Natural Resources for Human Health
eISSN: 2583-1194

Original Research

Received 29 May 2026
Revised 21 June 2026
Accepted 18 July 2026

Natural Resources for Human Health 2026, Vol. 6 (10s): 273–284

KEYWORDS:
Brain tumour; ROI; 3D U-net; MRI

Segmentation of Brain Tumours through Volumetric Analysis Utilizing U-Net on MRI Brain Images

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ABSTRACT: The 3D U-Net structure has emerged as a first priority in segmenting of brain tumours especially defining regions of interests (ROIs) to measure volumes. This deep learning model has been specifically optimized to take in three-dimensional data, and thus it can be applied effectively to medical imaging work where spatial context is essential. Its symmetric encoder-decoder structure enables the extraction of both high-level semantic features and fine-grained spatial information. The 3D U-Net requires annotated volumetric data-sets, typically MRI data-sets, during training period to know how to differentiate between tumour and normal brain tissue. Through voxel-based classification, tumour boundary is accurately delineated, which helps to easily identify the ROI to perform further clinical assessment.

In addition to segmentation, the 3D U-Net will improve volumetric analysis quality and speed by delivering valid data on the tumour size and morphology which is the key aspect requiring improvement in terms of clinical decision-making. The skip connections between the encoder and the decoder pathway contribute towards the maintenance of spatial resolution which is a prevailing drawback of traditional convolutional networks, and enhance the overall segmentation accuracy. This aspect of providing a consistent and high-resolution understanding of the tumour characteristics in order to enable clinicians to customize their treatment strategy into better patient care and outcomes is made possible by the 3D U-Net.

1. INTRODUCTION

Volumetric analysis is a critical component in neuro-oncology, offering a quantitative framework for assessing the size, shape, and progression of brain tumours. The method is essential both in the acute diagnosis and long-term monitoring and assessing the response to treatment. Clinicians can now visualise brain structures in 3 dimensions through high-resolution imaging modalities like magnetic resonance imaging (MRI) and computed tomography (CT) and in such a way that allows a precise measure of tumour volumes. The measurements is very useful in determining the growth pattern of the tumour, how it infiltrates the surrounding tissue as well as the reactions of the tumour to the therapeutic interventions-such as surgery, chemotherapy and radiotherapy.

With the improvement of advanced tools of software and ML(machine learning) algorithms, the precision of volumetric measures has tremendously improved and proven reproducible. Automated segmentation methods, in particular, minimize human error and inter-observer variability, streamlining workflows and ensuring consistent results. In addition, volumetric information would be able to record tumour heterogeneity, with internal heterogeneity showing potential in combination with a link to biological aggressiveness or response to treatment or underlying genetics. Such information is crucial for personalized treatment planning. Volumetric analysis can help neurosurgeons define the tumour margins and save vital neighbouring structures in a surgical setting, enhance dose distribution to the tumours, and limit collateral damage in radiotherapy.

Beyond clinical practice, volumetric analysis is foundational to neuroimaging research. The comparability of studies regarding brain tumour biology is achieved by increasing the comparability of data due to volumetric measurements, which are standardised measurements. When integrated with histopathological data and ML frameworks, such features support predictive modeling of tumour progression alongside treatment outcomes—advancing the field toward precision medicine.

The significant development in this field is the use of deep learning segmentation tools, especially the 3D U-Net architecture. Specifically designed to operate on volumetric medical data, the 3D U-Net is based on an encoder-decoder architecture that has symmetrical branches. This design allows that given data to be captured with the global contextual information in mind as well as the fine details of anatomical structures. During training, it leverages annotated MRI datasets to perform voxel-wise classification, accurately distinguishing tumour tissue from healthy brain matter. Use of skip connection in the encoder and decoder pathways retains vital spatial information, enhancing segmentation faithfulness, and helps to reduce complexities. The capabilities can help yield high-precision tumour delineation that can empower clinicians with consistent and usable knowledge in a short amount of time.

Compelled by spreading computational capability and the expanding variety of annotated datasets, usefulness, such as the 3D U-Net, can now systematise cross-patient and cross-imaging modality. These innovations are accelerating clinical workflows, improving diagnostic accuracy, and enhancing individualized treatment planning. As volumetric analysis continues to evolve through deeper integration with artificial intelligence and algorithmic refinement, its role in brain tumour management is set to expand—transforming neuro-oncology through more personalized, efficient, and effective patient care.

2. LITERATURE SURVEY

This literature survey synthesizes findings from recent journal articles, focusing on 3D brain Tumour segmentation, primarily using deep learning and multimodal MRI data. The survey highlights key methodologies, datasets, architectures, and performance metrics.

[1] We introduce a new segmentation framework—TransBTS—that efficiently integrates 3D CNN (convolutional neural network) with a transformer-based module for multimodal brain tumor (BT) segmentation from MRI data. This architecture leverages strengths of both 3D CNNs for catching localized spatial and intensity features and transformers for modeling global semantic dependencies across the entire volume. In our proposed pipeline, the 3D CNN initially extracts compact feature representations from input MRI sequences. These features are then passed to transformer encoder, which learns long-range contextual relationships across slices. By combining convolutional operations with attention mechanisms, TransBTS enhances model's capacity to comprehend both local as well as global features critical for accurate tumor delineation. We validated TransBTS on the BraTS 2019 and 2020 datasets, where it demonstrated strong segmentation performance, surpassing several contemporary approaches. The architecture employs stacked convolutional and transformer layers to progressively refine the segmentation resolution, leading to high-fidelity output masks. Looking ahead, we plan to explore more efficient attention mechanisms and memory optimization strategies within the transformer component to reduce computational overhead and enhance deployment feasibility in clinical environments.

