Efficient segmentation and classification of the tumor using improved encoder-decoder architecture in brain MRI images

Original Scientific Paper

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Abstract *– Primary diagnosis of brain tumors is crucial to improve treatment outcomes for patient survival. T1-weighted contrast-enhanced images of Magnetic Resonance Imaging (MRI) provide the most anatomically relevant images. But even with many advancements, day by day in the medical field, assessing tumor shape, size, segmentation, and classification is very difficult as manual segmentation of MRI images with high precision and accuracy is indeed a time-consuming and very challenging task. So newer digital methods like deep learning algorithms are used for tumor diagnosis which may lead to far better results. Deep learning algorithms have significantly upgraded the research in the artificial intelligence field and help in better understanding medical images and their further analysis. The work carried out in this paper presents a fully automatic brain tumor segmentation and classification model with encoder-decoder architecture that is an improvisation of traditional UNet architecture achieved by embedding three variants of ResNet like ResNet 50, ResNet 101, and ResNext 50 with proper hyperparameter tuning. Various data augmentation techniques were used to improve the model performance. The overall performance of the model was tested on a publicly available MRI image dataset containing three common types of tumors. The proposed model performed better in comparison to several other deep learning architectures regarding quality parameters including Dice Similarity Coefficient (DSC) and Mean Intersection over Union (Mean IoU) thereby enhancing the tumor analysis.*

Keywords*: UNet, ResNet, ResNext, Deep Learning, Transfer Learning, CNN, Brain tumor Segmentation*

1. INTRODUCTION

According to the published statistics from the American Society of Clinical Oncology Foundation, brain and other nervous system cancer is the 10th major reason for loss of life across the world. An estimated 308,102 individuals were detected with brain and nervous system cancer worldwide in 2020. Out of which, brain tumors alone account for 85% to 90% of all brain and nervous system cancer [1]. The brain is the complex and essential organ where all main functions of the human body like thought, speech, vision, and body activities are controlled. So as the tumor grows in the brain can affect these necessary activities. Specialists are taking efforts to learn about brain tumors and find the best treatment. To achieve the same, precise classification and tumor segmentation are necessary. Achieving high-level accuracy for the exact determination of tumors for saving lives requires a great amount of research. Generally, the diagnosis begins with Magnetic Resonance Imaging (MRI), which is a non-invasive process. MRI is a preferred way over other scanning techniques as it provides detailed images of soft tissues, but the manual segmentation of its images is quite a time-consuming and very challenging task. With recent advancements in technologies to enhance tumor detection deep learning methods can be integrated with different imaging modalities. The result of these methods extremely relies upon the quality of the image [2]. Using the deep learning algorithms on MRI images, the analysis and accuracy can be enhanced to far better levels in very less time. So, there is a very wide scope and need for research in this area.

Generally, deep learning techniques are categorized into supervised and non-supervised techniques. Supervised learning requires a massive amount of dataset which helps in better generalization. It is challenging in the medical field to gather huge datasets with labels as annotation requires extensive time from medical experts with multiple expert judgments to overcome human error. Along with this, privacy and legal issues, data interoperability, and data standards are the major challenges in the healthcare system [3]. Overfitting is another major challenge wherein the model performs well on the training dataset as compared to the test dataset. To resolve this training should be done on a larger dataset. To address the scarcity of data the data augmentation technique is used to raise the dataset artificially from the existing training dataset by applying random transformations which provide a diversity of data available for the training model [4, 5]. A pretrained model on the large standard dataset can be utilized for the different tasks as a feature extractor with a comparatively lesser available dataset is known as transfer learning, which removes the need of having a large dataset for model training and also reduces long learning time [6]. Contributions to this work are:

Traditional UNet architecture is improved by embedding three architectures ResNet 50, ResNet 101, and ResNext 50. To the best of our knowledge, such a combination of architecture has never been used before for brain tumor segmentation which inherently has the advantage of UNet and ResNet architecture.

Exhaustive experimentation on different hyperparameters like gamma, learning rate, type of optimizer, batch size, and step size is done to tune them to the best value which ultimately results in enhancing the performance of the proposed architecture. Also, comparative analysis between three models is done for several epoch values.

The given model is also tested in real-time for segmenting brain tumor MRI images obtained especially from renowned Nanavati Max Super Speciality Hospital, located in Mumbai, India, which is best known for providing medical service for 70 years to people across India. The results obtained are also verified by the radiological experts of the hospital.

2. RELATED WORKS

Various authors proposed several architectures for the segmentation and classification of brain tumors listed and compared their performance on the Dice Similarity Coefficient (DSC) or Accuracy measure in Table 1. Since we require a labeled dataset, supervised techniques are used.

Sérgio Pereira et al. [7] implemented the hierarchical system for whole tumor segmentation and intratumoral tissue segmentation. Histogram standardization is used as preprocessing method and implemented fully CNN-based UNet. Leaky Rectifier Linear Unit is used as nonlinear activation.

Saddam Hussain et al. [8] proposed an input concatenated CNN architecture using two types of patch-based training. To avoid overfitting max-out and dropout layers are used. Image normalization and bias field correction is used for preprocessing and morphological operators are used for post-processing to remove small false positives.

Mohammad Havaei et al. [9] implemented various two-path cascaded architectures with concatenations at different stages by exploiting simultaneous extraction of local as well as global features. To tackle tumor label imbalance two-phase training process is used. The final fully connected layer is replaced by a convolutional layer that speeds up the segmentation procedure. The segmentation time of the brain varies between 25 seconds to 3 minutes.

