

Brain Tumor Detection by Image Segmentation Using Customized UNet Deep Learning Based Model

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Abstract—Human brain is the most valuable organ that perform the most critical thinking and get the best solution methodology for real life problem. So, proper care should be taken to keep this valuable part be safe from being damaged by tumor disease. When a brain tumor is misdiagnosed, patients may receive the incorrect medical care, decreasing their chances of survival. Brain tumors are a deadly condition that, in its worst case, can have a very short life expectancy. In order to overcome these difficulties, the suggested framework uses CNN in large-scale trials to detect brain tumors utilizing the deep learning model's segmentation process. It is anticipated that the application of regularization strategies like augmentation and dropout will improve the precision of brain tumor identification with efficient manner. In this paper, we present a deep-learning method to detect brain tumors. We made use of a publicly available Kaggle brain tumor dataset that included color MRI pictures of both healthy and tumors brains that were afflicted. The dataset underwent preprocessing. A customized UNet CNN model was employed. Here, we customize the UNet model by adding 1 Convolution layer in downsampling and adding 1 De-Convolution layer in upsampling. With our suggested model, we achieved 99.80% train accuracy. For the validation and test phase, we achieved 99.78% & 99.75% accuracy, respectively.

Keywords—UNet, CNN, Conv2DTranspose, Conv2D, Dice-Coefficient, IoU, Deep-Learning.

I. INTRODUCTION

Brain malignancy is the cause of aberrant cell production that have the potential to become malignant brain cancer and harm the brain's structural integrity [1]. These tumors, also known as metastatic or secondary brain tumors, can be

benign (noncancerous), malignant (cancerous), alternatively composition of the two. Based on malignancies size & location, different people with brain tumors will suffer different signs and symptoms [2]. The main specific etiology of Brain malignancy is still not clear, although some threats or possible symptoms are considered for this disease. By considering all possible symptoms some are mentioned here like effect of excessive radiation ray, family trend that means found consecutive members of the ancestors, and a few abnormal genetic diseases. Chemotherapy, radiation therapy, and surgery are frequently used in the treatment of brain tumors. There are different category of brain tumor disease which is specifically depends on the shape & location of the brain malignancy. Before starting treatment, there is required to consider some issues to avoid the negative affect. Considering all cases some can be included here like patient's present health status, preferences, shape & size of the malignancy, etc [3], [4]. Brain tumors remain a significant medical problem despite advancements in therapy, with certain tumor forms linked to high death rates. Therefore, more accurate and effective diagnostic techniques are needed [5].

Brain tumors were categorized by Natak et al. [6] using dense Efficient-Net. The dataset they used was sourced from Kaggle and comprised 3260 varieties images. The dataset included MRI images of the pituitary, glioma, and meningioma, respectively. Poor lighting and noise levels made the photos of brain tumors look grainy. Their proposed solution uses a

consecutive implementation process. Here, at first they use normalization technique, second they use filters like Gaussian & Laplacian to turn low-pixel value images into brighter ones. Various image transformation techniques have been employed for enhancing data samples. Original sample image was updated 21 times to improve training. This enhanced the quantity of training data, accelerating the learning process of their model. Additionally, as a result of data augmentation, they were able to reduce overfitting as the volume of data increased. EfficientNet-B0, a 237-layer network, was used to classify brain tumors into meningioma, glioma, and pituitary cancers.

Concatenation-based deep learning architecture was presented by Noreen et al. [7]. They use publicly available Figshare brain tumor dataset. This brain dataset consists of 3064 MRI pictures from 233 different people. There are three distinct types of tumors in this dataset: pituitary tumors, gliomas, and meningiomas. They used two pre-trained models, DensNet201 and Inceptionv3. Inceptionv3 uses the C, D, and E inception blocks for feature extraction and feature concatenation. The softmax classifier received these concatenated features. For DensNet201 feature extraction and feature concatenation, the Denseblock—which consists of twelve (12), forty-eight (48), and thirty-two (32) convolutional layer blocks—has been utilized [8].

In this regard, deep learning techniques can aid in the development of more effective instruments for the early detection and management of brain cancers. Main goal of such kind of research work was using customized CNN [9], [10] to detect brain malignancy. To increase CNN's efficiency, a publically accessible dataset will be augmented using data augmentation approaches. Medical imaging modalities, including CT, PET, and MRI, are frequently used for the diagnosis and classification of brain cancers [11]–[13]. There are now methods for classifying and diagnosing brain tumors using deep learning and machine learning. The goal of this work is to develop a segmentation-based deep learning method for utilizing MRI scans to recognize brain tumors. The following are the precise contributions.

