

BRAIN TUMOR DETECTION USING DEEP LEARNING ALGORITHMS

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ABSTRACTS

Numerous studies utilizing machine learning techniques have been documented in the literature, focusing on the detection of brain tumors through the analysis of MRI data, with deep learning accounting for the majority of what has been done in the previous six years. The majority of them are intended to deal with 2D data. Because 3D models contain numerous tumor-free slice pictures, The performance of classification is comparatively inferior to that of 2D models. However, Glioma, a rapidly proliferating brain tumor, exhibits considerable heterogeneity in terms of its morphology, dimensions, and spatial distribution across different individuals. The manual delineation of a specific region of interest, namely the tumor, necessitates the involvement of a radiologist and is known to be an arduous and time-intensive process. In order to address this challenge, a novel approach known as SegNet(3Dunit modified) has been proposed. This method leverages the power of deep learning and employs an ensemble technique to achieve fully automated segmentation of brain tumors. Notably, the SegNet operates on four distinct 3D multimodal magnetic resonance imaging (MRI) scans, thereby enhancing its accuracy and reliability. The segmentation process is executed utilizing three encoder-decoder deep models renowned for their efficiency in segmentation. The outcomes of these models are evaluated using established segmentation metrics. Subsequently, a comprehensive statistical analysis of the models is conducted, leading to the development of an ensemble model. This ensemble model is designed by prioritizing the highest coefficients of Dice, Sensitivity, and specificity, employing a specific MRI modality. The proposed technique yields a satisfactory performance of the model, as evidenced by its sensitivity, specificity, and Dice scores, particularly for the BRATS 2020 dataset.

KEYWORDS: MRI, SEGNET, 3DUNIT, 3D models, 2D models, Deep learning, Segmentation, Brain Tumor.

1. INTRODUCTION

The World Health Organization (WHO) defines brain tumors as abnormalities that affect the central nervous system [1]. These tumors involve the uncontrolled growth of cells within the central nervous system and can also harm other brain areas, disrupting normal brain function. Medical professionals, particularly specialists and radiologists, rely heavily on medical imaging techniques to detect potential diseases in various clinical fields [2]. When it comes to in-depth examination of brain abnormalities, Magnetic Resonance Imaging (MRI) stands as the primary imaging technique [3]. MRI, an abbreviation for Magnetic Resonance Imaging, employs a magnetic field in conjunction with computer-generated radio waves to produce intricate and comprehensive visual representations of various organs and soft tissues residing within the human body [4]. By stimulating hydrogen atom protons with radio waves, the body's signals from these excited protons are processed by powerful computers to create cross-sectional images of the body in different orientations. The evaluation of brain MRIs by radiologists is conducted with the intention of diagnosing brain tumors. The education and training required for radiologists is a laborious and costly process [5]. Challenges in this field are further compounded by various factors,

including but not limited to, a scarcity of radiologists, inadequate expertise, time limitations, and exhaustion [6]. Furthermore, there has been a notable increase in the demand for radiological examinations in recent years, resulting in a large volume of images that radiologists must review. Given the diverse nature of brain tumors, the human evaluation process by radiologists is prone to errors [7]. Automated machine learning algorithms have emerged as a valuable tool in addressing the aforementioned challenges, as they can effectively aid clinicians and alleviate their burden. Notably, deep learning techniques have demonstrated exceptional efficacy and dependability in the detection of brain tumors, capitalizing on their achievements in diverse image-based classification assignments [8-11]. The conventional approach for detecting brain tumors through automation has relied on the utilization of Convolutional Neural Network (CNN) models that operate in two dimensions (2D). These models process individual MRI slices separately, which can be seen as a limitation due to the lack of contextual information between adjacent slices [12]. In contrast, models known as three-dimensional (3D) convolutional neural networks (CNNs) have been specifically developed to effectively analyze volumetric data. They excel in establishing connections between slices, leading to

enhanced performance, albeit at the cost of increased computational complexity due to the greater number of hyperparameters involved [13-15].

