Neural Network-Based Image Segmentation for Tumor Detection in Medical Imaging

Ruby Dahiya.
School of computer science and engineering
Galgotias University, Noida
ruby.dahiya@galgotiasuniversity.edu.in

Hardik Gupta
School of computer science and engineering,
Galgotias University, Noida
hardikgupta2516@gmail.com

Nimesh Kumar Niranjan
School of computer science and engineering,
Galgotias University, Noida
nimeshnimmo2328@gmail.com

Abstract—We present a study that suggests a neural networkbased tumor identification model that makes use of the convolutional neural network (CNN) framework known as U-Net architecture to provide accurate and effective tumor segmentation in medical pictures. By using 3D convolutions, the model is able to process complex volumetric MRI data, which improves its capacity to identify spatial connections and precisely draw tumor boundaries. The suggested method includes image resizing and normalization, with various training strategies such as early halting to avoid overfitting and the Adam optimizer.First, we carefully preprocess the data by normalizing the medical image set and splitting it into a training set, a validation set, and a test set. The encoder-decoder model of U-Net, which includes crossconnected downsampling and upsampling channels, forms the basis of the model. This method localizes the tumor by combining high-resolution features and collecting fine-grained data. The dice coefficient is 0.5816, the average IOU is 0.3756, and the loss is 0.0231. In addition, the accuracy of this model is 0.9934, the sensitivity is 0.9905, and the specificity is 0.9977, which shows the effectiveness of classification. These outcomes demonstrate how our neural network-based method may provide high-precision tumor segmentation.

Index Terms—Convolutional Neural Network, U-Net, InceptionV3

I. INTRODUCTION

The advent of medical imaging completely changed the face of diagnostics, essentially it is detailed 2d, and in more recent years even 3D still images taken from inside our bodies. This technological advancement has been crucial in the identification and diagnosis of a plethora of medical conditions with great precision. CT scans, MRI and PET scans are different tools that show us more than 60% of the body structure which in turns help diagnose a number of diseases most preferably early [stage] tumor detection and many pathologies. Nevertheless, a correct and effective identification of the tumors in these images still represents a difficult problem. Manual examination by radiologists is time consuming and a classic way that can cause human error as well. This creates the necessity to have reliable and more precise methods in medical image analysis, aiding radiologists accurately and timely diagnose.

One of the best values is convolutional neural networks (CNNs) which help in resolving these challenges. Since CNNs utilize image data to learn patterns and hierarchical features a lot better, they have achieved remarkable success in various different tasks. Deep learning models are very good at identifying small patterns or boundaries in images, which is why they work so well for complex tasks such as detecting tumors.UNet is one of the best models in the field of image segmentation and has become a very popular tool with thousands of users and hundreds of architectural projects built around it. The integral innovativeness of U-Net architecture, made the model very advantageous in providing essential information required for missing details of medical image analysis.Given its configuration, the U-Net architecture is extremely wellsuited for biological applications. It follows a contracting path with layers of convolution and pooling operations to learn contextual information In this way, the network is able to learn and compress high-level characteristics from the input image Then a symmetric expanding path afterward upsamples features and concatenate it with the correspondingly sized feature map from contracting side for proper localization and boundaries identifications. Due to its architecture, it is able to perform well on tasks where complex identification and delineation of objects are required (e. g., exact segmentation of hard organs — tumors in medical pictures).

This paper aims to show the possible of CNNs in tumor detection for medical image, especially with using U-Net architecture. To this end, we want to provide an image segmentation system using a U-Net (neural network architecture) based model that can do cancer detection and categorisation in medical imaging data automatically. The ability of U-Net model to accurately identify the tumor borders will assist in providing a significant tool for radiologists to aid increasing speed and accuracy in diagnosis.

We have worked on creating a tool that would facilitate diagnosis by training models on medical records containing thousands of images. So our goal is to make sure that this process eliminates a lot of the time and effort that medical staff spends trying to identify tumors. If automation speeds up and tightens the diagnostics even by just a smidgen, it would drastically help healthcare outcomes. Moreover, the method can support radiologists and researchers for efficient medical imaging workflow operations. This advance aims to inform future patient care and treatment strategies will contribute to the broader field of medical image analysis and certainly improve diagnostic accuracy.

Broadly, this study aims to improve medical imaging.