[2] Such research represents new multi-coding model for segmenting magnetic resonance 3D brain tumor pictures, yielding improved results in the BRATS 2020 database. To further illustrate efficacy of such strategy, we compare experimental outcome with those of other advanced techniques and also with outcomes of renowned team participating in BRATS 2020. (ME-NET), that has been enhancement in V structure suggested by MILTARI et al. A traditional V V network is having only 1 sampling path, making it challenging to extract magnetic resonance imaging images of 4 modalities. [16] To address this issue, we developed a novel architecture consisting of 4 codings with similar features. Input from 4 bass sampling pathways correlates with 4 modalities of brain tumors. This individual idea significantly enhances model's resource extraction capacity. Jump

connection amends corresponding modules of 4 coders and then combined on a resource map, after which they are input to decoder. Additionally, in UP-sampling process, corresponding low sampling internship maps are also combined to compensate for lost information. We additionally project categorical data loss function, including model optimisation function, as well as adjusted weight values of every output category by weight distribution, thus solving Voxel imbalance issues in foreground as well as background.

[3] For a challenge of segmenting Tumour regions from MRI images, U-Net segmentation version has been utilized in such investigation, that has been broadly standard structure [20], advanced by Olaf Ronneberger et al. To segment biomedical pics. U-Net employs one compact encoder or decoder structure, which concatenates functions from several encoder tiers with decoder layers twice. Demonstrates U-Net architecture. In fact, pre-processing step, normalisation, alongside rescaling have been applied to all 4 MRI sequences. Subsequently, each sequence is surpassed because schooling dataset is added to model. Respective manually segmented ROI (Seg) is utilized as floor reality for every sequence one by one.[18] Adam optimizer with mastering fee of 0.001 is utilized for schooling a version. For 4 sequences, 4 effects are formed, namely res-1, res-2, res-3, and res-4. Lastly, based on accuracy of every precise sequence, most suitable resulting model is obtained.

CNN-based 2D U-net segmentation version is suggested to segment brain Tumour from MRI images. Such a technique gets all MRI sequences, in my opinion, as educational information, as well as extracts ROIs (Tumour areas in Brain MRI).[20] Lowering computational value as well as boom efficacy, input pics are normalized as well as rescaled into single 128×128 image. We comprise 2D layers to combine data better. This model is skilled with "brain MRI dataset BraTS 2020" for all 4 MRI sequences (FLAIR, T1ce, T1, T2) to locate which collection provides optimal segmentation performance as per ground truth of MRI snapshots. Largest DSC rating (ninety-three 9 percent) is noted with T1 MRI sequence schooling on U-Net version. Outcomes are in comparison with preceding studies, indicating that this is a promising method, although it reduces computational complexity.

[4] In this study, we aim to utilize a set of U 3D networks with varying hyperparameters for brain tumor segmentation. Initial outcomes show that this model is effective. Additionally, we created linear model for survival forecasting utilizing both image as well as non-image features. Considering its simplicity, this model could significantly minimize adjustment and regression errors. A U 3D network-based structure was employed, as illustrated in Fig. 2. We applied zero filling to ensure that output spatial dimensions match those of input. Every coding block features a VGG network comprising 2consecutive 3D convolutional layers having a specified kernel size, after an activation function, as well as standard layers.

When it comes to segmentation, it's important to highlight that median metrics are considerably greater than average metrics. For instance, median data indices are 0.867, 0.923, 0.904 for WT, ET, & TC in final model set. Logically, maximum data index is one, and the minimum is zero. Hence, we notice that in some instances, data indices drop to zero for ET, TC, and 0.6 for WT. This is primarily because of low sensitivity, indicating that model struggles to identify relevant tumor regions. One possible explanation for these shortcomings is that the features of these regions differ significantly from those in training dataset. Nonetheless, it is encouraging because, in most cases, the quality of segmentation remains very high.

[5] Exactly, reproducible as well as effective tumor segmentation has capacity to enhance glioma treatment by allowing to deviate active tumor from necrotic tissue along with oath. Hence, great efforts were made to facilitate development of automated gliomse segmentation. Our set of rules is completed in addition to previously posted high-acting algorithms in segmentation of one and WT on Brats2017 Information set, and becomes one of top three athletes in segmentation of TC. Rules seen are also one of the highlights in line with forms in segmentation of WT, and one at Brats 2018 Facts Set. Our entire pipeline, along with all pre-treatment steps, took 5 min in steps with difficulty trial.

The dice rankings had been reduced slightly when created by the medical information kit. This decline in total performance has been anticipated because of practical issues associated with using clinical scans. For instance, variations in subject power (1.5t vs 3T), parameters for medical comic book series, and variability in submission also constitute the reduced total performance. [20] Despite the barriers, our deep mastery society was capable of sectional tumors as well as sub-components with fantastic consequences without the best vote, showing the promise for incorporation into scientific workflow. A3DDENSE UNET has been modified for MRI-based segmentation of gliomas. Algorithm could be easily integrated into scientific workflow. Our algorithm beat the top athletes in segmenting the WTandet.

[6] Current research presented one hybrid methodology which integrates handcrafted resources with CNN. Handcrafted resources integration with CNN resources in our suggested hybrid method has resulted in better segmentation performance. This method enabled us to take advantage of strengths of handcrafted as well as CNN resources for more accurate as well as robust tumor segmentation. CNN's thin adjustment on integrated features has further enhanced performance of our method. Comparative analysis reveals that proposed hybrid method exceeds handmade methods based on resource as well as CNN-based methods concerning segmentation accuracy, data punctuation, sensitivity, as well as specificity. This illustrates the efficacy of hybrid method in harnessing the advantages of artisanal traits along with DL approaches for BT segmentation.

Current research presents a hybrid technique for BT segmentation that integrates hand-crafted resources with CNNs. Methodology encompassed data gathering, pre-processing, resource extraction, CNN architecture, and merging of handmade with CNN resources. Suggested hybrid strategy exhibited enhanced performance relative to individual resource-based and CNN-based techniques. Combination of handcrafted as well as CNN features has resulted in enhanced accuracy and robustness, along with superior generalization abilities for invisible data. Although encouraging outcomes, suggested hybrid methodology possesses certain limitations. A limitation is complexity of hand-bred resource integration and CNNS, which may need extensive adjustment to get best performance. In addition, method still depends on accessibility of large training sets for training, that could be a challenge to get in medical field.