The utilization of deep learning techniques in the detection of brain tumors has emerged as a revolutionary approach in contemporary medical imaging. This paradigm shift addresses the challenges associated with human-based evaluation, particularly the potential for error and the increasing workload on medical professionals. Notably, the utilization of the Segnet model has yielded highly promising results, with scores such as 89.7% for the dice loss, 92.5 for specificity, and 88.7 for sensitivity in the Weight tumor dice slice, signifying its efficacy in precise tumor delineation.

2. RELATED WORKS.

The field of Tumor segmentation is an area of ongoing investigation, with recent advancements in deep learning techniques proving to be effective in healthcare image segmentation and information extraction. Pixel-based classification has emerged as the latest phenomenon in deep learning, with various researchers proposing different methods for brain Tumor segmentation. This section provides an analysis of a few critical research studies in this field.

One such study, referenced as [9], focuses on brain Tumor segmentation using a Deep Convolutional encoder model. The researchers utilize magnetic resonance visuals of the brain to segment Brain Tumors. By extracting attributes from complete images and improving calculations at adjacent intersections, this approach enhances the learning process and eliminates the need for patchwork selections.

Another study, referenced as [10], presents a technique for the early detection of brain cancers. The researchers examine magnetic resonance images to identify Tumor-bearing areas and classify them into different categories. Deep learning techniques, particularly in image classification, demonstrate efficient performance in this context.

In research [11], a model is developed that utilizes Brain imaging to recognize the nature of brain Tumors. A two-dimensional CNN is employed to accurately identify malignant Tumors with a 93 percent accuracy rate. The analysis includes data on the four most frequently detected brain Tumors.

Research [12] proposes a responsive and efficient Tumor segmentation framework. This strategy, implemented through a Cascades Classification Model, addresses

the problem of overfitting and reduces computation time. By utilizing two separate forms, this CNN architecture extracts both global and regional characteristics, resulting in significantly enhanced Tumor detection precision compared to existing algorithms. The proposed approach achieves average WT, increasing Tumor, and Tumor center dice scores of 92.3%, 94.5%, and 93.2%, respectively.

A method for integrating 2D and 3D MRI images was documented by the researchers in [13]. They recommended the application of DenseNet for classification and distinct 3D CNN architectures for segmenting multi-modal images. The proposed approach exhibited commendable performance on the test dataset, achieving an accuracy of 92% with the utilization of DenseNet and 85% with the individualized 3D CNN models. Kang et al. introduced the concept of brain tumor categorization.

3. DATASET

The datasets consist of two distinct classes, namely HGG and LGG, each containing four 3D MRI sequences and a corresponding ROI for a single patient or subject in NIfTI files. Furthermore, each 3D volume comprises 150 2D slices/images of MRIs from different sections of the brain, with each slice having a dimension of 240 x 240 and being in single channel grayscale format. During the collection of the BraTS 2020 dataset, it was

initially divided into training and validation sets. The validation set comprises 120 cases of both HGG and LGG classes, but the grade is not disclosed in the provided CSV file. Therefore, only the training dataset, which includes a total of 365 usable cases, is utilized in this research. Out of these cases, 291 belong to the HGG class, while 74 belong to the LGG class. It is worth noting that all three datasets exhibit a significant imbalance between the HGG and LGG classes, with a scarcity of LGG class being evident.

Structural MRI is commonly employed in brain tumor research due to its non-invasiveness and ability to provide high-resolution images of soft tissues. However, relying solely on a single structural MRI scan is insufficient for accurately distinguishing all tumor sub-regions, primarily due to the presence of imaging artifacts and the complexities associated with diverse tumor sub-regions. To overcome these limitations, multimodal MRI techniques are utilized to obtain additional information about various sub-regions of gliomas. These techniques include T1-weighted MRI (T1), T2-weighted MRI (T2), T1-weighted MRI with contrast enhancement (T1ce), and T2-weighted MRI with fluid-attenuated inversion recovery (T2 FLAIR). Each of these MRI scans serves a specific purpose in tumor characterization.

