



# Analysis Brain Tumor Segmentation Using a custom 3D UNet Model on Limited Dataset

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## ABSTRACT

Semantic segmentation plays a pivotal role within the theoretical domain, facilitating a meticulous and precise comprehension of medical scans at the pixel level. In this scholarly contribution, I shall elucidate the results of my research endeavours subsequent to the implementation of a custom 3D Net model. The essence of this work lies in the comprehensive evaluation and analysis of these models using the BraTS 2020 dataset. This endeavour aims to furnish medical professionals with essential insights for enhancing their understanding and enabling informed decision-making when faced with diverse medical challenges, especially when the data.

Keywords—BrainTumor, 3DUnet, DiceLoss, FocalLoss, MedSem, UniverSeg, Segmentation, MRI Scans, FCT, electron microscopy images, enhancing tumour, peritumoral edema, necrotic and non-enhancing tumour

## I. INTRODUCTION

This research paper introduces an implementation focused on the critical task of semantic segmentation within the realm of computer vision. Semantic segmentation involves the precise assignment of labels to each individual pixel within an image, and its applications span a wide range of fields, including autonomous driving, image and video analysis, medical imaging, and scene understanding. Notably, deep learning techniques have consistently demonstrated significant advancements and effectiveness in the domain of semantic segmentation.

The primary emphasis of this paper centres on the segmentation of brain tumours. We conduct a comprehensive comparative analysis of variable segmentation models while employing the BraTS 2021 dataset. The principal objective of this project is to provide valuable insights and comparisons intended for researchers and medical practitioners with a vested interest in brain tumour diagnosis through semantic segmentation.

Our exploration delves into the practical implementation of TensorFlow models, with a specific focus on the examination of the Unet [9] architecture. These neural networks have garnered attention as recent positions for semantic segmentation tasks.

The core aim of our investigation is to gain a comprehensive understanding of the architectural intricacies of these individual models and to elucidate their operational mechanisms.

To enhance the accessibility and utility of our work, we have undertaken meticulous documentation of the codebase. This documentation includes explicit and comprehensive instructions that facilitate ease of use. Moreover,

our documentation encompasses in-depth explanations of the training procedures applied in the context of our research. In the pursuit of efficiency, we have also harnessed pre-trained weights, which expedite the fine-tuning of the model on our specific datasets, streamlining the research process.

## II. LITERATURE SURVEY

The Brain Tumor Segmentation (BraTS) dataset undergoes updates and improvements from year to year. BraTS 2019 includes a substantial number of patient cases with high-resolution brain MRI scans. The dataset includes multi-modal images, including T1-weighted, T2-weighted, FLAIR, and post-contrast T1-weighted images. The tumor annotations in BraTS 2019 were carefully delineated by expert radiologists. The dataset provides ground truth segmentations for glioblastoma, astrocytoma, and oligodendroglioma tumors. BraTS 2019 was used as a benchmark for evaluating brain tumor segmentation algorithms, with participants in the BraTS Challenge submitting their segmentation results for evaluation. BraTS 2020, like its predecessor, is known for its large and high-quality dataset, providing a wide variety of multi-modal MRI images and expert annotations for brain tumor segmentation.

BraTS 2020 introduced new sub-tasks in the BraTS Challenge, including the segmentation of three tumor sub-compartments: enhancing tumor, peritumoral edema, and non-enhancing tumor. This addition aimed to further advance the field by encouraging the development of more fine-grained segmentation methods. BraTS 2020 also emphasized the importance of modeling tumor heterogeneity by providing more extensive annotations and adding more tumor types, making the dataset more representative of real-world clinical scenarios. The 2020 dataset continues to be highly relevant to clinical practice, as accurate brain tumor segmentation is crucial for diagnosis, treatment planning, and patient monitoring.

UNet is a convolutional neural network (CNN) architecture that was developed for semantic segmentation tasks in medical image analysis. It was introduced by Olaf Ronneberger, Philipp Fischer, and Thomas Brox in 2015. UNet has become a foundational architecture for various image segmentation tasks, particularly in the medical field, due to its effectiveness in capturing fine-grained details and preserving spatial context. Here's a brief overview of UNet's architecture. The encoder consists of several convolutional and max-pooling layers that progressively reduce the spatial dimensions and increase the depth of feature maps.