[7] Automated segmentation of BTs from 3-D magnetic resonance snapshots (MRIs) is essential for analysis, monitoring, as well as remedy making plans of sickness. Manual delineation practices need anatomical understanding, are luxurious, time-consuming, and could be incorrect because of human error. There, we define "semantic segmentation" network for Tumour subregion segmentation from 3-D MRIs utilizing encoder-decoder structure. Because of limited size of education dataset, variational autoencoder branch is introduced to rebuild entire photograph, aiming to regularize shared decoder as well as impose more limitations on its layers.

This study presents semantic segmentation network for BT segmentation from multimodal 3D MRIs, that achieved victory in "BraTS 2018" project. Although experimenting with community architectures, we attempted numerous other methods. For example, we've tried greater batch length of eight so that you can utilize "BatchNorm" (moreover utilise batch facts); nevertheless, because of GPU memory limits, this alteration needs to utilize smaller photo crop length, resulting in poor performance. We have additionally experimented with extra sophisticated information augmentation methods, together with random histogram matching, a ne image transforms, as well as random picture ltering, which don't show any extra enhancements. We have tried numerous information publish-processing techniques to tune segmentation predictions with CRF [14], nevertheless, we didn't find it helpful (it helped for some pics, however, it worsened some other image segmentation effects). Increasing network intensity in addition did not enhance overall performance; however, growing community width (wide variety of functions) continuously enhanced consequences. Utilizing "NVIDIA Volta V100 32GB GPU", we have been capable to double wide variety of functions in comparison to "V100 16GB version". Lastly, extra VAE branch facilitated regularizing shared encoder (in restrained statistics presence), that enhanced performance as well as assisted in always attaining correct schooling accuracy for one random initialization. Our BraTS 2018 checking out dataset outcomes are 0.7664, zero.8839, and zero.8154 common dice for greater Tumour center, complete Tumour, and Tumour middle, respectively.

[8] This section summarizes conduction of "3D-Znet model" through experiment series designed in determining optimal multimodal tumour mask segmentation utilizing "BraTS (2020)" public dataset, which includes stereotactic MR volumes. Data augmentation procedure had been essential to increase original sample of 369 raw volumes to bigger dataset of 1,845training volumetric samples through "3D affine transformations". Letting augmented dataset had been partitioned into 80%(training) & 20%(testing) sets. Subsequently, each stereotactic data was resized to 128 x 128 x 128 tensors for decreasing training complexity moreover fit combined "3D-Znet model" within the constraints of available RAM throughout the training data. All data samples include ground truth (annotated mask), that has been processed to generate 3 masks: ET (Enhanced Tumour), TC (Tumour Core), & WT (Whole Tumour). Outcomes of training prior mentioned method 3D-Znet demonstrated average 0.91 Dice correlation for entire tumor segmentation, 0.85 for tumor core, and 0.86 for segmentation of most challenging augmented tumor which reflects complete mean 0.87 Dice segmentation coefficient. Outcomes demonstrate compelling proof of proposed 3D-Znet DCNN method's efficacy in accurately segmenting various forms of BTs, with DCNN-generated tumor masks exhibiting substantial concordance having human expert delineations alongside other state-of-art models.

[9] This study presents a network that utilizes previously established transformer modules, augmented with advanced channel attention modules. This enables a full exploration of spatial and contextual information in MRI images, thorough exploitation of characteristics, and enhancement of representation of diverse tumor regions. Thus, we tackle the difficulty of precisely obtaining comprehensive information regarding the overall tumour architecture moreover attributes of particular subregions, hence improving segmentation accuracy. Our proposed network comprises 2 primary components: 3D-UNet backbone and 3D context-aware transformer module integrated into encoder-decoder architecture.

This research presents strong method from MRI images for multimodal brain tumor segmentation by integrating CoT for enhancing baseline architecture and enhance segmentation accuracy. CoT utilizes tumour features alongside contextual information by emphasizing self-attention blocks, hence improving output information synthesis as well as representation. "CNN-Transformer architecture" combines 3D-CNN benefits for local context modeling with enhanced capabilities of Transformers to capture long-range relationships. Consequently, 3D UNet+CoT model efficiently synchronizes features, mutually reinforcing the synthesis of important features. Hence, such model may comprehensively comprehend the tumor structure with accuracy, encompassing boundaries, locations, shapes, and sizes. Experimental findings confirm suggested method efficacy, attaining Dice scores of 81.2, 82.0, & 88.6% for TC, ET, and WT labels on BraTS2019, surpassing numerous other state-of-art techniques.

[10] We aimed to address a complex difficulty related to BT segmentation using 3-D MRI scans. We analyzed DL techniques moreover opted for a CNN to generate suitable responses for specified study challenge. We developed a novel structure for BT segmentation, utilizing established "U-Net architecture" alongside "Inception modules". This model attained a substantial rise in validation accuracy. Rise in validation accuracy has been attributed to implementation of multiple convolutional filters of diverse sizes within every Inception module. Throughout learning procedure, such filters can capture and preserve contextual information at various sizes. We contend that enhanced tumor segmentation accuracy is attributable to novel loss function derived from refined DSC. We evaluate our models utilizing DSC inside our suggested framework, moreover learning objective or loss function (Dice loss function) employed for training such algorithms is similarly as per DSC. Comprehensive research demonstrated that each component of the proposed structure fulfills its designated function in recognizing intricate patterns linked to tumors and enhances segmentation results. Furthermore, methodology defined in this study could be enhanced through the application of cascaded, ensemble, or alternative learning techniques. Primary conclusions of this study can be generalized and utilized across various biological picture segmentation and classification challenges, including image registration, disease quantification, moreover in other domains.

[11] This research presents an enhanced bio-inspired level set segmentation method for extraction of BT in MRI images. Proposed model employs a 2-step clustering approach for ascertaining precise beginning contour points for level set segmentation procedure which is a clustering methodology which integrates the k-means algorithm with dragonfly algorithm (DA) in the purpose of enhancing the level of tumour segmentation accuracy. As opposed to the randomly initialized population centroids, the proposed approach uses k-means to find an initial position of the DA, which allows defining optimal start-values. This is an important step because there is an intrinsic heterogeneity in tumour size, shape and structure thereby posing topological difficulties in contour identification. To deal with it, a two-stage dragonfly algorithm has been proposed in the paper aimed to provide an adequate initiation of the contour points. In pre-processing, the brain is initially separated out of the rest of the structures of the head. This is then followed by the detection of tumour edges based on 2-step DA whose edges have then been utilized as a starting point of the MRI sequence. In the last step, the entire tumour area is segmented throughout the volumetric slices through a level set technique which allows Three-Dimensional delineation of tumour.