Francisco Javier et al. [10] Proposed pixel-based classification with three different paths which are concatenated to give output out of four different classes through the fully connected layer. Overfitting is avoided by using elastic transformation as a data augmentation procedure.

Benjamin Maas et al. [11] proposed Two dimensional fully convolutional neural networks consisting of four encoders and decoders each. Skip connections like UNet architecture are employed at the encoder and decoder having similar spatial resolution. In the decoding stages, unpooling layers are used. To create a precise, consistent, and quicker network architecture for brain tumor segmentation it uses a modified cross-entropy loss function with an ADAM optimizer.

Mohamed Naser et al. [12] implemented a combined model for tumor segmentation, detection, and grading simultaneously of low-grade gliomas with Deep CNN using UNet with transfer learning from VGG-16. Rotation, zoom, shift, and horizontal flip are used as data augmentation techniques.

Mostefa et al. [13] Ensemble learning is used to develop a fully automatic deep learning model using incremental deep CNN with the advantage of GPU implementation. An efficient training method is implemented by considering the most important hyperparameters for best results.

Yongchao Jiang et al. [14] proposed an AIU-Net model. To improve network performance without adding extra parameters, receptive field expansion is done by adding Atrous convolution in the Inception module. It increases the depth and width of the architecture but has longer training and testing time. Residual connection is added for faster convergence between input and output.

Muhammad Sajjad et al. [15] implemented a computer-aided diagnosis system for tumor segmentation and classification using Deep CNN with extensive data augmentation techniques. Using a transfer learning approach pre-trained VGG-19 network is fine-tuned for

tumor classification. Two different datasets are used, and the accuracy achieved is compared which proves that the performance of the system is improved using data augmentation.

Amjad Rehman Khan et al. [16] used K means clustering to segment the region of interest and classification into benign or malignant by fine-tuning fully connected weights of VGG-19 with synthetic data augmentation.

Kang, J et. al [17] proposed a hybrid model for classification using pre-trained CNN and ML classifiers for deep feature extraction and tumor classification respectively. From exhaustive experimentation on several pre-trained CNN models, and ML classifiers on three datasets concluded with different combinations of these are better in the case of a smaller dataset with two classes, a large dataset with two classes, and a large dataset with four classes.

Zahid Ullah et al. [2] used a median filter, histogram equalization, and image conversion as preprocessing techniques for image enhancement. Discrete wavelet transform is used to extract features from enhanced images. From the proposed advanced deep neural network, human brain MRI images are classified as normal or pathological.

Table 1. Summarizes related work to brain tumor segmentation and classification

Author	CNN Architecture	Dataset	Performance Metric
S´ergio Pereira et al. 2016	Fully CNN-based UNet	BraTS 2013	DSC: 85%
Saddam Hussain et.al 2017	Input Concatenated CNN	BraTS 2013	DSC: 80%
Mohammad Havaei et.al 2017	two-path cascaded CNN	BraTS 2013	DSC: 88%
Francisco Javieret al. 2021	Three path output concatenation CNN	Nanfang Hospital	DSC: 82.8%
Benjamin Maas et al. 2021	Two dimensional CNN	Nanfang Hospital	DSC: 74.4%
Mohamed Naser et al. 2020	UNet	Private Data	DSC: 84%
Mostefa et al. 2018	Deep CNN	BraTS 2017	DSC: 88%
Yongchao Jiang et al. 2021	A-Inception based UNet	BraTS 2019	(Whole Tumor) DSC: 86.96% MIoU: 84.25%
Muhammad Sajjad et al. 2019	Deep CNN using extensive data augmentation	Radiopaedia Nanfang Hospital	Accuracy: 90.67% Accuracy: 94.58%
Amjad Khan et al. 2021	VGG-19	BraTS 2015	Accuracy: 94.06%

3. METHODOLOGY

3.1 DATASET

The dataset used is publicly available at figshare.com and Kaggle.com, which was presented by Cheng et al. [18]. The dataset is of 233 patients fetched from Nanfang Hospital, Guangzhou, and General Hospital, the Tianjing Medical University of China during the year 2005-2010. Dataset consists of 3064 T1 weighted improved contrast slices of three common types of tumors, Meningioma, Glioma, and Pituitary Tumor in sagittal, coronal, and axial views. Table 2 represents the number of slices with respect to the number of patients corresponding to each tumor type.

Table 2. Details of the Dataset

Dataset includes	Type of Tumors			Total
	Meningioma	Glioma	Pituitary	
Number of patients	82 patients	89 patients	62 patients	233 patients
Number of slices	708 slices	1426 slices	930 slices	3064 slices

3.2 PRE-PROCESSING

As CNN uses fewer pre-processing techniques as compared to other algorithms, data augmentation techniques are considered in pre-processing to improve the dataset and to avoid overfitting of the model and better generalization. Various data augmentation techniques like flipping, shifting, scaling, rotating, Grid and optical distortion, resizing, and random cropping on images are performed to increase data variability and flexibility. The dataset is randomly split into a training set, testing set, and validation set with the proportion of 0.80: 0.12: 0.08 respectively. With this proportion, the complete dataset is divided into a training set consisting of 2479 slices, a validation set consisting of 246 slices, and a test set consisting of 339 slices. During the training process, after every epoch, testing on the validation set is done to observe the model performance, by comparing the DSC score of the train and validation set. Here if they seem to divert from each other which eventually causes overfitting can be prevented by changing the model hyperparameters. The dataset images are in the size of 512×512. This size of the image is reduced to 128×128 before giving it as input to the architecture. The images are color normalized to have the intensities lying between 0 to1 using batch normalization which ultimately causes a reduction in the bit depth hence reducing the processing time and cost.