- To identify brain tumors through a segmentation-based deep learning model in an efficient manner.
- To increase the accuracy of the proposed model by customizing the existing efficient model.
- Expanding dataset & enhancing model's generalizability through the use of data augmentation tools.
- To assess the effectiveness of the suggested strategy.

Organization: The remainder of the paper is organized as follows: In Section II, the background and relevant literature are covered. The suggested model is thoroughly explained in Section III. The examination of the experiment results is mentioned in Section IV, and the conclusion is finally expanded upon in Section V.

II. RELATED WORKS

Arshia et al. [14] introduced DL technique for the categorization of brain malignancy. Their research, they use Figshare dataset consisted of 3064 brain MRI samples. Three quarters of the dataset were used for training, 15% for testing, and 15% for validation. During the preprocessing phase, they improved and honed the input data. To create high-resolution contrast images, they utilized the preprocessing

contrast stretching technique. They used three pre-trained CNN architectures (AlexNet, GoogleLeNet, and VGGNet) for feature extraction. To extract the discriminative visual features, each of the two transfer learning scenarios—fine-tune and freeze—is utilized separately for each architecture. AlexNet, GoogLeNet, and VGGNet obtained an accuracy of 97.39%, 98.04%, and 98.69% utilizing fine-tuning. For the freeze technique, AlexNet, GoogleLeNet, and VGGNet each obtained accuracy rates of 95.77%, 95.44%, and 89.79%. They have reached the highest accuracy of 98.69% among the optimized AlexNet and GoogleNet networks with the aid of the optimized VGG16 network. With an accuracy of 95.77%, AlexNet beat GoogLeNet and VGG16 while employing the transfer learning freezing strategy. Their study was limited solely by the complexity of time.

Hasan et al. [15] introduced DL technique to classify and identify brain malignancies. They used the Kaggle (Br35H) dataset for their research. This dataset contains 1500 brain MRI scans with tumors and another 1500 scans without tumors. After the changes were performed, there were 33 layers overall instead of just 22. The accuracy of their suggested model was 99.51%. Their investigation was limited by the inadequate size of the dataset they employed. Emrah Irmak [16] proposed a fully optimized deep CNN framework. He made use of four distinct, openly accessible datasets. For three classification tasks, he employed three CNN architectures. The CNN that is used for Classification-1 has 13 layers. The Second Classification, CNN, is comprised of 25 layers. The CNN's sixteen layers are used for Classification 3. Here, "Classification-1" denotes the identification of brain tumors, "Classification-2" denotes their classification, and "Classification-3" denotes their grading. On the other hand, learning rate, mini-batch size, and regularization are called fine adjustment hyperparameters. With a 99.33% accuracy rate, brain tumor identification was successfully accomplished. The accuracy of the classification of brain MR imaging was 92.66%. With a 98.14% accuracy rate, glioma brain tumors were correctly categorized into categories II, III, and IV. Another ideal and effective DL model was presented by Hamza et al. [17]. They made use of the Figshare dataset for their research. 1426 pictures from the Glioma class, 708 pictures from the Meningioma class, and 930 pictures from the Pituitary class were included in the collection. The pre-processing phase of their suggested methodology entails skull stripping and bilateral filtering procedures. Bilateral filtering removes noise while maintaining large, sharp edges, all without blurring. They used the Xception model for feature extraction. The STO algorithm was used to modify the hyperparameters in the Xception model. The ALSTM model was ultimately employed to categorize BT into several classes. To enhance the proposed model's BT classification performance, they intended to apply deep instance segmentation methods.

A deep Wavelet Autoencoder (DWA) based deep neural network for classifying brain MRI images for disease detection was proposed by Mallick et al. [18]. This study used the RIDER Neuro-MRI dataset, which includes imaging data from 19 recurrent glioblastoma patients who had repeat imaging examinations. Reference Imaging Database to Assess Treatment Response is referred to as RIDER. Their proposed DWA-DNN model attained an overall accuracy of 96% and an average ac-