Table 1: Implemented Methods and Findings Summary

Methods Used	Used Architecture	Outcomes
Ensemble Dual-Modality U-Net	U-Net, ensemble, Grad-CAM	Dice 97.73%, improved interpretability
ET UNet	U-Net + Transformer	DSC 0.854/0.862, improved HD95
3D-Z net	Dense VAE-Autoencoder	Enhanced feature reuse, robust segmentation

Natural Resources for
Human Health
eISSN: 2583-1194

MLU-Net	Frequency + MLP in U-Net	Higher efficiency, improved Dice/IoU
Bridged-U-Net-ASPP-EVO	U-Net + ASPP + EvoNorm	High segmentation accuracy
3D U-Net	Standard 3D U-Net	Widely used, strong baseline
CNN + IChOA	CNN + Feature Optimization	Improved robustness to modality variation

3. METHIODOLOGY

3.1 Data Acquisition and Preprocessing

The accumulated database of volumetric brain MRI data has been a core to the developmental research in neuroimaging especially on the study of brain tumours. An interesting case is the BraTS 2019 dataset that is imparticularly curated to aid the development and assessment of algorithms used to segment and classify the brain tumour. The data consist of MRI data of a heterogeneous group of multiple patients and represent a large variety of tumour types and grades. It consists of T1-, T2-weighted images, and FLAIR tests, which provide a detailed description of the morphology of the tumour and the brain configuration that surrounds it, turning out to be an invaluable tool in the prospect of developing machine learning algorithms with the goal of improving diagnostic quality and more focused treatment planning.

Beyond its clinical utility, the BraTS 2019 dataset serves as a standard benchmark in medical image computing. By providing uniform and well-annotated data, it enables objective comparison of algorithm performance across different studies, promoting consistency, reproducibility, and collaboration within the research community. The tumour segmentations that are created by experts also enhance its applicability in implementing supervised learning to enable research teams to design and test high fidelity segmentation models. With the ongoing complexity of the process being used to analyse brain tumour patients, high quality and well curated data such as BraTS 2019 will be critical in driving further changes in neuroimaging and helping patients.

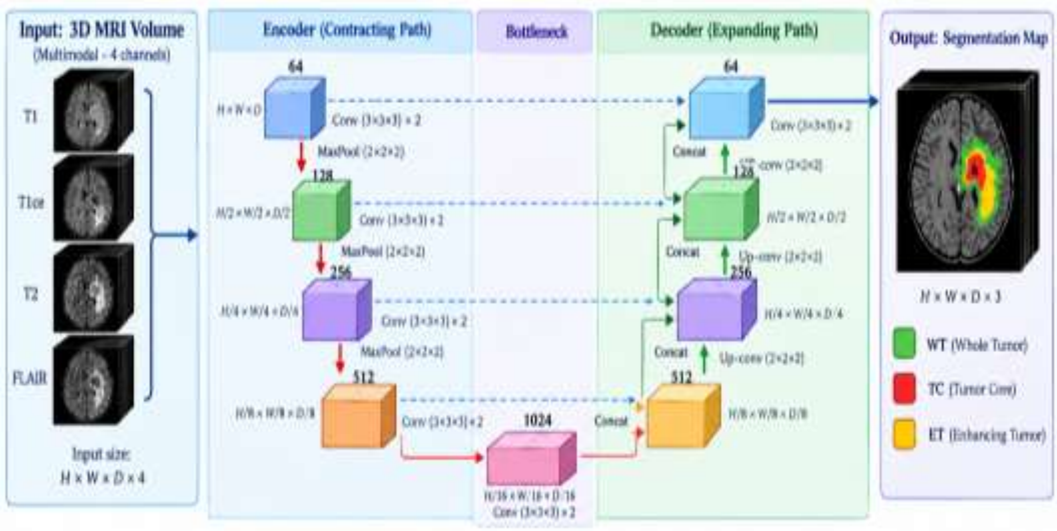
Preprocessing of brain magnetic resonance (MR) images is a critical step in the use of such datasets, as the quality and reliability of data are guaranteed by it later on in the analysis process. Preprocessing normally initiates by rectifying image artifacts and sharpening visual images. Noise, intensity inhomogeneities and patient movements during a scan are handled in techniques denoted by denoising, bias field correction, and motion correction respectively. Denoising algorithms decrease random intensity variations; however, bias field correction compensates for uneven signal intensities led by magnetic field irregularities. In clinical and research applications where the sample size is made up of human subjects, motion correction is of utmost importance since any movement, which is even minute, can corrupt structural integrity.

After artifact correction, the process of spatial normalization and segmentation takes place to simplify the analysis in subjects. Spatial normalization places collected images of individual brains on a standard template of anatomical space so that the result of comparisons and group sizes can be drawn on a population scale. Segmentation, on the other hand, consists of the outlining of important components of the brain, like the gray matter, the white matter, and the cerebrospinal fluid, which is necessary in retrieving quantitative biomarkers as well as the comprehension of normal and pathology of the brain. Together, such preprocessing steps create foundation for reproducible, robust neuroimaging research, letting subsequent analyses—like progression modeling, tumour detection, or therapeutic monitoring- have been grounded in reliable, high-quality data.