The decoder, on the other hand, comprises up-sampling and concatenation operations to recover spatial information and generate high-resolution feature maps. A distinctive feature of UNet is the inclusion of skip connections. These connections link corresponding encoder and decoder layers, enabling the model to retain and reuse feature information at different scales. This helps preserve fine details during the up-sampling process and contributes to more accurate segmentation.

In the middle of the network, there is a bottleneck layer, which typically has the highest feature dimensionality. This layer acts as a bottleneck in the information flow, forcing the network to learn compact and informative representations.

Depending on the specific segmentation task, UNet can have a SoftMax or sigmoid activation function in its final layer. For binary segmentation tasks, a sigmoid function is often used, while for multi-class segmentation, SoftMax is employed. UNet was initially designed for biomedical image segmentation, specifically for the segmentation of neuronal structures in electron microscopy images. However, it has been widely

adopted in various image segmentation tasks, including medical image segmentation (e.g., brain tumor and organ segmentation), industrial inspection, and satellite image analysis. Researchers often customize UNet to suit their specific segmentation tasks. This customization can involve modifying the architecture, incorporating attention mechanisms, or adjusting the loss function to optimize performance for particular applications. UNet is known for its simplicity, effectiveness, and efficiency. It is capable of producing high-quality segmentation results with relatively small amounts of training data. The skip connections allow it to capture both local and global context, making it suitable for tasks with varying scales and complex object shapes. While UNet is powerful, it may still face challenges with imbalanced datasets, handling class imbalance in segmentation tasks, and the precise delineation of object boundaries, which can be particularly important in medical image analysis.

Overall, UNet remains a popular choice for image segmentation tasks due to its architectural design and adaptability for various applications. Researchers and practitioners continue to build on its foundation by extending and customizing the architecture to address specific challenges in segmentation.

Our study involved the studying and understanding of experiments across several datasets to illustrate the robustness of the 3D-UCaps framework, encompassing iSeg-2017, LUNA16, Hippocampus, and Cardiac datasets. In our research, we have demonstrated that our method consistently surpasses previous Capsule networks and 3D-Unets. The key innovation, Dilated Dense Attention Unet [8] (DDA Unet), capitalizes on the inclusion of spatial and channel attention gates within each dense block. These gates enable selective focus on pivotal feature maps and regions. Furthermore, dilated convolutional layers have been employed to manage GPU memory efficiently and expand the network's receptive field.

Our investigation also entailed the implementation of various Unet Models for Image Segmentation, including Unet, RCNN-Unet, Attention Unet, RCNN-Attention Unet, and Nested Unet [9]. The introduction of Attention gates (AG) [10] has been a significant development in the realm of medical imaging, as it autonomously learns to concentrate on target structures of varying shapes and sizes. Models trained with AGs implicitly acquire the ability to suppress irrelevant regions in input images while accentuating salient features relevant to specific tasks. Consequently, there is no longer a need for external tissue/organ localization modules in cascaded convolutional neural networks (CNNs).

To address the demand for efficient skin lesion segmentation [11], we have designed a lightweight model that delivers competitive performance with minimal parameters and computational complexity. Our Recurrent Convolutional Neural Network (RCNN) and Recurrent Residual Convolutional Neural Network (RRCNN) models, named RU-Net and R2U-Net [12], draw on the strengths of UNet, Residual Networks, and RCNN. These architectures offer several advantages for segmentation tasks, including improved feature representation, making them well-suited for medical image segmentation on benchmark datasets like blood vessel segmentation in retinal images, skin cancer segmentation, and lung lesion segmentation.

The UNet 3+ model [13], which integrates full-scale skip connections and deep supervisions, has been developed to enhance segmentation accuracy. These skip connections merge low-level details with high-level semantics from feature maps of various scales. Deep supervision fosters the acquisition of hierarchical representations from the amalgamated full-scale feature maps. UNet 3+ is particularly advantageous for organs that appear at varying scales. In addition to boosting accuracy, this model reduces network parameters to enhance computational efficiency. We have also introduced a

hybrid loss function and a classification-guided module to refine organ boundaries and mitigate over-segmentation in non-organ images, thereby yielding more precise segmentation results.

Lastly, we introduce Swin-Unet [14], a pure Transformer-based approach for medical image segmentation. This model utilizes tokenized image patches and employs a Transformer-based U-shaped Encoder-Decoder architecture with skip-connections for local-global semantic feature learning. The encoder leverages hierarchical

Swin Transformers with shifted windows to extract context features, while the decoder, based on symmetric Swin Transformers, performs up-sampling to restore spatial feature map resolution. Experiments on multi-organ and cardiac segmentation tasks have shown that this pure Transformer-based approach outperforms methods relying on full-convolution or combinations of transformers and convolutions.