curacy of 93%. Comparably, the accuracy on average was low. Deep neural networks and multiclass SVM were employed by Maqsood et al. [19] for multi-modal brain tumor identification. Two datasets, figshare and Brain Tumor Segmentation (BraTS) 2018 were used to test their suggested technique for diagnosing brain tumors. They proposed a five-stage method for classifying and diagnosing brain cancers. Finally, the M-SVM classifier is used to classify brain tumors for both the BraTS 2018 and Figshare datasets. Their study was limited to 2D MRI scans and had two drawbacks: the feature selection process took some time. Glioblastoma patients' overall survival was predicted by Ahmed et al. [20] using ensembles [21] of convolutional neural networks derived from multimodal MRI. In their analysis, a subset of glioblastoma cases—163 instances for training and 46 cases for testing—from the BraTS 2019 training dataset was utilized. The system started with raw 3D MRI images, which were fed into a segmentation network that had already undergone training. Following feature extraction, a 3D CNN model applied to train classifier. The outcome of their recommended method has a very low accuracy of 57.1%.

By utilizing a deep learning network and 3D imaging of the tumor location, Karayegen et al. [22] were able to predict brain cancers on MRI images through semantic segmentation. They used semantic segmentation on 257 BraTS image data sets to construct a deep-learning network. Using the training, validation, and test images, labels were predicted and compared to the ground truth labels. Five distinct data sets were examined, each containing 155 MR slices that included a tumor. Their study's results showed that the average background prediction was 99.756% and the average tumor prediction ratio was 91.718. A novel convolutional neural network architecture was presented by Musallam et al. [23] for the automatic identification of brain malignancies. The first part of the image preprocessing technique involved cropping 100 pixels from either side of the image to remove distracting components like letters and blank areas in order to retrieve the precise brain object. The second phase of the proposed method efficiently deals with noise and enhances the image quality by using the non-local mean algorithm (NLM). When compared to Gaussian and Median algorithms, this increases the accuracy of the classification. The third step in the proposed method, called histogram equalization, splits the most common intensity values to eliminate interference from the images, finds minute features, and improves contrast in MRI photos. They developed a novel deep-learning model in their study that can solve common issues with similar models. This new model is composed of two components: the classifier and the convolutional component. The proposed architecture showed a remarkable competitive accuracy of 98.22%.

Using a constructed DL model based on magnetic resonance imaging, Alanazi et al. [24] suggested a framework to categorize brain malignancies and masses. Three distinct brain MRI scan datasets were used in the investigation. The initial dataset used in the study was named dataset-I and came from Kaggle. It was made publically available and had 3000 brain MRI scans with tumor and non-tumor diagnoses. The second & third dataset, known as dataset-II & dataset-III in the study, was obtained from Kaggle as well, and which consisted of 2870 samples & 3064 samples respectively. With pictures captured with the same MRI machine and data obtained from

an unknown MRI machine, their model achieved a high degree of accuracy, 95.75% and 96.89%, respectively.

Gomez-Guzm et al. [25] was used CNN model to categorize brain cancers on magnetic resonance imaging. The CNN models that were looked at in their investigation were EfficientNetB0, Xception, MobileNetV2, InceptionV3, InceptionResNetV2, Generic CNN, and ResNet50. They utilized a collection of MRI scans that were made public. It included 7023 MRI scans in JPG and grayscale format, showing four distinct types of brain cancer: pituitary tumors, meningiomas, gliomas, and no tumors. Following preprocessing approaches like downsizing and data augmentation, 9139 photographs were generated for training and testing. Training and validation methods made use of both the general CNN model and the pretrained CNN models. With a test score of 97.12%, the pre-trained model InceptionV3 demonstrated the highest accuracy in classifying brain tumors. Ayadi et al. [26] proposed a novel deep CNN model for classification of the brain tumor using MRI image dataset. There propose model shows 94.74% accuracy. In paper [27] Mahmud et al. proposed customized CNN based deep learning model for brain tumor detection and they achieved 93.3% accuracy. A tailored CNN deep learning model for brain tumor detection was proposed by Shraddha et al. [28]. They used MRI images and their model achieve a low level accuracy which was 87.42%

III. PROPOSED METHODOLOGY

A. Data Set Collection

We used 3D color MRI (Magnetic Resonance Imaging) dataset from Kaggle that is available to the public for this work. 3929 MRI pictures of various brain tumor kinds are included in the dataset; 2828 of these pictures were utilized for training, 708 for testing, and the final 393 for validation.

B. Preprocessing of the dataset

Pre-processing is an important step that entails changing the data so that it is appropriate for training. We normalized the photos to bring the characteristics into alignment with one another and set them up for future processing. This improves the training stability and performance of the model. We used rotation, flipping, and zooming to do data augmentation. Image data augmentation is a technique of making new, modified versions of the original photos to increase the diversity of an image collection.