The T1-weighted MRI scan defines the majority of the tumor, which is typically the region targeted for surgical removal. The areas of T1ce hyperintensity, in comparison to T1 and healthy White Matter (WM) areas in T1ce, delineate the enhancing tumor (ET). The appearance of the non-enhancing core (NCR) and the necrotic and enhancing tumor (NET) in T1ce is generally less intense than in T1, as it encompasses both the enhancing tumor core (ET) and the edema (ED). Lastly, the whole tumor (WT) is visualized through the hyper-intense FLAIR signal, providing a comprehensive

representation of the cancerous brain region.

In summary, while structural MRI is valuable in brain tumor research, the integration of multimodal MRI techniques, such as T1, T2, T1ce, and T2 FLAIR, allows for a more comprehensive understanding of the various sub-regions within gliomas. These techniques aid in the accurate identification and characterization of different tumor components, facilitating improved diagnosis and treatment planning.

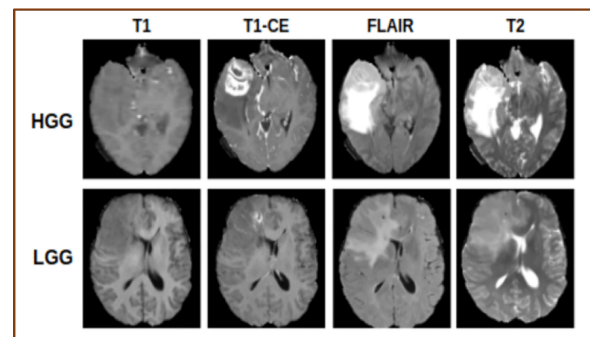


Figure 1 : an example of brain tumor from Brats2020 with all the modalities (T1, T1-CE, T2, and FLAIR)

4. PROPOSED METHODOLOGY

4.1 Data Preprocessing

The 'BratsDataset' class presented in this research methodology serves as a crucial tool for the preprocessing and loading of medical image datasets, with a specific focus on Brain Tumor Segmentation (BraTS) datasets. Building upon the PyTorch 'Dataset' framework, which is a versatile

asset that accommodates various phases of data handling. In its initialization method, the class takes in a DataFrame containing essential dataset information and specifies the phase. Furthermore, it defines data types for different MRI image modalities. Under the hood, the '**len**' method provides the count of samples in the dataset, while the '**getitem**' method handles the intricate process of loading and preprocessing images and masks based on the provided index . This includes center cropping, normalization, and, when applicable, data augmentation. Notably, the class incorporates intelligent preprocessing for masks, mapping distinct tumor regions to specific labels—whole tumor (WT), tumor core (TC), and enhancing tumor core (ET).

data augmentation is applied to the input images during the training phase to make the model more robust and reduce overfitting. The function defines a set of transformations that are randomly applied to the images with a certain probability. These transformations include:

Rotation: Images can be rotated by a specified angle, which helps the model learn to recognize objects from different angles.

Flipping: Images can be horizontally and vertically flipped. This mirrors the image,

providing variations in the orientation of objects within the image.

Cropping: a center cropping strategy is employed to extract a consistent region from all images. The method '**get_center_crop_coords**' calculates the coordinates for cropping a 3D volume centered within the original image volume. The dimensions of the cropped region are specified as (128, 128, 128), which means it extracts a cubic region of 128x128x128 pixels from the center of each image. This cropping helps focus the model on the most relevant information within the image and can improve computational efficiency by reducing the input size.

4.2 Model Architecture

The proposed model it is based on a modified 3Dunit model base, The provided code outlines a customized 3D U-Net architecture, a prominent deep learning model extensively employed for intricate tasks like medical image segmentation. The components of this architecture can be dissected as follows:

Input Parameters: It encompasses crucial specifications such as '**n_channels**' signifying the number of input channels, which, in this instance, is set at 4, indicating the potential presence of four data channels like multi-modal MRI. '**n_classes**' denotes the number of classes or categories

for segmentation, such as distinguishing between background, tumor, and healthy tissue. '**base_n_filter**' sets the foundation for the number of filters, dictating the model's capacity and intricacy.