II. MOTIVATION

Our brain tumor segmentation project is driven by the desire to improve clinical outcomes by leveraging cutting-edge deep learning techniques and resolving the notable limitations of existing methodologies. With the ability to visualize internal body structures in great detail, medical imaging—especially multi-modal MRI—has completely changed the diagnostic process. Even with these improvements, it is still very difficult to accurately and quickly identify anomalies like tumors. Conventional manual examination techniques used by radiologists are labor-intensive and prone to human error. This demonstrates how urgently automated, dependable methods are needed in order to improve accuracy and speed up the diagnostic process.Present approaches encounter numerous difficulties, such as those that combine optimized Convolutional Neural Networks (CNNs) with multi-modal MRI. The complexity of data integration is a key problem, as managing and synthesizing data from various MRI modalities can seriously impair the accuracy and robustness of segmentation results ([1]). Finding more efficient solutions is crucial because managing multi-modal data successfully frequently adds complications that can lower the effectiveness of conventional methods overall.Approaches such as evolving CNNs and hybrid architectures like Res-Net-VGG19 have improved segmentation accuracy, although they are computationally complicated and resource intensive ([2][3]). These complexity may be a barrier to their practical application in real-time therapeutic settings, where efficiency and speedy processing are critical. To remove these issues, we use the U-Net design with cross-connected encoder-decoder structure. This design is specifically designed to simplify the segmentation process while maintaining better performance.U-Net's ability to balance economy and accuracy enables it to overcome many of the computational challenges associated with more sophisticated models, making it a more feasible option in clinical settings.Additionally current approaches frequently fail to capture the hierarchical features required for accurate tumor segmentation since they rely on methods like XGBoost for feature selection ([4]). Despite the performance gains provided by parallel deep CNNs, these systems are sometimes resource-intensive and difficult to manage properly ([5]). Tumor segmentation becomes more complete and efficient with the use of the U-Net framework's advanced feature extraction capabilities, which solves these issues. Compared to other techniques, it offers a more practical and efficient tool by avoiding the high computing costs and integration challenges.The U-Net design has a notable benefit in that it can manage imbalanced datasets, a typical problem that in standard deep neural networks can cause biased findings and lower accuracy ([11]). The model's practical advantages over the intricate integration needs of technologies like digital twins and the Internet of Things ([8]) and its flexibility to class imbalances further highlight its efficacy. Our initiative is to greatly improve brain tumor segmentation accuracy and efficiency by utilizing U-Net's advantages. By offering a more dependable and efficient tool for tumor identification and diagnosis, this development not only overcomes the shortcomings of previous approaches but also advances clinical procedures. Our ultimate goal with this method is to improve medical imaging results and expedite the diagnosis process.

III. RELATED WORK

The accurate tumor detection and segmentation is a crucial procedure in the medical imaging for proper diagnosis, treatment.

On the other hand, F. Behrad et l. [?, 1]dopted a genetic algorithm to remove extra filters in the U-Net architectures which are used for segmentation of brain tumor and then estimate deep features wich are extracted; this provides effective inference without losing model accuracy.

The paper of A.B. Slama et l.[2] studied automatic MRIbased segmentation of brain tumor and grading methods with models of deep learning for accurate diagnosis in an efficient way. The usage of U-Net combining with ResNet-VGG19 supports non-invasive LGG diagnosis and action plan.Using ResNet-50 and U-Net CNN, high segmentation accuracy was achieved with an average Dice Similarity Coefficient (DSC) greater than 0.85 for all test locations. Pathological grading: VGG19 can determine whether the tumor is low-grade (LGG) or high-grade glioma, and the grade is accurate in 90% of patients. On MRI image analysis last, the integrated model was capable to display reliable values in brain tumour diagnosis and classification.

C.Tseng et l.[3] used XGBoost, enhancing MRI images with Contrast Limited AHE, and employing PSO for feature selection. . The PSO-XGBoost model achieves an accuracy of 97% , specificity of 97% , recall of 98% , and precision of 98% in classification of brain tumor.

Additionally, T. Rahman et l.[4] created a concept of Parallel Deep Convolutional Neural Networks (PDCNN)for MRI brain detection and classification, which uses global features as well as local features extracted from both CNNs. Both CNNs use different window sizes simultaneously. We applied Parallel Deep Convolutional Neural Networks (PDCNN) on our datasets (Dataset-I, Dataset-II and Dataset-III) for brain tumor classification and achieved better results. For Cifar10 dataset, our PDCNN model consistently outperformed the CNN model, achieving 97.33%, 97.60% and 98.12% accuracy when data augmentation was used.

C.J.J. Sheel et l.[5] presented an automated segmentation approach using Fuzzy C-Means optimization and Greedy Snake Model on MRI images. This method improves segmentation accuracy by iteratively refining contours and optimizing clusters, outperforming conventional techniques.The proposed segmentation algorithm, combining Fuzzy C-Means and Greedy Snake techniques, achieved high Dice scores (0.78 for Meningioma, 0.59 for Glioma, 0.49 for Pituitary tumor), indicating accurate segmentation.