C. Proposed Model

After pre-processing of the data set we divide it train, test, and validation as well as we do some data augmentation. Then we train our proposed customized Unet model using train dataset. We perform 50 epoch for training our model. After training we perform evaluation of our proposed model through some metric like dice-coefficient, accuracy, IoU. The following Fig. 1 shows the proposed model workflow.

D. Customized UNet Model

We customized the pre-trained Unet model for making the proposed model. The modification explain as follows. The pre trained Unet model use down sampling & up sampling portion where both contain 4 convolution layers and 4 De-Convolution layers respectively as well as each layer consists of consecutive two sequential convolution & De-Convolution layer for down

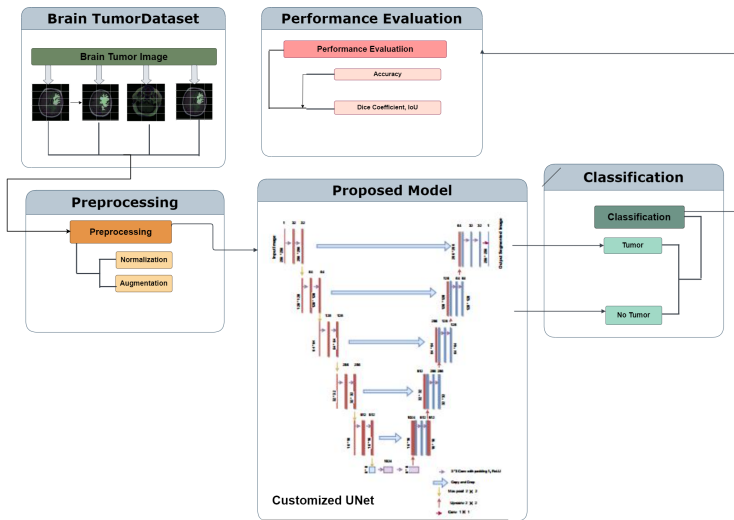


Fig. 1. Proposed Model diagram

& up sampling respectively. It employs stride 1 and 2×2 max pooling with 3×3 filter size. Every layer filters number for down-sampled section is doubled in comparison to the layer before it. On the other hand, in up sampling it is totally opposite comparing to the down sampling that means in every layer of the up sampling number of filters is decreased twice. In our customized Unet model used 5 Convolution layers for downsampling and 5 De-Convolution layers for up sampling portion. We add extra one layer in both down sampling and up sampling portion of the model where the number of filters was 32 with 3×3 filter size. Also, we used padding same. So, in our proposed model filter size is start from 32 and increased twice for each layer where the 6th layer filter size was 1024 for down sampling part. For up sampling part the filter size decreased twice and for the 5th layer filter size was 32. In every convolution layer for down sampling as well as every de convolution layer for up sampling we use Relu activation function. We use activation function sigmoid for the output layer which used 1×1 filter size for convolution to predict the class label. In down sampling we use Conv2D for convolution and for up sampling we use Conv2DTranspose to perform de convolution operation during the training phase. The following Fig. 2 shows the proposed customized UNet model architecture in details.

Convolutional 2D layer: For processing 2D input, a 2D Convolutional layer uses sliding convolutional filters. The input is convolved by the layer by moving the filters along the input in both vertical and horizontal directions, figuring out through the multiplication of input & weights, and then adding a bias term.

Max Pooling layer: From the feature map region that the filter covers, the largest element is chosen using a pooling technique called max pooling. Thus, it will provide most noticeable features from the prior feature map.

Conv2DTranspose: The opposite of convolution is called transposed convolution, sometimes referred to as fractionally-strided convolution or deconvolution. It works by enlarging the feature maps generated by a convolutional layer to improve an image's spatial resolution.