3.3 NETWORK STRUCTURE

In the proposed system of tumor segmentation and classification, the type of tumor is identified, and also finds the exact location of the tumor in the given MRI images. To achieve this objective, improvised UNet architecture with embedded ResNet 50, ResNet 101, and

ResNext 50 is designed. UNet architecture is specifically designed for the segmentation of medical images with a small dataset and typically consists of encoding and decoding layers [19]. Instead of using traditional UNet encoding layers three variants of ResNet like ResNet 50, ResNet 101, and ResNext 50 are used. As shown in Fig. 1., the decoding layers are designed in such a way that they complement the encoding layers.

In the decoding layer, the upsampling is done through transpose convolution. Optimization is done using an ADAM optimizer with a learning rate of 1e-4 for training. Model is built on Kaggle using Python Programming Language. As a free resource, Kaggle is having execution time limitations and even cannot be run for larger epochs for experiments.

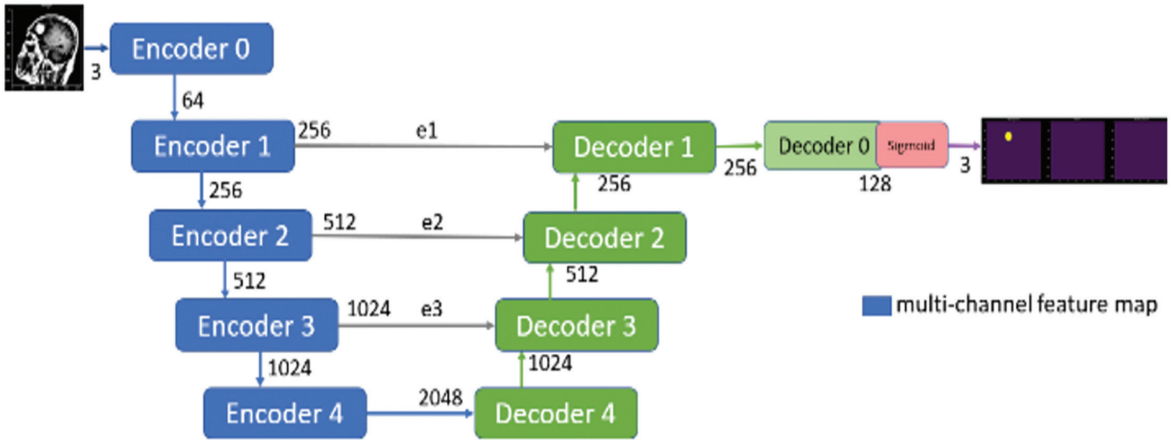


Fig. 1. Proposed modified UNet Architecture with ResNet/ResNext as a backbone architecture

4. EXPERIMENTS AND RESULT ANALYSIS

4.1 PERFORMANCE EVALUATION METRICS

For semantic segmentation to find the performance of the model the most popular metric is the Dice Similarity Coefficient (DSC). DSC is represented in Eq. (1) and computes spatial overlap between predicted segmentation and available ground truth to quantify the performance of image segmentation methods.

$$DSC=(2|A\cap B|)/(|A|+|B|) \quad (1)$$

Where A represents the ground truth and B represents the predicted segmentation. Metric values range between 0 and 1. 0 means no overlapping between predicted segmentation and available ground truth, while 1 means perfectly overlapping between predicted segmentation and available ground truth.

$$IoU=J(A, B)=(|A\cap B|)/(|A\cup B|) \quad (2)$$

Another most commonly used metric for the evaluation of a model is Jaccard Index or Intersection over Union (IoU) represented in Eq. (2). IoU is calculated as the area of overlap to the area of union between the predicted segmentation and available ground truth. The Mean IoU (MIoU) is calculated by taking an average of IoU of each class which is used in performance measurement in segmentation algorithms [20].

4.2 EXPERIMENT 1 (FOR HYPERPARAMETER TUNING)

The Deep Learning model has a set of parameters and hyperparameters. Parameters are updated at every backpropagation step using an optimization algorithm. Hyperparameters need to be set for deciding model structure and training strategy. For manual finding evaluation of the best hyperparameters for the model is a difficult task. The first experiment is carried out by considering ResNet 101 as the backbone architecture for transfer learning with 10 epochs to decide on the proper tuning of hyperparameters like gamma, learning rate, optimizer, step size, and batch size to achieve the best performance. An epoch consists of a cycle to train complete data. The learning algorithm will work a number of times through the entire training dataset equal to a number of epochs.

4.2.1. Gamma

With 1e-4 learning rate, Adam Optimizer, 64 Batch Size, 80 Step Size training time required for various values of gamma are almost the same, and mean loss on the train (MLT) is minimum at gamma=0.1 is shown in Table 3. So, Gamma 0.1 is considered for further experiment as it also gives better metric values for individual tumor types as illustrated in Fig. 2(a).