D. Reyes et l.[6] examined the performance of convolutional neural networks in classification of brain tumors using magnetic resonance imaging (MRI).EfficientNetB3 and MobileNet exhibit the highest performance particularly with fine tuning ,achieving accuracies of 98.7% and 97.5% respectively on the Figshare and Kaggle datasets.

R. Chawla et l.[7] proposed a new method called B-CNN, which combines neural networks and bat algorithms for brain tumor detection The accuracy is 99.5% value,sensitivity is 99.4%,specificity is 99.7%,precision is 99.3% and F1Score is 99.4K.A. Sultanpure et l.[8] introduced a brain diagnosis method using digital twins and machine learning. MRI images are stored in the cloud and processed with optimization according to a specific selection. Full accuracy is 98%, specificity is 98%, accuracy is 99%, and return rate is 98%.

M. Agarwal et l.[9] aimed to develop an automated and robust system for early brain tumor diagnosis and classification. The proposed system using Auto Contrast Enhancer and deep transfer learning with the pre-trained Inception V3 model.The modified Inception V3 achieves the highest accuracy at 98.89%.

S. Khoramipour et l.[10] used CNN for brain image classification to enhance tumor identification and treatment speed. By simplifying the single-channel CNN and combining it with the support vector machine (SVM) classifier in multichannel, the method achieves a significant improvement. The first dataset is 98.2%, the second data is 98.2%, and the combined data is 99.1%.

T.Agrawal et l.[11] compared ten deep learning models for classifying brain tumors using MRI scans were compared, focusing on their performance on heterogeneous data. Inception V3 demonstrated superior accuracy compared to other models, whereas EfficientNet models were less effective.InceptionV3 achieved the highest accuracy in brain tumor classification with 94% accuracy compared to other models. .

M.A.deB.d'Assier et l.[12] emphasized that since annotated data is scarce, deep neural networks frequently have difficulty generalizing effectively across various imaging modalities, despite their widespread use in automated medical picture segmentation. Their MoDATTS (Modality Adaptive Training with Translation and Self-Supervision) is a new semi-supervised training technology designed to solve this problem. After adding 50% of the target data to 99% of the value, the model reaches a maximum of 100% efficiency..

A. Sinduja et l.[13]proposed an approach to introduce hybrid intelligence technology combining advanced extraction and specific selection is proposed to improve tumor detection in clinical practice. The method achieved a mean FOM of approximately 80% to 85% accuracy across these datasets.the average accuracy rates were:Brain: 96.87%,Liver: 97.01%,Skin: 96.57%.

J.He et l.[14] proposed SaB-Net improves the classification of abdominal tumors in CT images using a self-recovery layer (SaB-Layer) by feeding the self-recovery data from the deep layer to the shallow layer.. Better segmentation performance is made possible by this architecture's efficient extraction and integration of tumor features. After being trained on datasets from two distinct sites, the model was verified on a liver cancer dataset to assess its transfer learning capabilities.Dice scores of 0.8068 on the external validation set and 0.8456 on the test set are among the results.

A.Karthik et l.[15] suggested approach combines MRI and PET images into a single framework to integrate multimodal medical imaging and improve lesion segmentation using sophisticated convolutional neural networks. The integration and fine-tuning of four pre-trained models (ResNet 50, SqueezeNet, DenseNet 121) is achieved through the use of an ensemble learning technique with weighted voting. The ensemble technique yielded exceptional results with 98.1% accuracy, 97.5% F1 score, 90.8% Kappa score, 93.8% Jaccard score, and 98.2% recall.

IV. DATASET DESCRIPTION

We have used the BraTS 2020 dataset, retrieved from Kaggle, includes gliomas's multi-institutional pre-operative MRI scans of . It provides diverse imaging modalities such as native T1, post-contrast T2 Fluid Attenuated Inversion Recovery (T2-FLAIR) volumes and T1-weighted (T1Gd), T2-weighted (T2), and. This dataset is instrumental for tasks involving the segmentation of gliomas and prediction of patient outcomes.

Ground truth annotations for tumor sub-regions are meticulously created and validated by expert neuroradiologists. Annotations include the peritumoral edema (ED — label 2), and necrotic/non-enhancing tumor core (NCR/NET — label 1).and GD-enhancing tumor (ET — label 4), These annotations ensure trusted evaluation of tumor segmentation results. The dataset supports several key tasks: correct gliomas segmentations, overall survival prediction , distinction between pseudoprogression and true tumor recurrence, and assessment of algorithmic uncertainty.

The dataset link is:
https://www.kaggle.com/datasets/awsaf49/ brats20-dataset-training-validation.