Activation Functions: The architecture employs '**LeakyReLU**' activation for introducing non-linearity after convolutional layers. Additionally, '**Softmax**' is utilized for probability normalization, typically in the output layer for multi-class segmentation tasks.

Context Pathway: This pathway comprises multiple convolutional and normalization layers, adept at capturing high-level context information from input data. Levels 1 to 4 progressively down sample the input data while amplifying the filter count. Level 5 extends this by further down sampling and then upscales the data.

Localization Pathway: The localization pathway is constituted of convolutional layers, normalization, and up sampling operations. It collaboratively integrates contextual information from the context pathway with up sampled features to generate the final segmentation map.

Output: The culmination of this architecture is a final output layer, capable of producing a segmentation map. This map may consist of multiple channels, each dedicated to a distinct class. Predictions are

consolidated from both the localization pathway and skip connections.

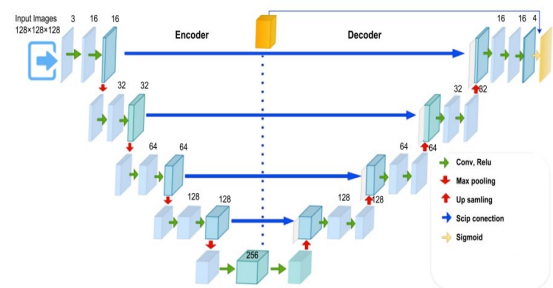


Figure 2 : Model's Architecture

This specialized architecture is meticulously crafted for the purpose of discerning and delineating structures within 3D medical images, exemplified by its proficiency in identifying brain tumors within MRI scans. During training, it harnesses ground truth labels to optimize its parameters, honing its ability to make precise segmentations. The incorporation of skip connections and multi-scale processing equips it to capture both local and global context information, elevating its effectiveness in addressing intricate tasks.

It's imperative to recognize that training such a model demands substantial labeled data and computational resources. Furthermore, precise configuration of model hyperparameters, choice of appropriate loss functions, and optimization techniques is indispensable to tailor the model to the specific task and dataset at hand.

Working with SegNet for brain tumor detection represents a significant leap forward in the field of medical imaging and diagnostic technology. SegNet, a deep learning architecture tailored for semantic image segmentation tasks, has shown great promise in accurately delineating and classifying complex structures within medical images. The intricacies of identifying and precisely delineating brain tumors present a critical challenge in the realm of healthcare, often necessitating rapid and accurate assessments for timely intervention. By leveraging the capabilities of SegNet, medical professionals can streamline the process of identifying tumor boundaries, distinguishing between healthy and affected tissues, and facilitating a more targeted and effective treatment approach. This collaborative effort embodies the convergence of advanced computational techniques with medical expertise, underscoring the potential for AI to revolutionize personalized patient care and significantly improve clinical outcomes in the challenging landscape of brain tumor diagnosis and treatment.

4.3 Loss functions

Dice loss function: The particle coefficient (Dice) is a commonly used metric in image segmentation to address the issue of imbalanced data. The calculation of this coefficient is based on the dice loss

function, which is expressed through a specific formula.

$$D = \frac{2 \sum_i^N p_i g_i}{\sum_i^N p_i^2 + \sum_i^N g_i^2}$$

Here p_i and g_i represent pairs of corresponding pixel values of prediction and ground truth. During the training of a 3D MRI segmentation model, the goal is to minimize the Dice loss. Optimization algorithms, such as stochastic gradient descent (SGD) or Adam, are used to adjust the model's parameters to minimize this loss. The model learns to generate segmentations that maximize the overlap with the ground truth segmentations.

Specificity: it is defined as the true negative rate or the specificity coefficient, measures the ability of a test or model to correctly identify true negatives or non-disease cases. It calculates the proportion of actual negatives (those without the condition) that are correctly identified as negatives by the test or model.