From this it is evident that the UNet models are used extensively in medical segmentation fields

### III. METHODOLOGY

The Brain Tumour Segmentation (BraTS) dataset is widely used in the field of medical image analysis, particularly for brain tumour segmentation, due to several compelling reasons. The BraTS dataset encompasses various types of brain tumours, including glioblastoma, astrocytoma, and oligodendroglioma, among others. It includes multiple MRI modalities, such as T1-weighted, T2-weighted, FLAIR, and post-contrast T1-weighted images. This diversity in tumour types and imaging modalities allows researchers to test the robustness and adaptability of segmentation algorithms across different clinical scenarios. The BraTS dataset is substantial in size, with a substantial number of patient cases, and it is meticulously annotated by experts.

The dataset includes both training and testing subsets, facilitating the development and evaluation of segmentation algorithms. The large, high-quality dataset minimizes the risk of overfitting and enhances the generalization of models to real-world clinical data. Brain tumour segmentation is a challenging task due to the complex shapes and infiltrative nature of tumours. The BraTS dataset includes ground truth segmentation that are carefully delineated by radiologists, providing a valuable benchmark for algorithm evaluation. Researchers can compare the performance of their methods against these expert annotations to assess the accuracy and reliability of their segmentation models.

The BraTS Challenge, associated with the dataset, has been held annually and has become a benchmark for the evaluation of brain tumour segmentation algorithms. Researchers from around the world participate in this challenge, contributing to a collaborative and competitive environment that drives innovation in the field. It allows for fair comparisons between different approaches and encourages the development of state-of-the-art methods. Brain tumour segmentation is of critical importance in clinical practice.

Accurate tumour segmentation plays a crucial role in the diagnosis, treatment planning, and monitoring of brain tumour patients. Algorithms developed and validated on the BraTS dataset can potentially be integrated into clinical workflows, aiding radiologists and healthcare professionals in making informed decisions. The BraTS dataset is publicly available, making it accessible to researchers, enabling them to conduct experiments and develop segmentation models without the need for extensive data collection and annotation, which can be costly and time-consuming. The BraTS dataset has evolved over the years, incorporating new challenges, sub-datasets, and updated annotations. This continuous development ensures that it remains a relevant and up-to-date resource for the research community. The BraTS dataset is a valuable resource for brain tumour segmentation

research due to its diversity, size, expert annotations, benchmark status, clinical relevance, and accessibility. It serves as a foundation for the development and evaluation of state-of-the-art segmentation algorithms, ultimately contributing to improved medical diagnosis and treatment for brain tumour patients.

### A. Dataset

The BraTS 2020 [4][5][6][7] dataset is a widely recognized and extensively employed dataset in the domain of medical image analysis, primarily focusing on the segmentation of brain tumours. This dataset encompasses multimodal Magnetic Resonance Imaging (MRI) scans stored in the NIfTI file format. These scans encompass four distinct MRI sequences, each serving a specific purpose:

- a) Native (T1): Comprising T1-weighted MRI scans.
- b) Post-contrast T1 (T1CE): Encompassing Post-contrast T1-weighted MRI scans.
- c) T2-weighted (T2): Incorporating T2-weighted MRI scans.
- d) T2 Fluid Attenuated Inversion Recovery (T2-FLAIR): Encompassing T2-FLAIR MRI scans.

It is noteworthy that these MRI scans have been acquired from various clinical protocols and scanners spanning multiple institutions. Notably, data contributors to this dataset have emanated from a total of 19 different institutions, attesting to its broad representation.