Table 3. Comparison of training time and MLT for different values of Gamma

Gamma	Training Time	MLT
0.05	00:33:04	0.384912
0.075	00:32:56	0.371084
0.1	00:32:59	0.343684
0.15	00:32:43	0.344272
0.2	00:32:43	0.349402
0.75	00:33:16	0.47495

4.2.2. Learning rate

The most important hyperparameter to tune for best results is the learning rate. With gamma 0.1, Adam Optimizer, 64 Batch Size, and 80 Step Size extremely poor performance for very lower and higher values of learning rate is observed. Table 4 compares different metrics like MIoU, DSC and individual class dice score for Meningioma, Glioma, and Pituitary type of tumor (PT). It is observed that the learning rate 1e-4 gives better results with less training time. Very poor performance is observed for learning rates 1e-2 and 1e-5 are not considered for comparison as shown in Fig. 2 (b).

Table 4. Comparison of metrics for various learning rates

Learning Rate	MIoU	DSC	Meningioma	Glioma	Pituitary Tumor
1e-2	Very Poor Performance all readings zero				
1e-3	60%	59.88%	71.15%	57.38%	64.08%
1e-4	74%	73.69%	79.32%	66.85%	67.55%
1e-5	Very Poor Performance all readings zero				

4.2.3. Optimizer

For loss reduction, different optimizers of adaptive learning rate like Adam, Adagrad, RMSprop, and Adamax are tried for the selection of the best optimizer as shown in Table5. Adam optimizer gives the best results as illustrated in Fig. 2(c) with a similar mean loss in train and training time as compared to other optimizers.

Table 5. Comparison of metrics for various optimizers

Optimizer	MIoU	DSC	Meningioma	Glioma	Pituitary Tumor
Adam	74%	73.69%	79.32%	66.85%	67.55%
Adagrad	15%	15.14%	33.04%	26.87%	17.43%
RMS Prop	72%	71.59%	77.27%	64.74%	80.29%
Adamax	55%	54.81%	55.79%	49.67%	37.08%

4.2.4. Batch size

A number of samples used to make predictions that are compared with expected output variables to calculate error is known as Batch size.

Table 6. Comparison of metrics for different batch size

Batch Size	MIoU	DSC	Meningioma	Glioma	Pituitary Tumor
8	71%	70.83%	86.30%	60.70%	76.34%
16	71%	70.68%	83.26%	61.43%	66.47%
32	76%	75.79%	82.01%	68.30%	76.74%
64	74%	73.69%	79.32%	66.85%	67.55%

A large batch size decreases the quality of the model to generalize while requiring more memory space and too small batch size makes learning too stochastic. In this experiment batch sizes, 32 and 64 give better metric values on the test dataset as shown in Table 6 and graphically illustrated in Fig. 2 (d). A batch size greater than 64 is not supported by available resources.

4.2.5. Step size

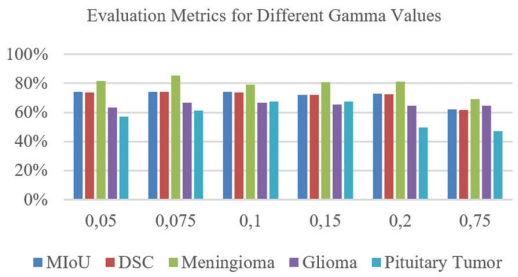
Step size consists of several iterations required to train the complete available dataset. Step size varies concerning batch size for the training process. For batch size 64, step size 80 gives a maximum MIoU of 74% shown in Fig. 2(e) and for batch size 32, step size 240 gives a maximum MIoU of 77% shown in Fig. 2(f) as listed in Table 7 and Table 8 respectively.

Table 7. Comparison of metrics for different step sizes with batch size 64

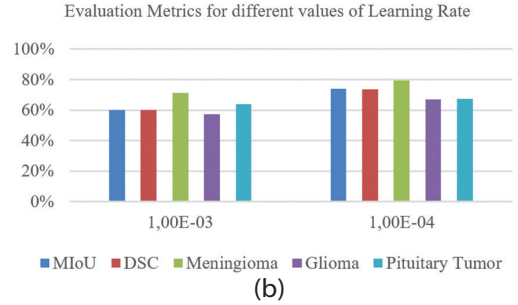
Step Size	MIoU	DSC	Meningioma	Glioma	Pituitary Tumor
20	67%	67.07%	76.97%	63.31%	60.50%
40	70%	70.02%	81.59%	65.79%	56.61%
60	62%	61.55%	72.91%	65.86%	39.81%
80	74%	73.69%	79.32%	66.85%	67.55%
120	73%	73.04%	77.91%	68.68%	70.34%
150	71%	71.00%	83.69%	64.47%	61.11%

Table 8. Comparison of metrics for different step sizes with batch size 32

Step Size	MIoU	DSC	Meningioma	Glioma	Pituitary Tumor
120	73%	72.76%	83.15%	64.76%	68.13%
180	73%	73.32%	82.08%	66.44%	77.49%
240	77%	76.70%	86.48%	69.01%	79.91%
280	72%	71.70%	83.13%	67.88%	70.52%
320	73%	73.14%	83.51%	64.52%	77.04%
360	72%	72.02%	84.54%	65.29%	79.02%



(a)