Specificity is calculated as follows:

$$\text{Specificity} = (\text{TN}) / (\text{TN} + \text{FP})$$

A high specificity indicates that the test or model has a low rate of false positives, meaning it accurately identifies individuals who do not have the condition.

Sensitivity: it is the true positive rate or the sensitivity coefficient, measures the ability

of a test or model to correctly identify true positives or disease cases.

It calculates the proportion of actual positives (those with the condition) that are correctly identified as positives by the test or model.

Sensitivity is calculated as follows:

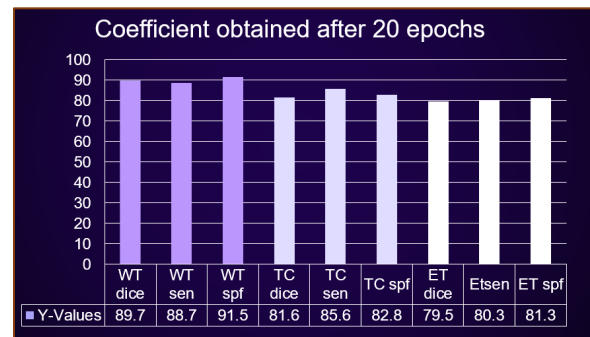
$$\text{Sensitivity} = (TP) / (TP + FN)$$

A high sensitivity indicates that the test or model has a low rate of false negatives, meaning it accurately identifies individuals who have the condition.

5. RESULTS

The dataset for the BraTS 2020 study comprises a total of 369 cases, encompassing 76 individuals diagnosed with low-grade glioma (LGG) and 293 individuals diagnosed with high-grade glioma (HGG). Each patient in the BRATS dataset has access to four distinct MRI sequences, namely T1-weighted (T1), T1 with gadolinium-enhanced contrast (T1c), T2-weighted (T2), and FLAIR. These sequences collectively contribute to a comprehensive collection of 2470 MRIs, with 1759 images allocated for training purposes, 247 images designated for validation, and 494 images reserved for testing. Employing the proposed methodology for brain tumor segmentation prediction, we have successfully predicted

the BraTS 2020 dataset in LGG-HGG grade patients, as depicted in the accompanying figure.



The average values of the coefficient Dice score, Sensitivity and Specificity after the validation of each class are presented in the figure below as well.

In the table below we have put together the tested multiple deep learning algorithms on the Brats2020 dataset

4 epochs	Slice	DS	SPF	SEN
	WT	81.9	82.8	82.8
	TC	63.9	84.6	51.9
	ET	39	32.2	0.1
20 epochs	WT	89.7	91.5	88.7
	TC	81.6	81.6	85.6
	ET	79.5	80.3	81.3

As seen in the table, the mean validation loss dice score 81.6%, and 84.46% of sensitivity and 80.36% respectively to WT, TC, ET.

Based on the MRI slices, the performance outcome of the SEGNET model on the Brats2020 dataset can be determined.

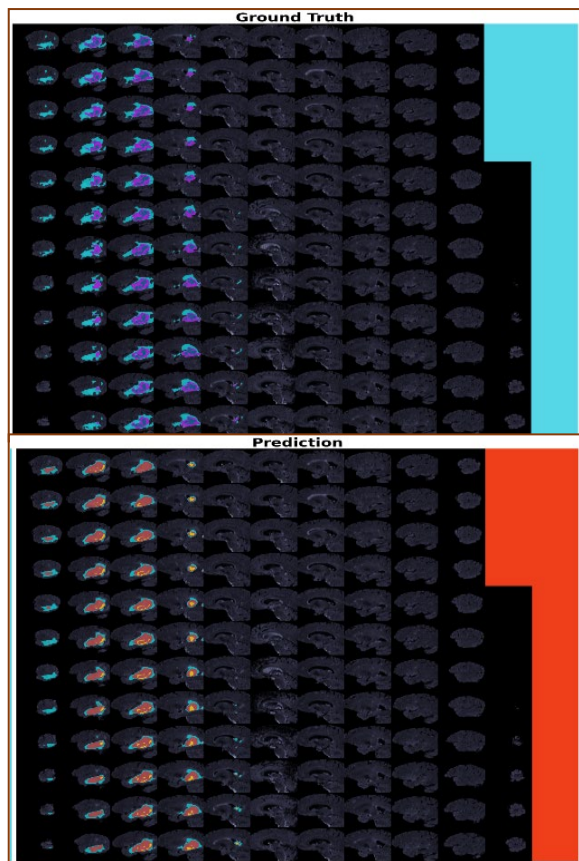


Figure 3: the prediction of the proposed model for (20 epochs)