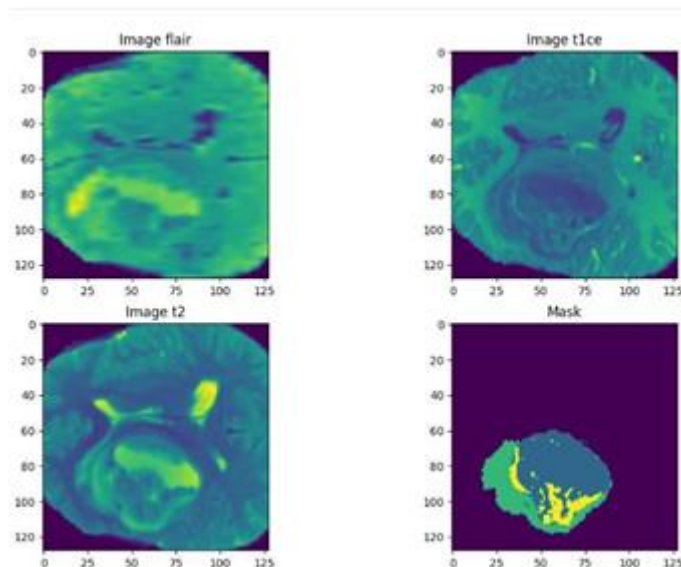
An intrinsic facet of this dataset is the meticulous manual segmentation undertaken by one of four raters. This segmentation process adheres to a rigorously standardized annotation protocol. These initial annotations are subsequently subjected to comprehensive review and validation by experienced neuro-radiologists. The annotations encapsulate diverse tumour regions, classifying them as follows:

1. GD-enhancing tumour (ET), identified and labelled as 4.
2. Peritumoral edema (ED), designated with the label 2.
3. Necrotic and non-enhancing tumour core (NCR/NET), demarcated and marked with the label 1.

To ensure uniformity and compatibility for research and analytical purposes in the domain of brain tumour segmentation, the dataset has undergone crucial pre-processing steps. These steps encompass co-registration to a common anatomical template, interpolation to a uniform resolution of  $1\text{mm}^3$ , and skull-stripping. Such pre-processing measures have been diligently executed to guarantee the consistent formatting of the data, thus rendering it amenable to research and analysis within the realm of brain tumour segmentation.

### B. Procedure

The primary objective of this endeavor is to streamline the process of model development while maximizing efficiency. In pursuit of this goal, we will embark on a series of data preprocessing steps aimed at preserving pertinent information while upholding model accuracy. A notable challenge encountered in this regard pertains to discrepancies in the number of scans and available masks due to erroneous labelling within segmentation masks. Consequently, we have been compelled to exclude a specific scan from the dataset. The initial phase of our data preprocessing entails the removal of T1G images, as their expected contribution to the model's performance is deemed negligible.



**Fig1 Plotting Post-contrast T1, T2-weighted T2, Fluid Attenuated Inversion Recovery and given segmentations**

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Subsequent to the exclusion of these images, we will undertake cropping of the scans to retain only the relevant pixels, eliminating redundant empty space. Furthermore, scans characterized by an empty space of less than 8% will be selectively removed from consideration. Our next step involves the conversion of the NIfTI images into the .ndy format, essentially saving them as NumPy arrays. This process will be accompanied by resizing and scaling to align with the model's requirements. Additionally, we will consolidate the three input arrays into a single combined array.

Given that TensorFlow lacks a built-in data generator tailored to NumPy arrays, we will develop a straightforward custom data generator to facilitate data handling. This custom data generator will consist of two core functions: the first function will be responsible for loading the NumPy array from the specified path, while the second function will

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function will be responsible for loading the NumPy array from the specified path, while the second function will manage batching and yield these batches as needed.



$$L_{dice} = \frac{2 * \sum p_{true} * p_{pred}}{\sum p_{true}^2 + \sum p_{pred}^2 + \epsilon}$$

**Fig2DiceLoss**

Subsequent to the meticulous data preparation process, the processed data will be channelled into a custom 3D Unet model. Notably, our selection of loss functions will encompass both the dice loss and focal loss. This choice also offers us the flexibility to incorporate custom weights into the loss functions in the future, as circumstances may require.

$$Focal Loss = - \sum_{i=1}^{i=n} (i - p_i)^{\gamma} \log_b(p_i)$$

**Fig 3FocalLoss**

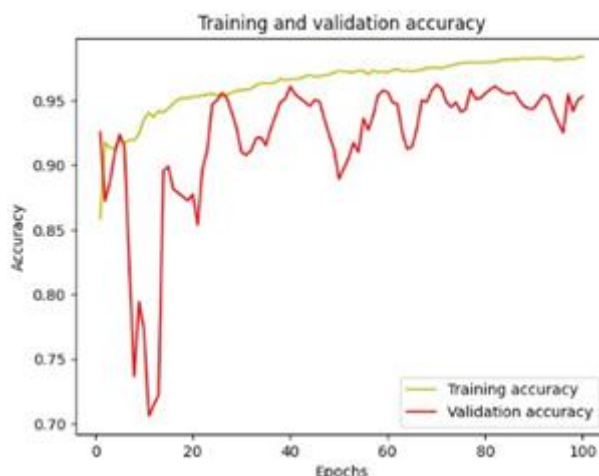
This structured and methodical approach is poised to expedite the development and refinement of our model, all the while upholding its accuracy and ensuring the optimal utilization of the available data resources.