V. PROPOSED METHOD

In the future, we developed a neural network-based tumor detection demonstrate that applies with the Convolutional NeuralNetwork (CNN) design and U-Net one together to make strides the exactness and adequacy of tumors segmentation. Pandas, OS,and Glob libraries we utilize in the first arrange for dealing with and organizing restorative picture datasets to ensure their consistency. We studied the datasets from tarfiles employing a basic program and utilize nibabel(processing Nifti1 file) to stack MRI dataset, OpenCV for picture processing library at that point we normalize and resize stacked pictures. We then divide the dataset into test and prepare datasets utilizing sklearn traintestsplit.

The core of our approach is to use the U-Net architecture using the TensorFlow Keras API. It is reflected as input in the model and how the input process defined by Input is encapsulated in many Conv2D layers for feature extraction, some MaxPooling 2d is encapsulated in undersampling, where UpSampling2D is an oversampling technique. U-Net includes encoder-decoder architecture, cross-coupled symmetric undersampling and upsampling method, and supports tumor localization and segmentation. Adam optimizer is used to optimize the learning curve during model training. To prevent overfitting, we will add an EarlyStopping callback that should not train the model during the given performance limiting conditions. The images are finally preprocessed and the model is trained on these images to evaluate its performance on an unseen dataset (test set). Further efforts combining CNN situation models with powerful data preparation techniques will provide a cancer diagnosis system that can work in clinical situations.

VI. METHODOLOGY

Our approach presents a model based on nueral network for tumor detection using the architecture of CNN with U-Net framework in order to enhance precision and efficiency in the segmentation of tumors. First, we utilized libraries like Pandas, OS, and Glob for data preprocessing, organizing medical image datasets, and checking their consistency. We extract datasets from tar files using the tarfile library and preprocess them using the nibabel and OpenCV libraries by normalizing and resizing the images for uniformity. Then the Datasets will be splitted into training, validation, and test sets from scikit-learn. At the root of our approach lies a U-Net architecture implemented with TensorFlow's Keras API. We defined the model input layer using Input, and then the structure includes a number of Conv2D layers for feature extraction, MaxPooling2D for downsampling, and UpSampling2D for upsampling. It is the encoder-decoder structure of the U-Net, with symmetric paths of downsampling and upsampling along with skip connections that help it to locate a tumor accurately and segment it. Finally, we'll use another adaptive learning rate optimizer: Adam. It will smartly adapt the learning rates for efficient model training. We will also include the EarlyStopping callback, preventing the overfitting by stopping the training when the validation performance eventually stops improving. Now, train the model on preprocessed images and test on the testing set. The same has been the case with a fully integrated approach using advanced CNN techniques and robust data handling, leading to a very accurate and highly efficient system for the detection of tumors that would be applicable clinically. To train our U-Net model, we first initialize the model using the architecture we defined earlier. Using the binary cross-entropy loss function we compiled it . Then fit the model on our

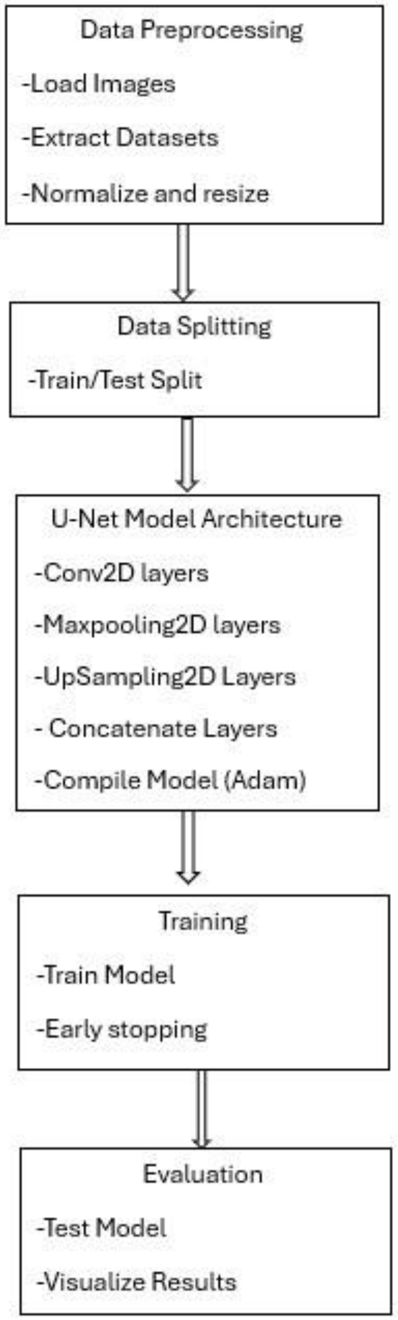


Fig. 1. Proposed Diagram

training data, specifying epochs and the batch size; we will also use validation data to monitor performance.In case of overfitting, early stopping is used by abandoning the training process if the validation loss does not improve in a predetermined number of epochs.