The presented figure displays the compelling results of the Segnet model applied to the testing dataset over 20 epochs. Two distinct images are juxtaposed within the frame. The first image, representing the ground truth, serves as the benchmark for accuracy in brain tumor detection. The second image showcases the Segnet model's predictions, revealing an astonishing similarity to the ground truth.

This striking parallel underscores the model's remarkable

proficiency in accurately identifying and delineating brain tumor regions, signifying a significant leap forward in the application of deep learning for precise medical imaging analysis.

Due to insufficient computational power, we wouldn't be able to train the model on a maximum weight of epochs, as for this training duration it took about 10hours for the 20 epochs.

	Training loss curve
	Validation Loss curve

The training and validation graphs of the proposed model on the Multimodal MRIs for the tow experiments

On the 2 epochs

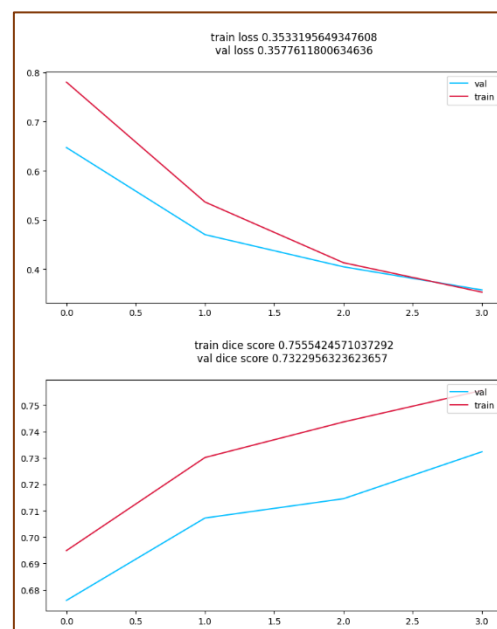


Figure 4: Figure 5: training and validation for the SegNet model over 2 epochs.

A loss score is a numerical value that quantifies the dissimilarity between the predicted output of a model and the ground truth (the actual target). In image segmentation and analysis, the predicted output typically consists of pixel-wise or region-wise labels, and the ground truth represents the true labels or annotations.

During the training phase of the model, the primary objective is to minimize the loss score. Models are optimized by adjusting their parameters (weights and biases) to make the loss as small as possible. This process is performed through techniques like gradient descent. By minimizing the loss, the model learns to make more accurate predictions.

The model performed a train set of 75% vs the validation of 72 %, in the other hand the loss function is yet to be minimized the average loss score is 0.36.

Due to the model training time, we run the training once more, hence we upgraded the number of epochs to 30:

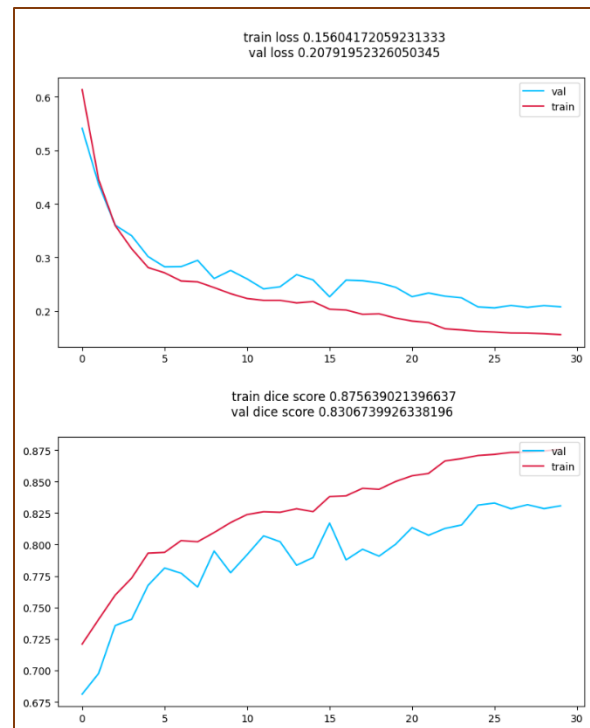


Figure 5 : Model's training and validation (loss score, Dice score) at 30 epochs

Loss scores are not only useful during training but also for evaluating the performance of a model. A lower loss score generally indicates a better-performing model. It provides a quantitative measure of how well the model is capturing the patterns and features in the images. As the figures show comparing to the number of epochs, it is precisely shown that the model's loss have been optimized to 0.15 over the 30 epochs, and as for the training loss is improved according to the overall model's performance.

According to the table below we have compared the performance of the proposed model with other deep learning models.

The results shown the segnet model out performance over the other models.

In the fast-evolving landscape of brain tumor detection, the integration of sophisticated deep learning methodologies has emerged as a pivotal breakthrough. Having delved extensively into the implementation of multiple algorithms, including SEGNET, 3D UNIT, and UNIT, our proposed research methodology pursuit of comprehensive solutions is evident. Notably, the SEGNET model, upon meticulous refinement, has yielded highly promising outcomes, evident from the comprehensive assessment metrics.

With a striking 89.7% for the dice loss, 92.5 for specificity, and 88.7 for sensitivity in the Weight tumor dice slice, the model showcases a commendable capability to precisely identify tumor regions. Similarly, the Tumor core slice's results, scoring 81.6% for the dice score, 89.6 for specificity, and 89.6 for sensitivity, underscore the model's adeptness in comprehending the intricate nuances of the tumor core. Moreover, the Enhancing tumor slice's performance, registering 80.5 for the dice loss, 88.3 for specificity, and 84.3 for sensitivity, reflects the model's proficiency in capturing the intricate aspects of tumor enhancement.

By meticulously fine-tuning the SEGNET model and amplifying its functionalities, the model’s performance has not only

SEGNET	Slice	DS	SPF	SEN
	WT	89.7	92.5	88.7
	TC	81.6	89.6	89.6
	ET	80.5	88.3	84.3
U-NET	WT	86	84	88.7
	TC	81.6	81.6	85.6
	ET	79.5	80.3	81.3
3D UNIT	WT	71.9	79.1	71.2
	TC	51.4	82.7	66.5
	ET	36.5	81.1	40.5

underscored the importance of nuanced analysis but also demonstrated the immense potential of deep learning in enhancing the precision of brain tumor detection. This strategic approach highlights a nuanced understanding of the complexities involved in interpreting complex medical imagery, thereby underscoring the research methodology’s significant contribution to the advancement of brain tumor diagnosis.

6. CONCLUSION

In the challenging domain of brain tumor diagnosis, the convergence of advanced

imaging methodologies and automated deep learning algorithms marks a transformative milestone in medical science. Amidst the limitations and challenges faced by traditional radiological assessments, the remarkable results obtained from the Segnet model underscore the pivotal role of artificial intelligence in augmenting diagnostic accuracy. With the Segnet model achieving impressive scores, including 89.7% for the dice loss, 92.5 for specificity, and 88.7 for sensitivity in the Weight tumor dice slice, the potential for automated detection is indisputably validated. Furthermore, the shift from 2D CNNs to 3D CNNs has broadened the scope for comprehensive analysis, offering a more nuanced understanding of complex brain structures and anomalies. As the field continues to embrace cutting-edge deep learning techniques, the future of seamless and reliable brain tumor detection appears increasingly promising, poised to significantly enhance patient care and transform the landscape of modern healthcare.