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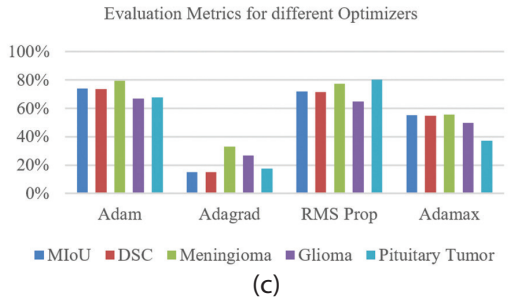

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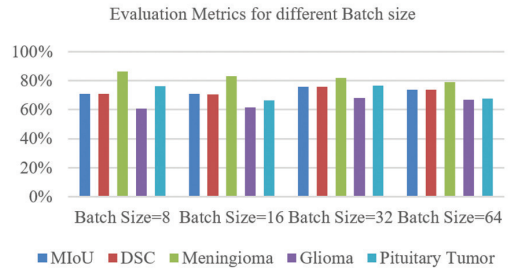

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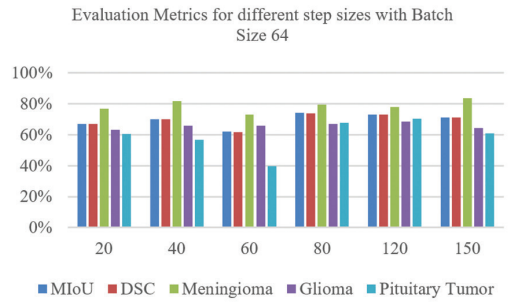
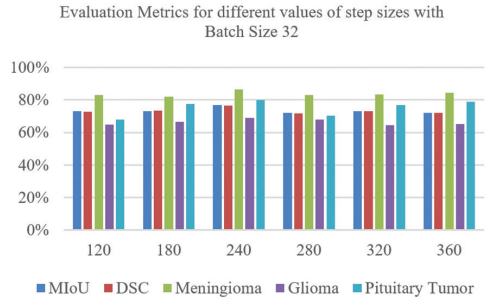


(e)



(f)

Fig. 2. Comparison of Evaluation Metrics for Hyperparameter Tuning using ResNet 101 as the backbone for UNet with 10 Epochs, for different: (a) Gamma (b) Learning Rate (c) Optimizer (d) Batch Size (e) Step Size with Batch Size 64 (f) Step Size with Batch Size 32

4.3 EXPERIMENT 2 (FOR LARGER STEP SIZE)

From the results of the first experiment, the second experiment is designed for ResNet 101 with batch size 32 and step size 240 considering gamma 0.1, learning rate as 1e-4 using ADAM optimizer for 10, 20, 30, 50, and 100 epochs as shown in Table 9. With different values of epochs, metric performance is not improved as expected as illustrated in Fig. 3

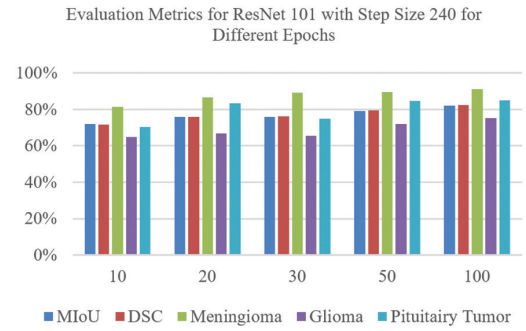


Fig. 3. Comparison of Evaluation Metrics for ResNet 101 with step size 240 for a different number of epochs

Table 9. Comparison of metric values for ResNet101 with step size 240 for a different number of epochs.

Epochs	MIoU	DSC	Meningioma	Glioma	Pituitary Tumor
10	72%	71.64%	81.37%	64.80%	70.25%
20	76%	75.94%	86.59%	66.86%	83.44%
30	76%	76.04%	89.29%	65.44%	75.04%
50	79%	79.33%	89.53%	71.99%	84.75%
100	82%	82.32%	91.23%	75.24%	85.10%

Table 10. Comparison of proposed architectures

Network	Backbone architecture	Number of Convolutional layers	Training Time in hours (for 100 epochs)
ResUNet1	ResNet50	53	03:59:49
ResUNet2	ResNet101	104	05:27:13
ResUNet3	ResNext50	53	07:35:30

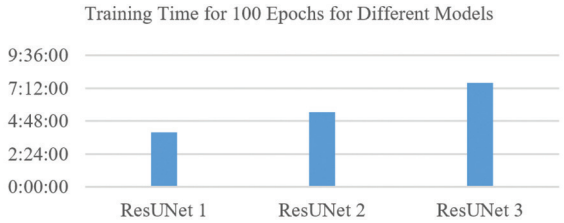


Fig. 4. Comparison of Training Time for different models evaluated at 100 epochs

4.4 EXPERIMENT 3 (COMPARISON OF BRAIN TUMOR SEGMENTATION AND CLASSIFICATION USING DIFFERENT MODELS)

These architectures as listed in Table 10, experimented with 10, 15, 20, 30, 50, and 100 epochs. It is observed that we must increase the number of epochs to reduce the mean loss on training to improve on metrics like DSC and MIoU, while training time goes on increasing. ResUNet2 and ResUNet3 for 100 epochs give maximum MIoU of 85% and 84% respectively as listed in Table 11. While training time required for ResUNet3 is very huge as compared to ResUNet2 as illustrated in Fig. 4. From

Fig. 5, ResUNet2 for 100 epochs should be preferred with a DSC of 83.69% and Mean IoU of 85%. Fig. 6. Illustrates how the proposed architecture reached very fast to its maximum performance and demonstrates consistency between training DSC score, validation DSC score, and loss. Due to hardware and time limitations on the Kaggle model with ResNext 101 using batch size 64 is not able to execute even for 10 or lesser epochs. A model with ResNext 101 executed with batch size 32 is not further evaluated due to the very large training time as compared with other models for 10 epochs.

