors, 255 images of Glioma tumors, 367 images of pituitary tumors, and 200 images of no tumors. Further, the images considered for the training samples for Meningioma Tumor, Glioma, and Pituitary Tumor, not a Tumor, Overall taken images were 200, 100, 200, 110, and 610, respectively. The images considered for the testing samples for Meningioma Tumor, Glioma, and Pituitary Tumor, not a Tumor, Overall taken images were 140, 155, 167, 90, and 552, respectively.

**Table 1: Dataset settings for proposed model implementation.**

| S. No. | Tumor Class          | Total count | Training sample | Testing sample |
|--------|----------------------|-------------|-----------------|----------------|
| 1      | Meningioma Tumor     | 340         | 200             | 140            |
| 2      | Glioma               | 255         | 100             | 155            |
| 3      | Pituitary Tumor      | 367         | 200             | 167            |
| 4      | Not a Tumor          | 200         | 110             | 90             |
| 5      | Overall taken images | 1162        | 610             | 552            |

### 3.5. Evaluation Metrics:

For the proposed deep ensemble model implementation, multiple metrics that involve accuracy, precision, F1-score recall, and specificity have been considered. The performance of the suggested deep ensemble model is assessed utilizing the following metrics.

$$Accuracy = \frac{TP+TN}{TS} \quad (1)$$

$$Precision = \frac{TP}{TP+FP} \quad (2)$$

$$Recall = \frac{TP}{TP+FN} \quad (3)$$

$$SPC = \frac{TN}{FP+TN} \quad (4)$$

$$F1\ Score = 2 * \frac{Precision*Recall}{Precision+Recall} \quad (5)$$

Here, FP is the False positive, FN is the False Negative, TP is the true positive, and TN is the true negative.

## IV. SIMULATION RESULTS

Selecting the right verification method is crucial for the dataset of 1162 scanned pictures. With 80% of the picture dataset being utilized for training samples and the remaining 20% being utilized for verification samples, we decided to implement a holdout verification method. The method known as the holdout verification approach is the greatest utilized strategy which yields favourable outcomes. To assist with the algorithm training more quickly, the given holdout technique often entails dividing the sample between a train set plus a test set. This deep ensemble model has been trained using the train samples, and its effectiveness was assessed using the test samples taken from the Kaggle dataset images. In the adopted holdout approach, 20% of image data was utilized as the testing samples as well as rest of the 80% of image samples were arbitrarily chosen to be the training sample for the model training process. This ensemble model is trained by utilizing the 610 image train samples, as well as its effectiveness is then assessed on

552 testing image samples. This proposed deep ensemble model contains more dataset samples in generalization when 80% of data is used for training purposes, this might aid in its ability to generalize to fresh, unexplored datasets.

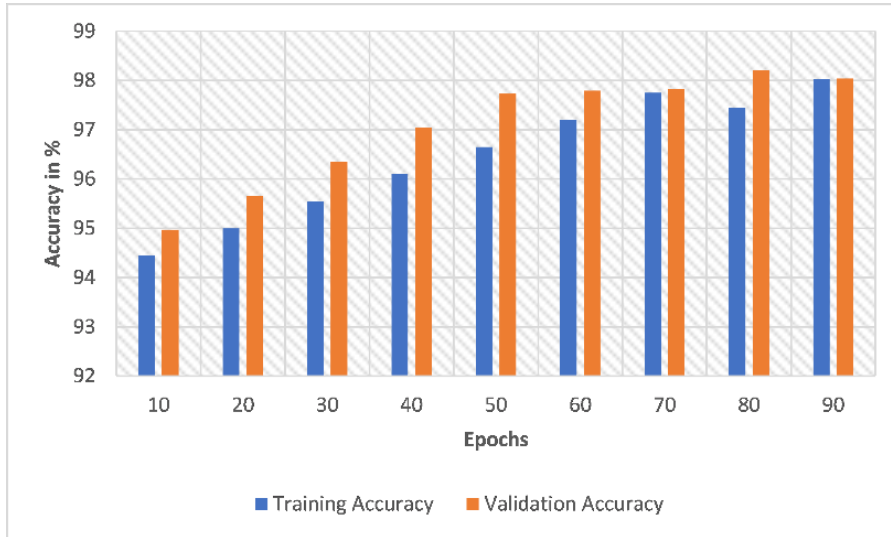


Figure 3: Evaluated accuracy of the proposed model.

Figure 3 shows the evaluated accuracy of the deep ensemble model. The accuracy of this ensemble model in training on epoch 10, 20, 30, 40, 50, 60, 70, 80, and 90 is 94.45%, 95%, 95.55%, 96.1%, 96.65%, 97.2%, 97.75%, 97.45%, 98.03%, respectively. The accuracy of this ensemble model in testing on epoch 10, 20, 30, 40, 50, 60, 70, 80, and 90 is 94.97%, 95.66%, 96.35%, 97.04%, 97.73%, 97.79%, 97.83%, 98.2%, and 98.04%. All the scores are found enhanced for correct detection of the tumor’s classes in real-time.