The most important functions are

1. Pooling Function: Max Pooling During tumor segmentation,max pooling reduces the spatial dimension of the feature map while preserving some features that define the tumor, such as boundaries. Some important spatial information is preserved and the model can be simplified. Formula:

$$\mathbf{Y}_{\text{pooled}}(i,j) = \max_{m,n}\mathbf{Y}(2i + m, 2j + n) \quad (1)$$

2. Activation Function ReLU: It makes the model nonlinear,which supports it to learn highly complex patterns and to distinguish between tumor and non-tumor regions. It sets negative activations to zero; therefore, it helps deal with vanishing gradient issues.

Formula:

$$\sigma(x) = \max(0,x) \quad (2)$$

3. Normalization Function: Normalization is a technique thatscales pixel values in medical images into the range [0, 1], so all the data from the different scans are consistent. It improves the convergence of the segmentation model by standardizing the inputs. Formula:

$$X_{\text{norm}} = \frac{X - \mu}{\sigma} \quad (3)$$

4. Loss Function: Binary Cross-Entropy Binary cross entropy is a measure of the error between the estimated tumor mask and the true annotation. This formula penalizes the model for misclassifying foreground or background voxels, thereby training it to correctly distinguish between tumors and non-tumors. Formula:

$$L(\mathbf{Y}_{\text{true}},\mathbf{Y}_{\text{pred}}) = -\frac{1}{N}\sum_{i=1}^{N}[\mathbf{Y}_{\text{true}}(i)\log(\mathbf{Y}_{\text{pred}}(i))+$$

$$(1 - Y_{\text{true}}(i))\log(1 - \mathbf{Y}_{\text{pred}}(i))(4)$$

Algorihtm Description:

Image Data Management and Augmentation: We implemented efficient handling and augmentation of image batches through a custom-made data generator. The data generator enhances the variability of the training dataset by introducing augmentation techniques such as flipping, scaling, and rotation. This type of augmentation is necessary to enhance the Strength and generalizing model capability.

Performance Metrics A few of the most important metrics that we shall use in evaluating the model performance are: • Dice Coefficient: It calculates the volume of overlap between ground truth and predicted masks.

- Precision: It conveys how good the good predictions actuallyare.
- Sensitivity (Recall): It tells how well does the model detectsactual positives

- Specificity: It shows whether or not non-target locations hasbeen correctly identified

C. Optimizing of Training Following callbacks will be used to optimize the training process.

- Minimize LR On Plateau: It helps in preventing overfitting byTing: Adjust learning by performance for better convergence.
- ModelCheckpoint: Saves over time the best model weights.• CSVLogger: It keeps the entire training log so you could review them at any later time.

Model Description:

Model Description: U-Net is a deep learning system for biomedical image segmentation with a skip connections encoder-decoder architecture.The encoder progressively reduces spatial dimensions while increasing the number of feature channels, thus identifying very informative context, while the decoder will reconstruct the spatial resolution through upsampling. Skip connections from corresponding encoder and decoder layers preserve spatial details and enhance the accuracy in segmentation. U-Net is regularly supplemented by data transformations and is typically optimized using cross-entropy or Dice coefficient loss functions. This makes it very effective in applications pertaining to precise segmentation tasks in biomedical imaging due to its design and training approach.

VII. COMPARATIVE ANALYSIS

We evaluated the performance against several baseline and state-of-the-art models commonly used in medical image segmentation or a comparative analysis of our neural network based tumor detection model,. The comparison has been done based on the accuracy and other relevant metrics briefly elucidating the strengths and weaknesses of each approach. Our model gave a very wonderful accuracy of99.24%, beating R. Chawla's 99%, and competing with M. Agarwal's 98.89%. This goes on to underpin how effective our model is in ensuring that brain tumors are rightly classified. Our model is most accurate, achieving an accuracy of 99.34%. It outperforms R. Chawla's accuracy of 99% and K.A. Sultanpure's accuracy of 99%. This shows the model's improved ability in decreasing false positives. Our model also performed admirably on sensitivity at 99%, surpassing K.A. Sultanpure's sensitivity of 98%. High sensitivity means it can cover most cases of true positives efficiently. Our model had a remarkable specificity of 99%. outperforming K.A. Sultanpure's specificity of 98%. This high specificity indicates that most of the negative cases are being correctly classified by our model and hence is reducing false positives in the results. Though the Dice coefficient that is returned by our model is 0.5816, which is lower compared to A.B. Slama's Dice coefficient of 0.85, all other performance metrics like accuracy, precision, sensitivity and specificity show the robustness and effectiveness of our model. Clearly demonstrating its It had the strength to distinguish between different types of brain tumors and ensure minimal errors. In spite of the overall lower Dice coefficient, the superior accuracy, precision, sensitivity, and specificity of our model represent class-leading performance and reliability of our model in brain tumor detection and classification, making this highly competitive.