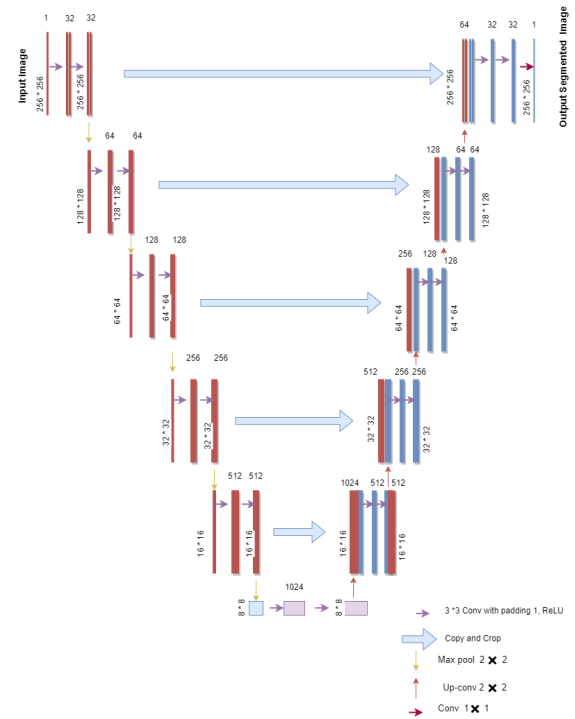


Fig. 2. Proposed customized UNet Model

ReLU: An activation function called a rectified linear unit (ReLU) addresses the problem of vanishing gradients and introduces non-linearity to deep learning models. The purpose of the ReLU layer is to increase the nonlinearity of the pixel data in the image.

IV. RESULT ANALYSIS

A. Implementation Result

We implement our proposed customized Unet deep learning model in Kaggle cloud server. For training, we used a total of 2828 color 3D images, which belong to 2 classes.

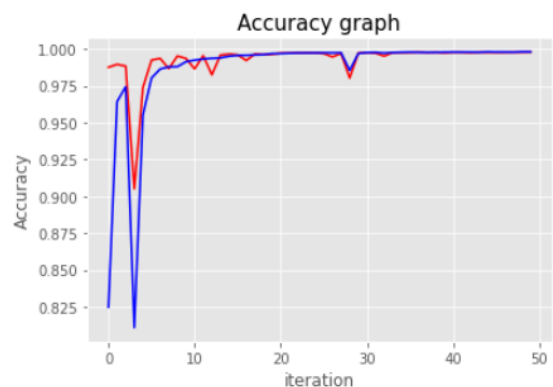


Fig. 3. Accuracy of the proposed Model

We set our batch size to 32. So, the steps per epoch was 89 according to the training dataset images. Before run the model we set some hyperparameter like initial learning rate

0.0001, optimizer algorithm as Adam, to calculate loss we use dice coefficient function. In Adam optimizer algorithm we set beta1 parameter as 0.9, beta2 parameter as 0.999, learning rate is same as initial learning rate, for decay parameter we assign this value by calculating division of learning rate with batch size. To keep track best weight parameter & save the model when gain best accuracy, we use Modelcheckpoint method in callback. We use validation dataset in training phase of the model to track the validation accuracy. For validation we use 708 3D color image data. On the 50th epoch, the training accuracy was 99.80% and validation accuracy was 99.76%. After training and validation we evaluate our model through test dataset which has 393 3D color images. We get 99.75% test accuracy when evaluate our test dataset. In Fig. 3 shows the training and validation accuracy & Fig. 4 shows training and validation loss.

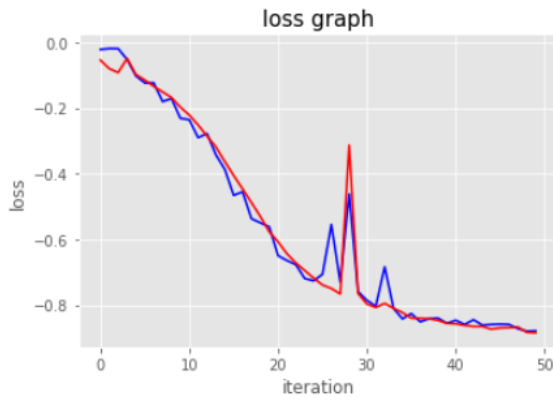


Fig. 4. Loss of the Proposed Model

On the other hand, Fig. 5 shows the evaluation result of our proposed model, which shows the three different images. First one is the original color image, second one is the mask image which shows in gray color & where white color segment is the detected brain tumor part & if there is no brain tumor in the color image then all part of the image is black. The third image is the predicted result image where shows yellow color segment as the detected brain tumor part. If there is no brain tumor then the image has no yellow color segment.

B. Performance Evaluation Metric

Accuracy: The percentage of a model's predictions that are accurate relative to all others is measured using an evaluation metric known as accuracy. The accuracy score is calculated by dividing the total number of forecasts by the number of correct guesses. The following figure shows the accuracy of the proposed model.