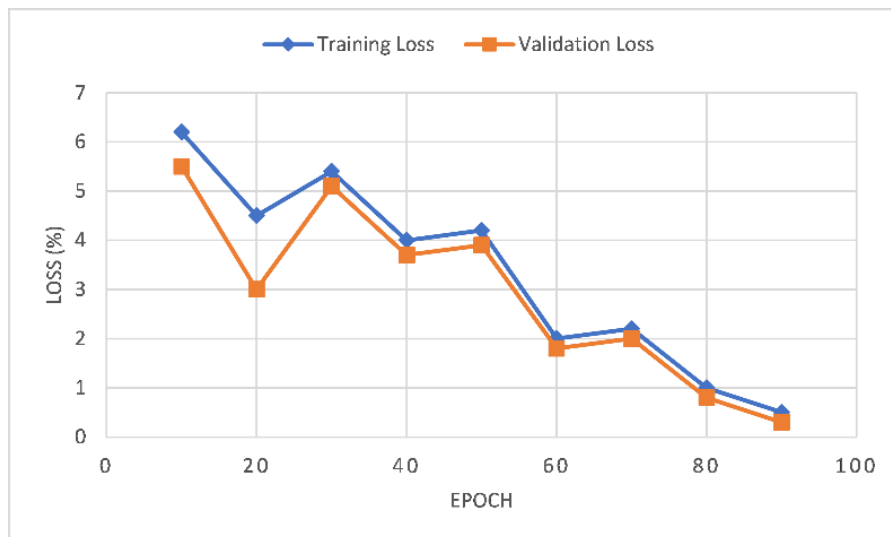


Figure 4: Evaluated loss of the proposed model

Figure 4 shows the evaluated loss of the proposed model. This proposed deep ensemble model is very good in brain tumor prediction as it attains less train loss on epochs 10, 20, 30, 40, 50, 60, 70, 80, and 90 are 6.2, 4.5, 5.4, 4, 4.2, 2, 2.2, 1, and 0.5. Further, this deep ensemble method receives less loss in test phase on epoch 10, 20, 30, 40, 50, 60, 70, 80, and 90 are 5.5, 3, 5.1, 3.7, 3.9, 1.8, 2, 0.8, and 0.3.

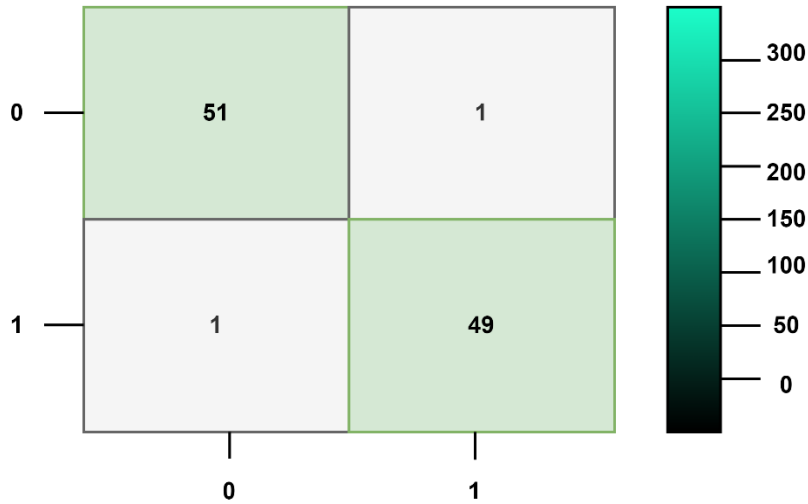


Figure 5: Shows the confusion matrix for the proposed deep ensemble model.

Figure 5 shows the confusion matrix for the proposed deep ensemble model. The matrix of confusion provides a performance assessment instrument utilized in DL, especially for addressing classification issues. Contrasting the forecasts of a categorization algorithm with the actual ground truth labeling, enables you to evaluate the accuracy as well as effectiveness of the model. Whenever you are interested in how well the algorithm is working and you have a sample with known labeling for classes, the confusion matrix may be quite helpful.

Table 2: Illustrates the overall analysis of all metrics for the proposed deep ensemble model.

| S. No. | Metrix      | Observed Values (%) |
|--------|-------------|---------------------|
| 1      | Accuracy    | 98.04%              |
| 2      | Precision   | 98.08%              |
| 3      | Recall      | 98.11%              |
| 4      | F1-score    | 98.25%              |
| 5      | Specificity | 98.00%              |

Table 2 summarizes the overall analysis of all metrics for the proposed deep ensemble model. It has been observed that the suggested deep ensemble model's overall accuracy, precision, Recall, F1-score, and Specificity are 98.04%, 98.08%, 98.11%, 98.25%, and 98.00%, respectively.

### V. CONCLUSION AND FUTURE WORK

Worldwide greater death rates may be significantly reduced by prompt identification of brain tumours. This accurate identification of brain tumors remains quite difficult because of the tumor's shape, shifting dimensions, and complicated chemistry. The categorization of MRI imagery has a significant impact on the medical diagnostic as well as therapeutic choices made for those suffering from brain tumors. A tumour fragmentation technique as well as early brain tumour detection employing MRI scans both seem encouraging. However, more work has to be done before the tumor site can be properly identified as well as categorized. In our work, we employed a range of MR brain tumor pictures for the objective of prompt cerebral tumor identification. Segmentation along with identification are significantly impacted by the proposed deep ensemble model as well. With the use of several MRI scans, we presented an enhanced CNN, KNN as well and VGG16-based model for the prompt identification of brain tumors and saw encouraging results. To guarantee the effectiveness of the ML-based models throughout the assessment procedure, we used several metrics. Researchers considered a few more ML algorithms in addition to the suggested approach while evaluating our results. Overall deep ensemble model accuracy, precision, recall, F1-score, and specificity were found to

be 98.04%, 98.08%, 98.11%, 98.25%, and 98.00%, respectively. Future research can be done on multimodal data fusion approaches and 3D Imaging and Reconstruction for quick identification of brain tumors.

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