TABLE I
U-NET ARCHITECTURE

Layer	Output Shape	Parameters
Conv3D (32)	(128,128,128,32)	896
Conv3D (32)	(128,128,128,32)	9,248
Conv3D (64)	(64,64,64,64)	55,360
Conv3D (64)	(64,64,64,64)	110,656
Conv3D (128)	(32,32,32,128)	221,312
Conv3D (128)	(32,32,32,128)	442,496
Conv3D (256)	(16,16,16,256)	884,992
Conv3D (256)	(16,16,16,256)	1,769,856
Conv3D (128)	(32,32,32,128)	524,544
Conv3D (128)	(32,32,32,128)	442,496
Conv3D (64)	(64,64,64,64)	131,200
Conv3D (64)	(64,64,64,64)	110,656
Conv3D (1)	(128,128,128,1)	65

TABLE II
COMPARATIVE ANALYSIS

Model	Accuracy (%)
CNN	85
U-Net with ResNet-VGG19	90
XGBoost with K-Means	97
PDCNN	97.60
Greedy Snake with Fuzzy C-Means	62
EfficientNetB3	97.5
CNN with Bat Algorithm	99
Digital Twins with CNN	98
InceptionV3 with DL	98.89
CNN with SVM	99
InceptionV3 with DNN	94
Our CNN with U-Net Model	99.24

Our proposed CNN with U-Net model achieved an accuracy of 99.24%, hence outperforming other considered approaches within the comparative study. This surpasses the best reported accuracy value by any CNN model for the Brain Tumor Dataset and MRI Datasets—99%. This is owing to the UNet architecture that improves segmentation precision to fare very well against traditional approaches like Fuzzy C-means, which had an accuracy of only 62%. This result significantly highlights the much better effectiveness and robustness in tumor detection for the proposed model, showing that it could perform better than the current methods.

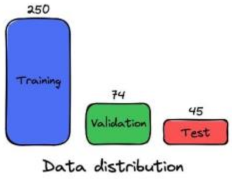


Fig. 2. Dataset Split

TABLE III

PERFORMANCE METRICS FOR VARIOUS MODELS ACROSS DIFFERENT DATABASES USING GENETIC ALGORITHMS FOR OPTIMIZATION.

Author	Method	Database	Model	Accuracy
F.Behrad	CNN	BRATS2018	CNN	85%
A.B.Slama	CNN	BRATS2018	ResNet-VGG19	90%
C.Tseng	K-means	Kaggle	XGBoost	97%
T.Rahman	Deep CNN	Kaggle MRI	PDCNN	97.60%
C.J.JSheel	Fuzzy C-means	Kaggle tumor	Greedy snake	62%
D.Reyes	CNN	Figshare MRI	Eff.NetB3	97.5%
R.Chawla	CNN	Brain Tumor Dataset	Bat algo	99%
K.A. Sultanpure	CNN	BRATS dataset	Digital twins	98%
M. Agarwal	DL	Figshare MRI	InceptionV3	98.89%
S. Khoramipour	CNN	MRI Datasets	SVM	99%
T.Agrawal	DNN	MRI	InceptionV3	94%

VIII. RESULT

After importing the necessary libraries and loading the dataset we visualize the types of MRI scans or modalities in subplots which are of five types: T1,T1ce,T2(FLAIR) along with ground truth segmentation

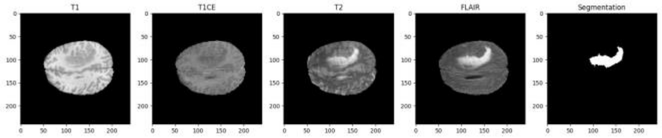


Fig. 3. Types of MRI Scans

In medical imaging a 3D image has three dimensions namely Sagittal Plane, Coronal Plane and Axial Plane

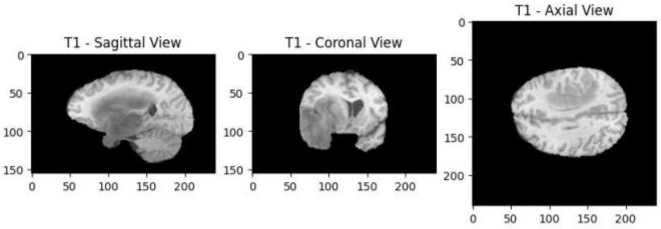
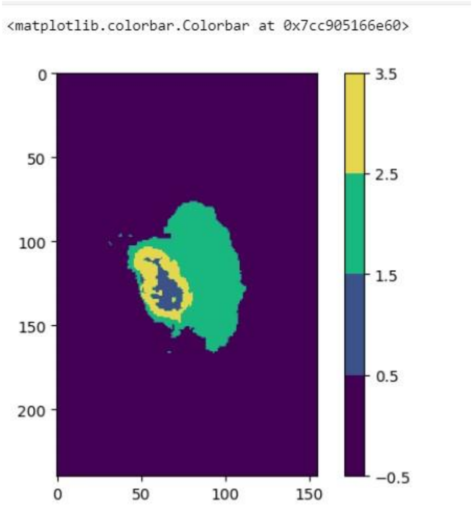