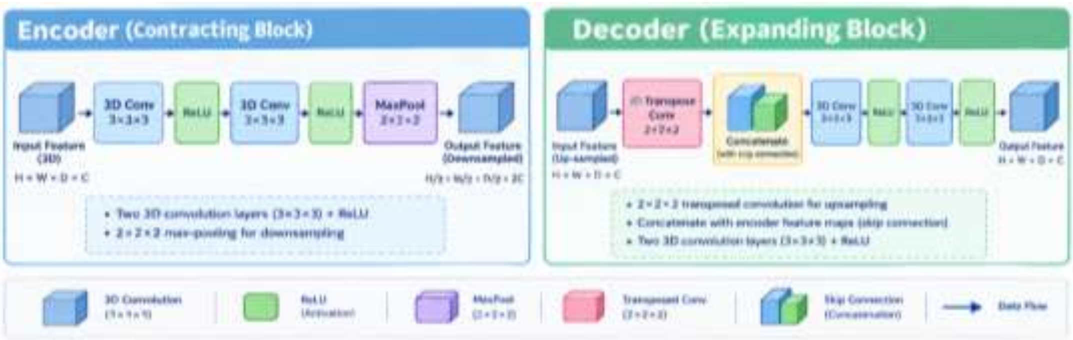
3.2 Model Architecture: 3D U-Net

The emerging architectures consisting of 3D U-Net as a model of volumetric processing of MRI scans is the step towards the medical imaging analysis as one of the most important fields of medicine. The 3D U-Net is an extension of the original U-Net (developed using 2D images) that uses three-dimension convolutional layers and can thus properly capture spatial hierarchies and context in the volume cases. This makes it specifically conducive to MRI scans which are always made up of stacked 2-D layers of slices making up a 3-D pattern. The model is effective in deriving concise details on these slices and thus it can provide an opportunity to segment these anatomical structures more precisely and effectively. The architecture uses skip connections between the decoder and encoder paths to maintain spatial resolution during learning complex representations, and this enhances high rates of segmentation, which is a necessary thing in the diagnosis, monitoring, and treatment of various medical diseases.

The technological development of computational ability and the subsequent increase in accessible large assembled volumetric MRI datasets have vastly contributed to the real-life implementation of 3D U Net. These advances have enabled training of more generalized and sturdy models that could be used to perform reasonably on various imaging protocols and work on a cohort of patients. Also, 3D end-to-end learning framework of the U-Net enables connecting the preprocessing-related methods like normalization, data augmentation, and intensity correction, into a direct training-related chain, further simplifying the whole process. This not only increases efficiency in processing but also makes real-time application in clinical settings a possibility. The 3D U-Net is another key to analysis in modern medical imagery that allows more accurate and earlier diagnosis due to continuous creation of improvements in its scalability and accuracy, which leads to improved patient outcomes.



(a)



(b)

Figure 1. (a) & (b) Tumour Segmentation Workflow with 3D-Unet

3.3 Training Procedure

The loss function is a fundamental component in the training of machine learning models, serving as a quantitative measure of the discrepancy between predicted outcomes and ground truth values. It directs the training by, via the optimization algorithm, telling it how wrong the predictions of the model are and hence allowing the updating of the parameters via backpropagation. Some of the popular loss functions are "Mean Squared Error (MSE) and Cross-Entropy Loss on regression and classification tasks, respectively. The choice of a suitable loss function plays a major role in the performance of a model" since it determines the gradients which are used to execute the learning as well as directly affect the generalization capacity of a model. An optimal loss function not only yields small prediction error but also heavily punishes misclassification so as to ensure enhanced accuracy and stability.

Optimizers together with loss functions act like a pair in the sense that they reduce the loss computed by updating the parameters of the model. The Stochastic Gradient Descent (SGD) algorithm, Adam, and RMSprop have different methods in weight updating and their own benefits in speed, convergence power, and the capacity to deal with sparse gradients. The dynamics of the learning are also influenced by the selection of the batch size, the number of training samples that one works on in each iteration. Batches can be smaller, which injects more noise into the estimation of the gradients, which can improve the generalization, or they can be larger, which will smoothen the updates of gradients but taking more computational resources. Also, validation is significant throughout training as it examines how well the model performs on unexamined data. This will assist in avoiding overfitting as well as keep the model with high-level attributes of generalization. Together, the careful selection and tuning of loss functions, optimizers, batch sizes, and validation strategies are pivotal for developing high-performing machine learning models.

3.4 Evaluation Metrics

They are quite necessary when the objectivity of the process of determining whether a model works or not is concerned, especially when application domains such as image segmentation and classification are of interest. One of the most common measures includes Dice Similarity Coefficient (DSC) and the intersection over union (IoU) which values the intersection of predicted (seg.) against the ground truth annotations. Dice coefficient of 0 to 1 is particularly good with segmentation into two segments, since it is the measure of similarity between two sets. IoU/ Jaccard Index, computes intersection to union ratio of predicted and true regions, offering a more nuanced perspective on model accuracy in segmentation contexts.

Additional metrics that are complementary to performance (precision, recall, and accuracy) also improve performance evaluation. Precision determines the correct proportion of the predicted positives among all the positively predicted, and recall reports how well the model can identify all the actual positives. Accuracy shows the entire proportion of the correct predictions of all classes. Such metrics together offer a comprehensive evaluation framework, highlighting different aspects of model effectiveness.

In order to have reliable and valid numerical values, the comparison of the results to experts annotated data or to known state of the art models is paramount. The difference between expert annotations and model outputs can be used to determine the gap in the performance of the model and further improvement of the algorithm. In addition, benchmarking helps the researchers to evaluate their models against the existing standards in the industry or academia which opens up transparency and iterative growth. Strict evaluation practices not only confirm the effectiveness of the model, but also advance research studies in machine learning, bringing innovations to the fore and improving the real use of the result.