Dice Coefficient or F1-score: The dice coefficient is derived from a prediction's accuracy and recall. The overlap between the predicted segmentation and the ground truth is then scored. It also penalizes false positives, which are a common issue in datasets containing significant class imbalances, like segmentation of medical images. The harmonic mean of recall and precision is the dice coefficient, or F1 score. Put differently, the calculation involves dividing the total number

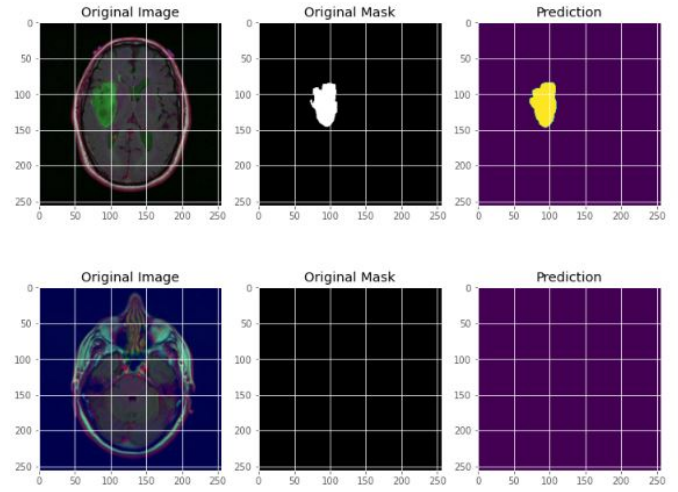


Fig. 5. Test Result of the Proposed Model

of pixels in both images by the product of $2 \times \text{intersection}$. The equation can be expressed as follows.

$$\text{Dice Coefficient} = \frac{2TP}{2TP + FP + FN} \quad (1)$$

Or it can also be rewrite as following way.

$$\text{Dice Coefficient} = \frac{2 * \text{Area of overlap}}{\text{Total area}} \quad (2)$$

Intersection over Union (IoU): The intersection over union (IoU) is the region where the expected segmentation and the ground truth converge.

The equation can be expressed as follows.

$$\text{IoU} = \frac{TP}{FP + TP + FN} \equiv \frac{\text{Area of overlap}}{\text{Total area}} \quad (3)$$

TABLE I
PERFORMANCE EVALUATION TABLE

| Phases | Accuracy | DiceCoefficient | IoU |
|------------|----------|-----------------|------|
| Training | 99.80% | 0.88 | 0.80 |
| Validation | 99.78% | 0.90 | 0.80 |
| Test | 99.75% | 0.90 | 0.80 |

TABLE II
COMPARISON OF OUR PROPOSED MODEL WITH SOME EXISTING MODELS

| Authors | Model | Accuracy |
|----------------------|--|----------|
| Proposed Model | Customized UNet-CNN | 99.78% |
| Ahmed et al. [20] | Ensembles of convolutional neural networks | 57.1% |
| Ayadi et al. [26] | CNN | 93.71% |
| Rehman et al. [14] | CNN, VGG19 | 92.67% |
| Mahmud et al. [27] | CNN | 93.3% |
| Shraddha et al. [28] | CNN | 87.42% |
| Irmak [16] | 25 layered CNN | 92.66% |

Table I shows the proposed model performance after training and testing in terms of Accuracy, Dice Coefficient or

F1-score, and IoU. In Table II, it shows the performance comparison of our proposed model with some existing models. Here, it has shown that our proposed customized UNet-CNN based deep learning model has better accuracy.

V. CONCLUSION

In order to develop a customized Unet CNN based model we add one Convolution layer in down sampling as well as add one De-Convolution layer in up sampling portion. Before implement our customized UNet-CNN based model, we required a significant number of instances or dataset. We used normalization and augmentation to preprocess the 3D color images before training the model. We included techniques like zoom, rotation, and horizontal flip. The suggested model's accuracy was 99.78%. The training period went by quickly. Epochs 1-7 showed overfitting, whereas later epochs rarely showed any signs of it. To lessen overfitting, we also wish to employ more regularization strategies. At present our proposed model only can detect whether there is a tumor or not through the segmentation based deep learning algorithm. Later, try to develop segmentation based DL methodology that can detect brain tumor as well as classify it's category that will help to diagnosis for the early stage treatment. This research work significance actually reflects on the implementation phase of smart healthcare where proper treatment required early stages.

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