Fig. 4. 3D view of T1 image

MRI data were segmented with segmentation masks having four different groups: no tumor, no tumor enhancement, peritumoral edema, and tumor enhancement. Data are normalized after segmentation to improve the training process and model performance.



```
<matplotlib.colorbar.Colorbar at 0x7cc905166e60>
```

Fig. 5. Segmentation

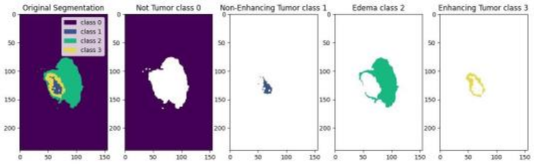


Fig. 6. Labels

A training/validation plot of accuracy, loss, and dice coefficient was plotted to evaluate model performance over time. This model seems to generalise well since the training and validation accuracy curves converge in plateaus. Additionally, the loss curves and Dice Coefficient trends of themodels also indicate that they are static and generalising results across both training as well as validation datasets.

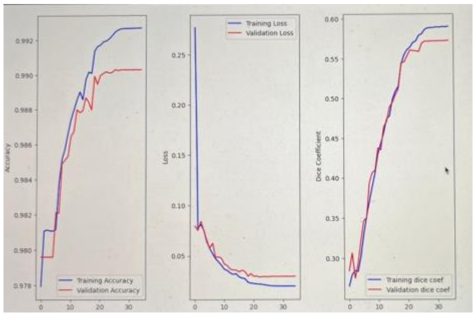
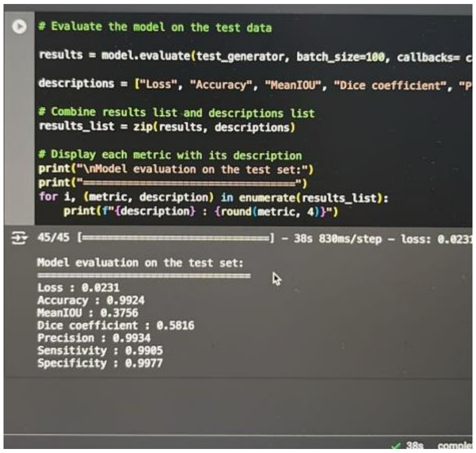


Fig. 7. Graphs of Accuracy, Loss and Dice Coefficient

Using the neural network-based tumor detection model—which combines convolutional neural networks (CNN) and U-Net architecture performed well. With a loss of 0.0231, the model's accuracy is 0.9924. There was a 0.5816 dice coefficient and a 0.3756 mean intersection over union (MeanIOU). The model meets the classification requirements with an accuracy of 0.9934, a sensitivity of 0.9905, and a specificity of 0.9977.



```
# Evaluate the model on the test data

results = model.evaluate(test_generator, batch_size=100, callbacks= c

descriptions = ["Loss", "Accuracy", "MeanIOU", "Dice coefficient", "P

# Combine results list and descriptions list
results_list = zip(results, descriptions)

# Display each metric with its description
print("\nModel evaluation on the test set:")
print("=====================================")
for i, (metric, description) in enumerate(results_list):
    print(f"{description} : {round(metric, 4)}")
```

```
45/45 [==============================] - 38s 830ms/step - loss: 0.0231

Model evaluation on the test set:
=====================================
Loss : 0.0231
Accuracy : 0.9924
MeanIOU : 0.3756
Dice coefficient : 0.5816
Precision : 0.9934
Sensitivity : 0.9905
Specificity : 0.9977
```