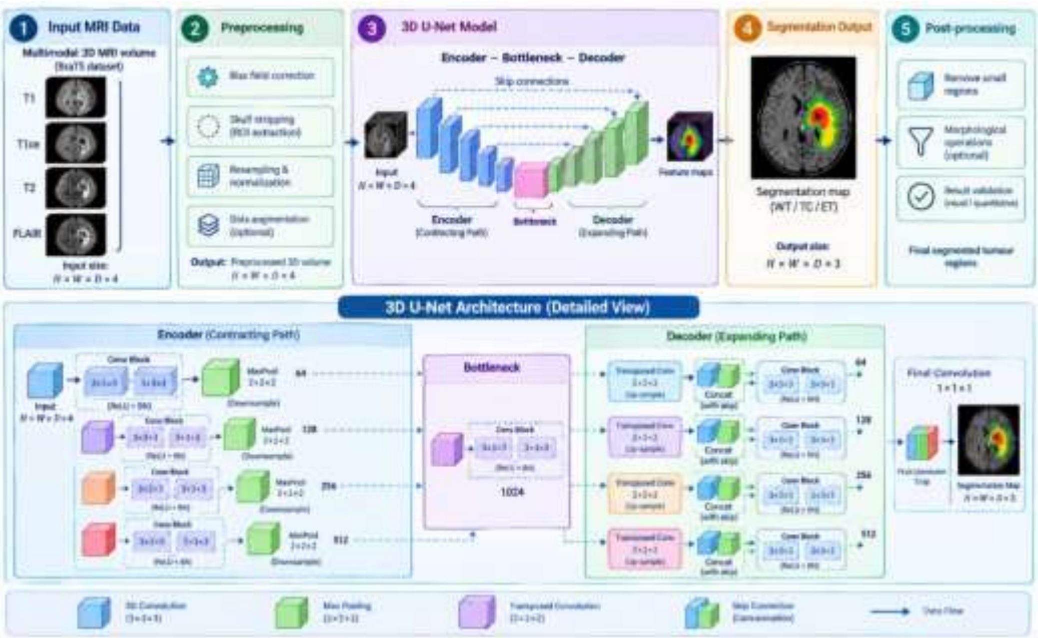


Figure 2. Process Flow of the Segmentation using 3D Unet

3.5 Flow Chart:

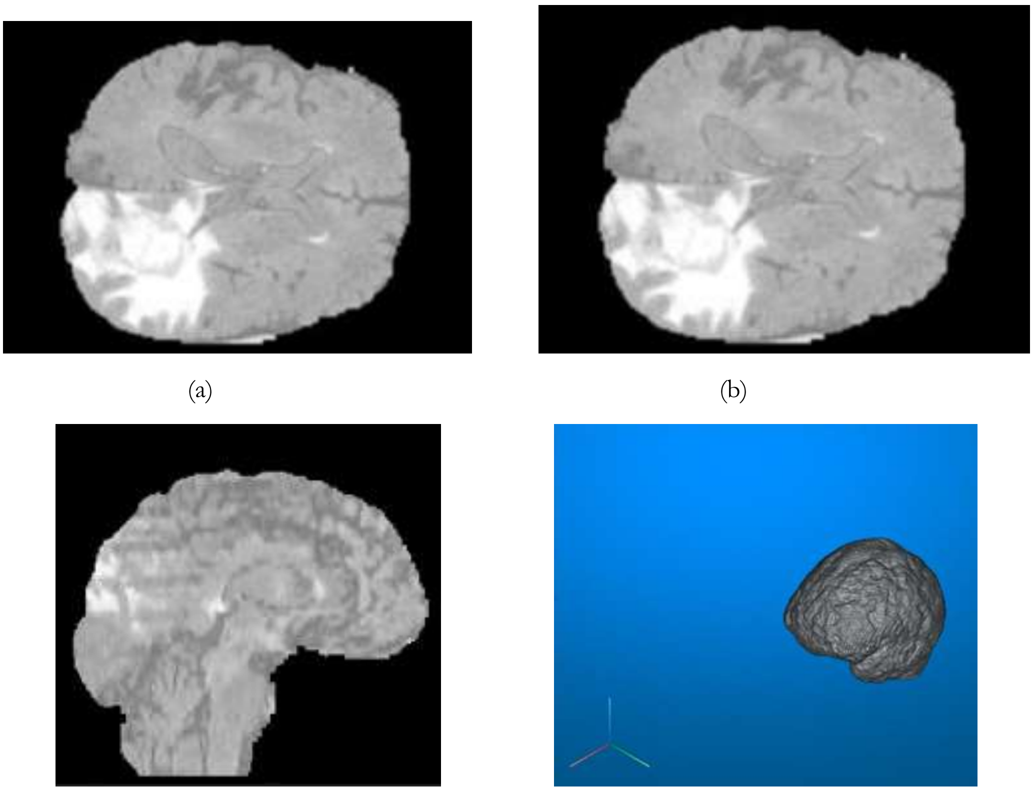
Figure 3. Flow Chart of the Different Processes in Segmentation of Brain Tumour

4. RESULTS

The segmentation of brain tumour with the utilization of orthogonal methods of cross-section slice, i.e., axial, coronal, and sagittal, gives a very healthy assessment of the efficiency of the 3D U-Net models. The views present a complete spatial view of the tumour and allow the assessment of the segmentation accuracy in detail in various anatomical planes.

4.1 Visual Examples of 3D U-Net Segmentation

Axial, Coronal, and Sagittal Views: Three-dimensional U-Net model produces the results shown on the images below, which are slices through the three orthogonal planes representing the brain tumour segmentation. Such cross-sectional images through axial, coronal and sagittal planes give prominence as to how the model can precisely outline the tumour boundaries in space.



(a) (b)

(c) (d)

Figure 4. (a) XY Plane, (b) YZ Plane, (c) XZ Plane (d)3D Volume

Subsequent images illustrates original MRI slices along with ground truth annotations moreover segmentation predictions developed by 3D U-Net model. Tumour areas have been clearly highlighted across coronal, axial, sagittal planes, providing comprehensive visual comparison. Such side-by-side presentation demonstrates model's ability to accurately replicate expert annotations moreover efficiently delineate tumour boundaries in 3-D space.

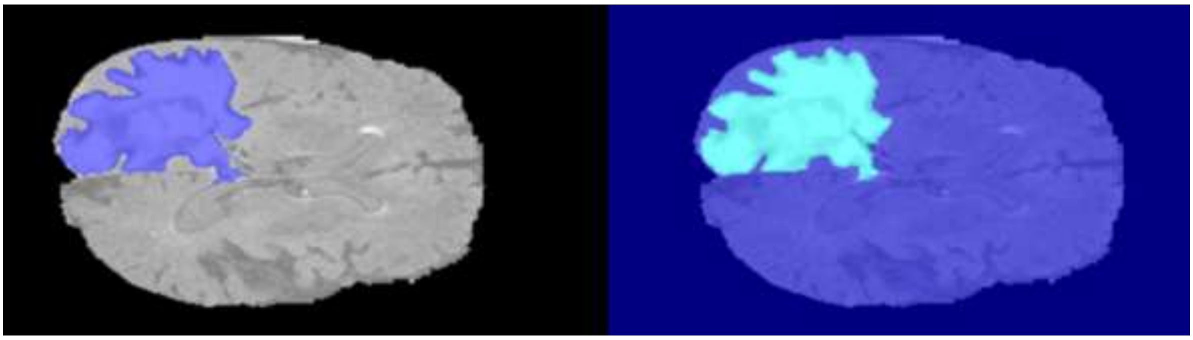


Figure 5. Segmentation of Tumour ROI Using Volumetric Analysis with Ground Truth Comparison