#### IV. RESULTS AND DISCUSSION

Upon a comprehensive analysis conducted on a restricted dataset, encompassing a total of 95 scans, our model has yielded a Mean Intersection over Union (Iou) score of 0.5692228. In forthcoming experiments, we intend to harness the full dataset and adopt a patch-based approach to further augment our model's performance.

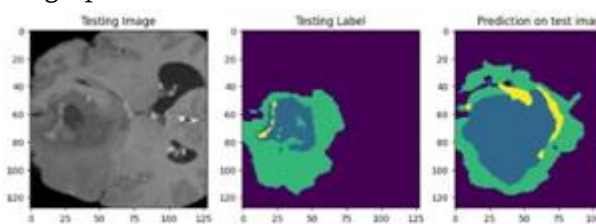
**Fig1.2Plotting Training and validation loss**

Furthermore, we plan to delve into the application and evaluation of the "Segment Anything Model" [7] developed by META. This model, while not originally designed for medical images, presents an noteworthy avenue for experimentation. An inherent challenge in this endeavor pertains to adapting the input layers to accommodate all three types of scans.



**Fig 1.3**PlottingTrainingandvalidationaccuracy

Followingtheimplementationoftheseexperiments,wewillundertakeacomprehensivecomparativeanalysisisthatpitsthe"SegmentAnythingModel" against our custom Unet architecture. AnticipationssuggestthatourcustomUnet,bolsteredbytheutilizationofthecompletedataset,willlikelyoutperformthe"SegmentAnythingModel,"yieldingsuperiorresults.



**Fig 1.4** Plotting Testing image, Testing Label andPredictionontestimage

In addition to these specific experiments, our paperoffersathoroughandexhaustiveanalysisofsemanticsegmentationusingwell-establishedmodels, namely UniverSeg, FCT, and Meds AM.These research findings furnish invaluable insightsfor both researchers and practitioners operating inthe intersection of medicine and machine learning.Ourstudyhighlightstheeffectivenessandresilienceof these models, underscored by their applicabilityin addressing diverse segmentation tasks within the domainofmedicalimageanalysis.

## V. FUTUREWORK

In the field of the medical image analysis, thesegmentationoftumors,mitochondria,orotherstructuresofinterestoftenreliesontheutilizationofdeeplearningarchitecturessuchasUNet,VNet,andvariousencoder-decodernetworks.Notably,continuous advancements have been made in thedevelopmentofUNet-basedarchitectures,includinginnovationslikeAttentionUNet,whichaimtoenhance the precision and efficacy of segmentationtasks.

Theprimaryobjectiveofthepresentresearchpaperistoestablishafoundationalframeworkthatwillserveasacornerstoneforforthcoming experiments. These experiments willrevolvearoundthecomparativeanalysisofstate-of-the-art



machine learning models, including but not limited to UniverSeg[3], FCT[1], and MedSAM[2], specifically in the context of medical image segmentation. It is important to note that although numerous novel and promising models have emerged in the machine learning community, their direct application to medical image segmentation is impeded by the distinct nature of the data they were originally trained on.

One pivotal avenue of exploration in this study involves the application of transfer learning techniques. The aim is to adapt and fine-tune these cutting-edge models on medical image datasets, thereby enabling a meaningful comparison of their segmentation performance against conventional, established architectures. The intent is to ascertain whether transfer learning can bridge the gap between these disparate domains and potentially leverage the rich representations learned by state-of-the-art models in more general image analysis tasks for the specific domain of medical image segmentation.

Additionally, an important innovation in this research involves extending the input modality of the models. Rather than operating solely on 2D images, we intend to equip these models with the capability to process 3D stacked arrays. This modification is motivated by the inherent advantages of 3D information in capturing spatial relationships and contextual details. By allowing these models to operate in a three-dimensional space, we anticipate that they will acquire a more comprehensive understanding of medical image data, thus facilitating the extraction of pertinent features and improving segmentation accuracy.

In conclusion, this study endeavors to provide a solid foundation for future investigations in medical image segmentation. By adapting state-of-the-art machine learning models to the medical domain through transfer learning and enhancing their capacity to process 3D data, we aim to advance the state of the art in this critical field and contribute to the development of more accurate and effective tools for medical image segmentation.

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