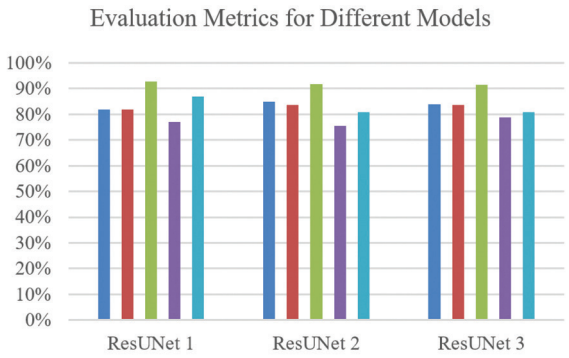


Fig. 5. Comparison of Evaluation Metrics for different models

Evaluation metrics are determined for three types of tumors namely Meningioma, Glioma, and Pituitary Tumor. Comparative analysis is presented in Table 12 for evaluating the effectiveness of the proposed model. It is evident from Table 12 that the proposed ResUnet 2 architecture outperforms other existing models on the same dataset in terms of DSC and Mean IoU.

Table 11. Comparison of metric values for different models

Different Models	MIoU	DSC	Meningioma	Glioma	Pituitary Tumor
ResUNet1	82%	81.84%	92.81%	77.18%	87.02%
ResUNet2	85%	83.69%	91.67%	75.45%	80.91%
ResUNet3	84%	83.68%	91.42%	78.87%	80.81%

Visual results of our model performance for three types of tumors are shown in Fig. 7. Tumor is segmented and classified for random test samples for Meningioma, Glioma, and Pituitary Tumor. The region detected is shown in yellow and it is compared with the ground truth available. The images of brain tumors acquired from Nanavati Super Speciality are applied to the proposed Model ResUNet2 trained on the online available dataset using Command Line Interface (CLI). Segmentation results and performance obtained are verified and demonstrated in Fig. 8. Execution time at different instances varies between 14 to 20 seconds.

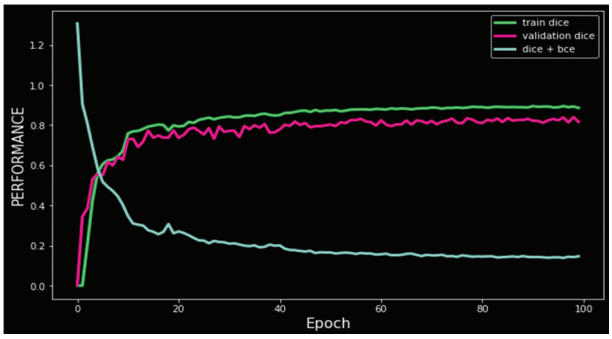


Fig. 6. Proposed architecture performance

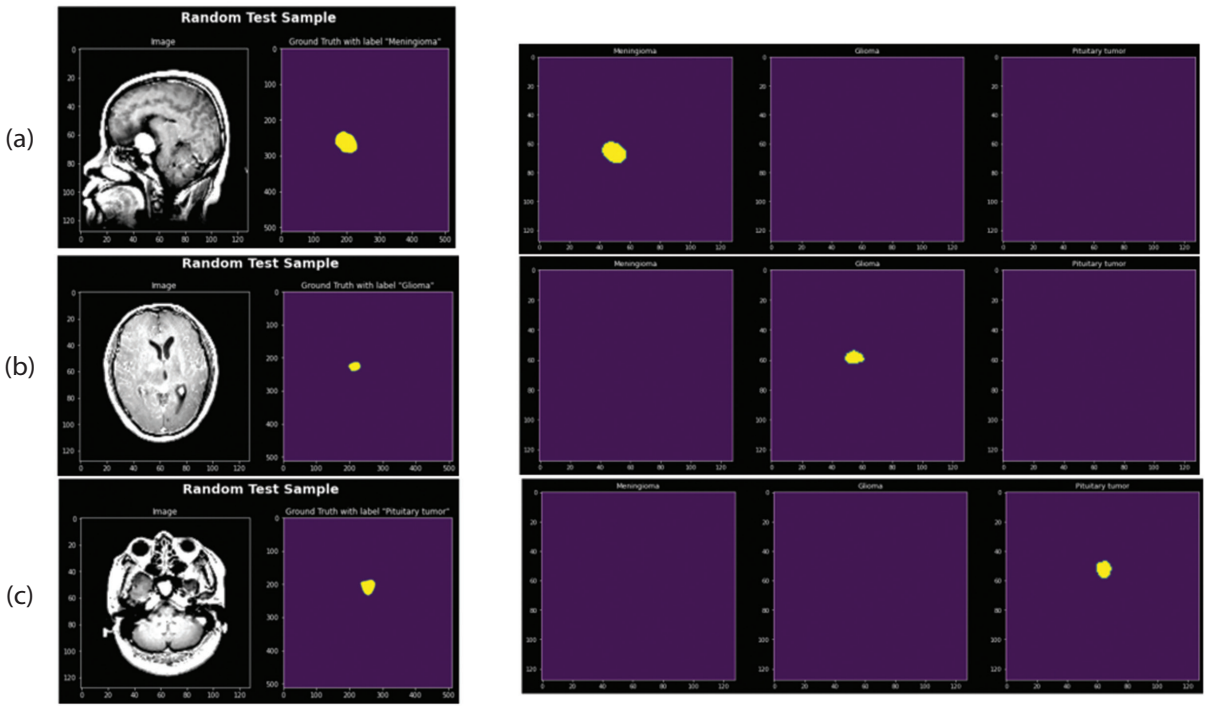


Fig.7. Ground truth versus Segmented and classified image for (a) Meningioma (b) Glioma and (c) Pituitary Tumor