These visualizations offer a clear comparison between the predicted segmentation and the ground truth, effectively in exhibiting the capacity of the model to perform in defining tumour boundaries and to provide a beneficial delineation across axial, coronal and sagittal planes. Orthogonal cross-sectional slices are effectively needed to achieve a complete assessment of 3D U-Net application in the segmentation of brain tumours. This provision of segmented regimes in three anatomical perspectives allows researchers and clinicians to access the spatial accuracy and uniformity of the model in detail and helps to make it clinically viable and reliable.

5. CONCLUSION

The application of the 3D U-Net architecture for the segmentation of volumetric MRI scans represents a significant advancement in medical imaging. Specifically designed to process three-dimensional data, the 3D U-Net leverages deep convolutional layers and a symmetric encoder-decoder structure to effectively capture both spatial hierarchies and contextual information. It also keeps fine anatomical details and preserves high-level contextual information, hence it would be possible with respect to accurate segmentation in clinical limitations where accurate delineation of anatomy is imperative to diagnosis and treatment planning.

The effectiveness of 3D U-Net has been validated across diverse datasets, demonstrating its robustness and adaptability to varying imaging modalities and pathological conditions. The reason it can reasonably be applied in clinical practice is that its implementation would be incredibly helpful in terms of improved efficiency, radiologist workload reduction, and decreased risk of human error. Newer and newer attempts are being made to optimize the architecture, to better train it, and to improve generalizability over the different sets of patients. In the end, the fact that 3D U-Net and other deep learning models continue evolving means that improved, automated, and more precise diagnostic solutions may be achieved by making medical imaging more personal and accurate.

ACKNOWLEDGEMENTS

The authors would like to express their sincere gratitude to our supervisor Dr. Naveen B for the invaluable guidance, continuous encouragement, and insightful suggestions provided throughout the course of this research work. We also extend our heartfelt appreciation to our co-author Mrs. Lakshmi D L for the significant contributions, constructive discussions, and dedicated support. Their expertise and cooperation greatly enhanced the quality of this study.

AUTHOR CONTRIBUTIONS

Goutham V: Conceptualization, Data Curation, Methodology, Formal and Laboratory Analysis, Writing—Review & Editing.

Naveen B: Conceptualization, Supervision, Writing and Reviewing.

Lakshmi D L: Investigation, Methodology, Data Curation, Formal Analysis, Writing—Review & Editing

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

ETHICS STATEMENT

Ethical approval was not required for this study.

DATA AVAILABILITY STATEMENT

We have used the BraTS 2021 dataset. http://www.braintumorsegmentation.org/ [38-39]

REFERENCES

[1] TransBTS: Multimodal Brain Tumour Segmentation Using Transformer Wenxuan Wang1, Chen Chen2, Meng Ding3, Hong Yu1, Sen Zha1, Jiangyun Li1 arXiv:2103.04430v2 [cs.CV] 26 Jun 2021

[2] ME-Net: Multi-Encoder Net Framework for Brain Tumour Segmentation Wenbo Zhang 1,*, Guang Yang 2, 3, *†, He Huang 1, Weiji Yang4, Xiaomei Xu1, Yongkai Liu 5, Xiaobo Lai 1,†, Electrical Engineering and Systems Science , Image and Video Processing, arXiv:2203.11213.

[3] Brain Tumour Segmentation from 3D MRI Scans Using U-Net, Sidratul Montaha, Sami Azam, A. K. M. Rakibul Haque Rafid, Md. Zahid Hasan & Asif Karim, Published: 11 May 2023, Volume 4, article number 386, (2023)

[4] Brain Tumour Segmentation using an Ensemble of 3D U-Nets and Overall Survival Prediction using Radiomic Features, Xue Feng et, al., Computer Science, Computer Vision and Pattern Recognition, arXiv:1812.01049

[5] A Fully Automated Deep Learning Network for Brain Tumour Segmentation by Chandan Ganesh Bangalore Yogananda, Tomography 2020, 6(2), 186-193; https://doi.org/10.18383/j.tom.2019.00026

[6] Brain Tumour Segmentation from MRI Images Using Handcrafted Convolutional Neural Network, by Faizan Ullah et. al., Diagnostics 2023, 13(16), 2650; https://doi.org/10.3390/diagnostics13162650

[7] 3D MRI brain Tumour segmentation using autoencoder regularization Andriy Myronenko NVIDIA, Santa Clara, CA arXiv:1810.11654v3 [cs.CV] 19 Nov 2018.

[8] Multimodal Stereotactic Brain Tumour Segmentation Using 3D-Znet by Mohammad Ashraf Ottom et. al., Bioengineering 2023, 10(5), 581; https://doi.org/10.3390/bioengineering10050581

[9] Brain Tumour Segmentation in MRI Images with 3D U-Net and Contextual Transformer Thien-Qua T.NguyenS et. al., arXiv:2407.08470v1 [cs.CV] 11 Jul 2024

[10] Deep Learning Hybrid Techniques for Brain Tumour Segmentation by Khushboo Munir et. al., Sensors 2022, 22(21), 8201; https://doi.org/10.3390/s22218201

[11] 3D-MRI Brain Tumour Detection Model Using Modified Version of Level Set Segmentation Based on Dragonfly Algorithm by Hassan A. Khalil, et. al., Symmetry 2020, 12(8), 1256; https://doi.org/10.3390/sym12081256

[12] Brain Tumour segmentation using multi-scale attention U-Net with EfficientNetB4 encoder for enhanced MRI analysis, by Preetha R, Jasmine Pemeena Priyadarsini M & Nisha J S , Scientific Reports volume 15, Article number: 9914, 2025

[13] Multiclass MRI Brain Tumour Segmentation using 3D Attention-based U-Net, by Maryann M. Gitonga, arXiv:2305.06203, https://doi.org/10.48550/arXiv.2305.06203, 2023

[14] Advancements in deep learning techniques for brain Tumour segmentation: A survey, by Chandrakant M. Umarani, S.G. Gollagi, Shridhar Allagi, Kuldeep Sambrekar, Sanjay B. Ankali, https://doi.org/10.1016/j.imu.2024.101576, 2024

[15] An improved 3D-UNet-based brain hippocampus segmentation model based on MR images, Volume 24, article number 166, 2024, Qian Yang, Chengfeng Wang, , Kaicheng Pan, Bing Xia.