7. REFERENCES

1. Cosgrove, N., Vareslija, D., Keelan, S., Elangovan, A., Atkinson, J. M., Cocchiglia, S., Bane, B. T., Singh, V., Furney, S., Hu, C., Carter, J. M., Hart, S. N., Yadav, S., Goetz,

M. P., Hill, A. D. K., Oesterreich, S., Lee, A. V., Couch, F. J., & Young, L. S. (2022). Mapping molecular subtype specific alterations in breast cancer brain metastases identifies clinically relevant vulnerabilities. **Nature Communications**, 13, 514. [Link](<https://www.nature.com/articles/s41467-022-27987-5>).

2. Zhao, G., Feng, Q., Chen, C., Zhou, Z., & Yu, Y. (2021). Diagnose Like a Radiologist: Hybrid Neuro-Probabilistic Reasoning for Attribute-Based Medical Image Diagnosis. **IEEE Transactions on Pattern Analysis and Machine Intelligence**, 44(12), 7400-7416. [DOI](<https://doi.org/10.1109/TPAMI.2021.3130759>).

3. Olson, P. N. (1994). **MRI in Practice**. John Wiley & Sons, 193(1), 202.

4. Ottens, T., Barbieri, S., Orton, M. R., Klaassen, R., van Laarhoven, H. W. M., Crezee, H., Nederveen, A. J., Zhen, X., & Gurney-Champion, O. J. (2022). Deep learning DCE-MRI parameter estimation: Application in pancreatic cancer. **Medical Image Analysis**, 80, 102512. [DOI](<https://doi.org/10.1016/j.media.2022.102512>).

5. Mohsen, H., El-Dahshan, E.-S.-A., El-Horbaty, E.-S.-M., & Salem, A.-B.-M. (2018). Classification using deep learning neural networks for brain tumors. **Future Computing and Informatics Journal**, 3, 68-71. [DOI](<https://doi.org/10.1016/j.fci.2017.12.001>).

6. Abdelaziz Ismael, S. A., Mohammed, A., & Hefny, H. (2020). An enhanced deep learning approach for brain cancer MRI images classification using residual networks. **Artificial Intelligence in Medicine**, 102, 101779. [DOI](https://doi.org/10.1016/j.artmed.2019.101779).
7. Shahamat, H., & Saniee Abadeh, M. (2020). Brain MRI analysis using a deep learning based evolutionary approach. **Neural Networks**, 126, 218-234. [DOI](https://doi.org/10.1016/j.aeunet.2020.03.017).
8. Poyraz, A. K., Dogan, S., Akbal, E., & Tuncer, T. (2022). Automated brain disease classification using exemplar deep features. **Biomedical Signal Processing and Control**, 73.
9. Koc, M., Sut, S. K., Serhatlioglu, I., Baygin, M., & Tuncer, T. (2022). Automatic prostate cancer detection model based on ensemble VGGNet feature generation and NCA feature selection using magnetic resonance images. **Multimedia Tools and Applications**, 81(5), 7125-7144.
10. Vaibhavi, P., & Rupal, K. (2018). Brain Tumor Segmentation Using K-means-FCM Hybrid Technique. In **Ambient Communications and Computer Systems: RACCCS 2017** (pp. 341-352). Springer Singapore. [DOI](10.1007/978-981-10-7386-1_30).
11. Sharif, M. I., Li, J. P., Amin, J., & Sharif, A. (2021). An improved framework for brain Tumor analysis using MRI based on YOLOv2 and convolutional neural network. **Complex Intelligent Systems**, 7, 2023-2036. [DOI](10.1007/s40747-021-00310-3).
12. Yahyaoui, H., Ghazouani, F., & Farah, I. R. (2021). Deep learning guided by an ontology for medical images classification using a multimodal fusion. In **Proceedings of the International Congress of Advanced Technology and Engineering (ICOTEN 2021)**, 1-6.
13. Agravat, R. R., & Raval, M. S. (2021). A survey and analysis on automated glioma brain tumor segmentation and overall patient survival prediction. **Archives of Computational Methods in Engineering**.