Table 12. Comparison of proposed architecture with other architectures evaluated on same data

Author/ Architecture	DSC	Mean IoU
Francisco Javier et. al. [10] Multi-pathway CNN 2021	82.8%	-
Benjamin Maas et. al [11] Quick Tumor Net 2021	74.4%	-
Zahra Sobhaninia et. al [21] 2018 Single LinkNet for all directions	73%	-
Zahra Sobhaninia et. al [21] 2018 Separately trained Linknet networks for each direction	76%	-
Zahra Sobhaninia et. al. [22] 2020 Cascaded Dual-Scale LinkNet	80.03%	-
Ahmad Thias et.al. [23] 2019 morphological geodesic active contour (MGAC)	-	72.66%
Proposed Architecture **(ResUnet2)**	**83.69%**	**85%**

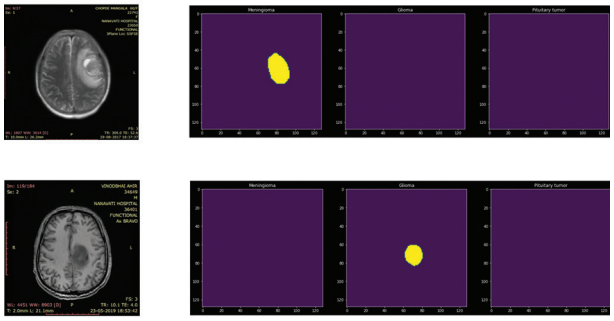


Fig. 8. Segmentation of Brain Tumor images obtained from Nanavati Super Speciality Hospital

5. RESULTS DISCUSSION

Proposed an improved UNet architecture by embedding three architectures ResNet 50, ResNet 101, and ResNext 50 which inherently has the advantage of UNet and ResNet architecture. Also, Various data augmentation techniques on images are performed to increase data variability and flexibility. A Pre-trained model helps in a significant reduction in training time because it just needs to fine-tune the weights of the model instead of learning them from scratch.

The experimental results were obtained for tumor segmentation and classification on the tumor dataset. The first experiment is designed for proper tuning of hyperparameters which helps in finding suitable hyperparameters like gamma, learning rate, type of optimizer, batch size, and step size. With extensive experimentation, we settle to gamma as 0.1, 1e-4 as learning rate, Adam optimizer for batch size 32 or 64 with a number of step sizes to train model through the available dataset. In the second experiment, performance is evaluated for backbone ResNet101 on batch sizes 32 and 64. Though batch size 32 with step size 240 gives the best MIoU 77% for 10 epochs, performance is not improved as we increase epochs towards 100. From the analysis of the first two experiments, we concluded that the best batch size is 64 with step size 80. The third experiment shows and compares the effectiveness of the use of transfer learning with ResNet 50, ResNet 101, and ResNext 50 in segmentation using deep learning. From the analysis of this experiment, ResUnet2 gives the best results in important performance evaluation metrics with average training time. ResUnet2 gives a Mean Test DSC Score of 83.69% and a Mean IoU Test of 85% which is significantly better than existing methods. A maximum number of slices present in glioma type of tumor, but MRI images obtained from these scans are having variation in intensities throughout the dataset, because of this, the DSC score obtained for meningioma and pituitary type of tumor is better as compared to glioma type of tumor. The best-pretrained model is used for the segmentation of tumor images obtained from Nanavati Super Speciality Hospital, the same validated by expert radiologists. The average execution time is 17 seconds.

6. CONCLUSION

In this paper, we proposed a unique fully automatic encoder-decoder architecture for brain tumor segmentation and classification which lead to better results and is a step ahead of improvisation over basic UNet architecture. The three extensive experiments with three proposed architectures on a publicly available MRI dataset were executed and tested through standard performance metrics and compared with previously published results on the same dataset, the best performance was achieved using ResNet2 architecture for 100 epochs with freely available resources with Dice Similarity Coefficient of 83.69% and Mean Intersection over Union of 85% and thereby assisting in better tumor analysis.

7. REFERENCES:

[1] "Types of Cancer, Brain tumor", Brain Tumor: Statistics, https://www.cancer.net/cancer-types/brain-tumor/statistics (accessed: 2022)

[2] Z. Ullah, M. Farooq, S. Lee, D. An, "A hybrid image enhancement based brain MRI images classification technique", Medical Hypotheses, Vol. 143, 2020.

[3] M. Razzak, S. Naz, A. Zaib, "Deep Learning for Medical Image Processing: Overview, Challenges and Future", Book on Classification in BioApps, SpringerLink, 2017, pp 323-350.