[16] nnSegNeXt: A 3D Convolutional Network for Brain Tissue Segmentation Based on Quality Evaluation, by Yuchen Liu, Chongchong Song, Xiaolin Ning et.al., Bioengineering 2024

[17] Brain MRI Segmentation using Template-Based Training and Visual Perception Augmentation, by Fang-Cheng Yeh, Electrical Engineering and Systems Science, Image and Video Processing, 4 Aug 2023

[18] Xinyang Liu; et.al "Automatic Segmentation of Rare Pediatric Brain Tumours Using Knowledge Transfer From Adult Data", 2023 IEEE 20th International Symposium on Biomedical Imaging (ISBI).

[19] M.W. Wagner et al., "Radiomic features based on MRI predict progression-free survival in pediatric diffuse midline glioma/diffuse intrinsic pontine glioma", Can Assoc Radiol J, pp. 8465371221109921, 2022.

[20] Pseudo Computed Tomography generation using 3D deep learning – Application to brain radiotherapy - TheraPanacea, Apr. 2023, [online] Available: https://www.therapanacea.eu/pseudo-computed-tomographygeneration-using-3d-deep-learning-application-to-brainradiotherapy/.
[21] Mohammad Raihan Goni, "Salient feature extraction using Attention for Brain Tumour segmentation", 2022 IEEE International Conference on Computing (ICOCO)
[22] Anurag Goswami et.al, "An Analysis of Image Segmentation Methods for Brain Tumour Detection on MRI Images", 2020 IEEE 9th International Conference on Communication Systems and Network Technologies (CSNT)
[23] Toufique A. Soomro et.al , "Image Segmentation for MR Brain Tumour Detection Using Machine Learning: A Review, IEEE Reviews in Biomedical Engineering.
[24] Enhao Wang et. al, "TransUNet with Attention Mechanism for Brain Tumour Segmentation on MR Images", 2022 IEEE International Conference on Artificial Intelligence and Computer Applications (ICAICA).
[25] Riyanto Sigit, Zainal Arief and Mochamad Mobed Bachtiar, "Development of Healthcare Kiosk for Checking Heart Health", EMITTER International Journal of Engineering Technology, 2015.
[26] V. Dhanve and M. Kumar, "Detection of brain Tumour using k-means segmentation based on object labeling algorithm", 2017 IEEE InternationalConference on Power Control Signals and Instrumentation Engineering (ICPCSI), pp. 944-951, 2017.
[27] S. Bauer, R. Wiest, L. P. Nolte and M. Reyes, "A survey of MRI-based Medical Image Analysis for Brain Tumour Studies", Physics Medicine Biology, vol. 58, pp. 97-129, Jul. 2013.
[28] S. Hussaina, S. M. Anwara and M. Majidb, "Segmentation of Glioma Tumours in Brain Using Deep Convolutional Neural Network", Neurocomputing, vol. 282, pp. 248-261, Mar. 2018.
[29] N. Kaur and M. Sharma, "Brain Tumour detection using self-adaptive K- means clustering", 2017 International Conference on Energy Communication Data Analytics and Soft Computing (ICECDS), pp. 1861-1865, 2017.
[30] https://www.researchgate.net/publication/320554561_Digital_Image_Processing_Techniques_-_A_Survey.
[31] "About your brain Tumour surgery for pediatrics,"2021. Accessed:Jun. 25, 2022. [Online]. Available: https://www.mskcc.org/cancer-care/patient-education/pediatric-brain-surgery
[32] T. Imtiaz et al.: Automated Brain Tumour Segmentation Based on Multi-Planar Superpixel Level Features Extracted, IEEE Access, Digital Object Identifier 10.1109/ACCESS.2019.2961630.
[33] L. Zhao and K. Jia, Multiscale CNNs for brain Tumour segmentation and diagnosis, Comput. Math. Methods Med., vol. 2016, Mar. 2016, Art. no. 8356294.
[34] N. Nabizadeh and M. Kubat, Brain Tumours detection and segmentation in MR images: Gabor wavelet vs. statistical features, J. Comput. Elect. Eng., vol. 45, pp. 286301, Jul. 2015.
[35] Center for Biomedical Image Computing and Analytics, University of Pennsylvania, "Image processing portal- https://ipp.cbica.upenn.edu/," A web accessible platform for imaging analytics, 2015.
[36] F. Isensee, P. Kickingereder, W. Wick, M. Bendszus, and K. H. Maier Hein, "Brain Tumour segmentation and radiomics survival prediction: Contribution to the BRATS 2017 challenge," in Proc. Int. Conf. Med. Image Comput. Comput.-Assist. Intervent Brainlesion Workshop, 2017, pp. 287–297.
[37] X. Zhao, Y. Wu, G. Song, Z. Li, Y. Zhang, and Y. Fan, "A deep learning model integrating FCNNs and CRFs for brain Tumour segmentation," Med. Imag. Anal., vol. 43, pp. 98–111, 2018.
[38] U.Baid, et al., The RSNA-ASNR-MICCAI BraTS 2021 Benchmark on Brain Tumor Segmentation and Radiogenomic Classification, arXiv:2107.02314, 2021.
[39] B. H. Menze, A. Jakab, S. Bauer, J. Kalpathy-Cramer, K. Farahani, J. Kirby, et al. "The Multimodal Brain Tumor Image Segmentation Benchmark (BRATS)", IEEE Transactions on Medical Imaging 34(10), 1993-2024 (2015) DOI: 10.1109/TMI.2014.2377694