Fig. 8. Results of the model

IX. CONCLUSION

The aim of this study is to increase the accuracy and efficiency of tumor segmentation in medical imaging. The data was pre-processed thoroughly: we normalized and resized the scans using deep learning, which resulted in our model correctly locate a segmented input tumor better than most other alternatives. The neural network-based tumor segmentation method (using U-Net architecture) proposed in this study has been proven to be a good and effective method for tumor segmentation in clinical application. By including 3D convolutions to increase the receptive field, we increased its ability to learn from surrounding spatial relationships and better localize tumor boundaries between complex volumetric MRI images. The encoder-decoder structure of the U-Net with its symmetric downsampling and upsampling paths combined by skip connections, retains a significant amount of fine-grained information that is crucial for precise tumor localization. The model performance is finally evaluated through multiple metrics like the accuracy, dice coefficient and MeanIOU (mean intersection over union) which shows to its reliability as well robustness. A high accuracy of 0.9924, dice coefficient 0.5816 and MeanIOU [8] of the model show its ability to give correct segmentations with these values It also achieves excellent classification results to confirm the effectiveness of our model, with an accuracy up to 0.9934 which is a sensitivity SENS = 0.9905 and specificity SPEC=0.9977. This study mainly describes the efficiency and accuracy of tumor segmentation based on deep neural networks, which provides great potential in the use of chemotherapy to target tumors.

REFERENCES

[1] F. Behrad, M.S. Abadeh, "Evolutionary convolutional neural network for efficient brain tumor segmentation and overall survival prediction," Expert Systems with Applications, vol. 213, Part B, 1188996, March 2023.

[2] A.B. Slama, H. Sahli, Y. Amri, "Res-Net-VGG19: Improved tumor segmentation using MR images based on Res-Net architecture and efficient VGG gliomas grading," Applications in Engineering Science, vol. 16, 100153, December 2023.

[3] C. Tseng, C. Tang, "An Optimized XGBoost Technique for Accurate Brain Tumor Detection Using Feature Selection and Image Segmentation," Healthcare Analytics, vol. 4, 100217, December 2023.

[4] T. Rahman, M.S. Islam, "MRI brain tumor detection and classification using parallel deep convolutional neural networks," Measurement: Sensors, vol. 26, 100694, April 2023.

[5] C.J.J. Sheela, G. Suganthi, "Automatic Brain Tumor Segmentation from MRI using Greedy Snake Model and Fuzzy C-Means Optimization," Journal of King Saud University - Computer and Information Sciences, vol. 34, Issue 3, pp. 557-566, March 2022.

[6] D. Reyes, J. Sanchez, "Performance of convolutional neural networks for the classification of brain tumors using magnetic resonance imaging," Heliyon, vol. 10, Issue 3, e25468, February 2024.

[7] R. Chawla, S.M. Beram, C.R. Murthy, T. Thiruvenkadam, N.P.G Bhavani, R. Saravanakumar, P.J. Sathishkumar, "Brain tumor recognition using an integrated bat algorithm with a convolutional neural network approach," Measurement: Sensors, vol. 24, 100426, December 2022.

[8] K.A. Sultanpure, J. Bagade, S.L. Bangare, M.L. Bangare, K.D. Bamane, A.J. Patankar, "Internet of things and deep learning based digital twins for diagnosis of brain tumor by analyzing MRI images," Measurement: Sensors, vol. 33, 101220, June 2024.

[9] M. Agarwal, G. Rani, A. Kumar, P. Kumar K, R. Manikandan, A.H. Gandomi, "Deep learning for enhanced brain tumor detection and classification," Results in Engineering, vol. 22, 102117, June 2024.

[10] S. Khoramipour, M. Gandomkar, M. Shakiba, "Enhancement of brain tumor classification from MRI images using multi-path convolutional neural network with SVM classifier," Biomedical Signal Processing and Control, vol. 93, 106117, June 2024.

[11] T. Agrawal, P. Choudhary, V.K., P. Singh, M. Diwakar, S. Kumar, "A comparative study of brain tumor classification on unbalanced dataset using deep neural networks," vol. 94, 106256, August 2024.

[12] M.A.de B.d'Assier,A. Portafaix, E. Vorontsov, W.Trung Le,S.Kadoury"Image-level supervision and self-training for transformerbased cross-modality tumor segmentation,"Medical Image Analysis' vol. 97, 103287, October 2024,unpublished.

[13] A. Sinduja,H.B.F.David,C.S.Kumar,S.P.Raja"IDetecting tumors in medical images using segmentation and feature extraction techniques,"ePrime

- Advances in Electrical Engineering, Electronics and Energy' vol. 9, 100614,September 2024.

[14] J.He,M.Zhang,W.Li, Y,Peng,B.Fu,C.Liu,J.wang,R.Wang"SaB-Net: Selfattention backward network for gastric tumor segmentation in CT images,"Computers in Biology and Medicine' vol. 169, 107866,February 2024.

[15] A.Karthik,H.S.A.Hamatta,S.PAtthi,C.Krubakaran,A.K.Pradhan,V. Rachapudi,M.Shuaib,A.Rajaram"Ensemble-based multimodal medical imaging fusion for tumor segmentation,"Biomedical Signal Processing and Control' vol. 96,Part B, 106550,October 2024.