[4] A. Buslaev, V. Iglovikov, E. Khvedchenya, A. Parinov, M. Druzhinin, A. Kalinin, "Albumentations: Fast and Flexible Image Augmentations", Information, Vol. 11, No. 2, 2020.

[5] A. Krizhevsky, I. Sutskever, G. Hinton, "ImageNet Classification with Deep Convolutional Neural

Networks", Communications of the ACM, Vol. 60, No. 6, 2017, pp. 84-90.

[6] J. Wacker, M. Ladeira, J. Nascimento, "Transfer Learning for Brain Tumor Segmentation", arXiv:1912.12452v2, 2019.

[7] S. Pereira, A. Pinto, V. Alves, and C. Silva, "Brain Tumor Segmentation Using Convolutional Neural Networks in MRI Images", IEEE Transactions on Medical Imaging, Vol. 35, No. 5, 2016, pp. 1240-1251,

[8] S. Hussain, S. Anwar, M. Majid, "Brain Tumor Segmentation using Cascaded Deep Convolutional Neural Network", Proceedings of the Annual International Conference of the IEEE Engineering in Medicine and Biology Society, Jeju, Korea, 11-15 July 2017, pp. 1198-2001.

[9] M. Havaei, A. Davy, D. Warde-Farley, A. Biard, A. Courville, Y. Bengio, C. Pal, P. Jodoin, H. Larochelle, "Brain tumor segmentation with Deep Neural Networks", Medical Image Analysis, Vol. 35, 2017, pp.18–31

[10] F. Pernas, M. Martínez-Zarzuela, M. Antón-Rodríguez, D. González-Ortega, "A Deep Learning Approach for Brain Tumor Classification and Segmentation Using a Multiscale Convolutional Neural Network", Healthcare, Vol. 9, 2021, pp. 1-14.

[11] B. Maas, E. Zabeh, S. Arabshahi, "QuickTumorNet: Fast Automatic Multi-Class Segmentation of Brain Tumors", Proceedings of the International IEEE/EMBS Conference on Neural Engineering, Italy, 4-6 May 2021, pp.81-85.

[12] M. Naser, M. Deen, "Brain tumor segmentation and grading of lower-grade glioma using deep learning in MRI images", Computers in Biology and Medicine, Vol. 121, 2020.

[13] M. Naceur, R. Saouli, M. Akil, R. Kachouri, "Fully Automatic Brain Tumor Segmentation using End-to-End Incremental Deep Neural Networks in MRI images", Computer Methods and Programs in Biomedicine, Vol. 166, 2018, pp. 39-49.

[14] Y. Guan, M. Aamir, Z. Rahman, A. Ali, W. Abro, Z. Dayo, M. Bhutta, Z. Hu, "A framework for efficient brain tumor classification using MRI images", Mathematical Biosciences and Engineering, Vol. 18, No. 5, 2021, pp. 5790-5815.

[15] A. Sajjad, S. Khan, M. Khan, W. Wu, A. Ullah, S. Baik, "Multi-Grade Brain Tumor Classification using Deep CNN with Extensive Data Augmentation", Journal of Computational Science, Vol. 30, 2019, pp. 1-13.

[16] A. Khan, S. Khan, M. Harouni, R. Abbasi, S. Iqbal, Z. Mehmood, "Brain tumor segmentation using K-means clustering and deep learning with synthetic data augmentation for classification", Wiley Periodicals LLC, 2021, pp. 1-11.

[17] J. Kang, Z. Ullah, J. Gwak, "MRI-Based Brain Tumor Classification Using Ensemble of Deep Features and Machine Learning Classifiers", Sensors, Vol. 21, 2022.

[18] J. Huang, S. Cao, R. Yang, W. Yang, Z. Yun, Z. Wang, Q. Feng, "Enhanced Performance of Brain Tumor Classification via Tumor Region Augmentation and Partition", PLOS ONE, 2015.

[19] O. Ronneberger, P. Fischer, T. Bro, "U-net: Convolutional networks for biomedical image segmentation", Proceedings of the International Conference on Medical image computing and computer-assisted intervention, 2015, pp. 234-241.

[20] S. Minaee, Y. Boykov, F. Porikli, A. Plaza, N. Kehtarnavaz, D. Terzopoulos, "Image Segmentation Using Deep Learning: A Survey", IEEE Transactions Pattern Analysis and Machine Intelligence, Vol. 44, No. 7, 2021, pp. 3523-3542.

[21] Z. Sobhaninia, S. Rezaei, A. Noroozi, M. Ahmadi, H. Zarrabi, N. Karimi, A. Emami, S. Samavi, "Brain Tumor Segmentation Using Deep Learning by Type Specific Sorting of Images", arXiv:1809.07786v1, 2018.

[22] Z. Sobhaninia, S. Rezaei, N. Karimi, A. Emami, S. Samavi, "Brain Tumor Segmentation by Cascaded Deep Neural Networks Using Multiple Image Scales", Proceedings of the 28th Iranian Conference on Electrical Engineering, 2020.

[23] A. Thias, A. Mubarok, A. Handayani, D. Danudirdjo, T. Rajab, "Brain Tumor Semi-automatic Segmentation on MRI T1-weighted Images using Active Contour Models", Proceedings of the International Conference on Mechatronics, Robotics and Systems Engineering, Bali, Indonesia, 4-6 December 2019, pp. 217-221.