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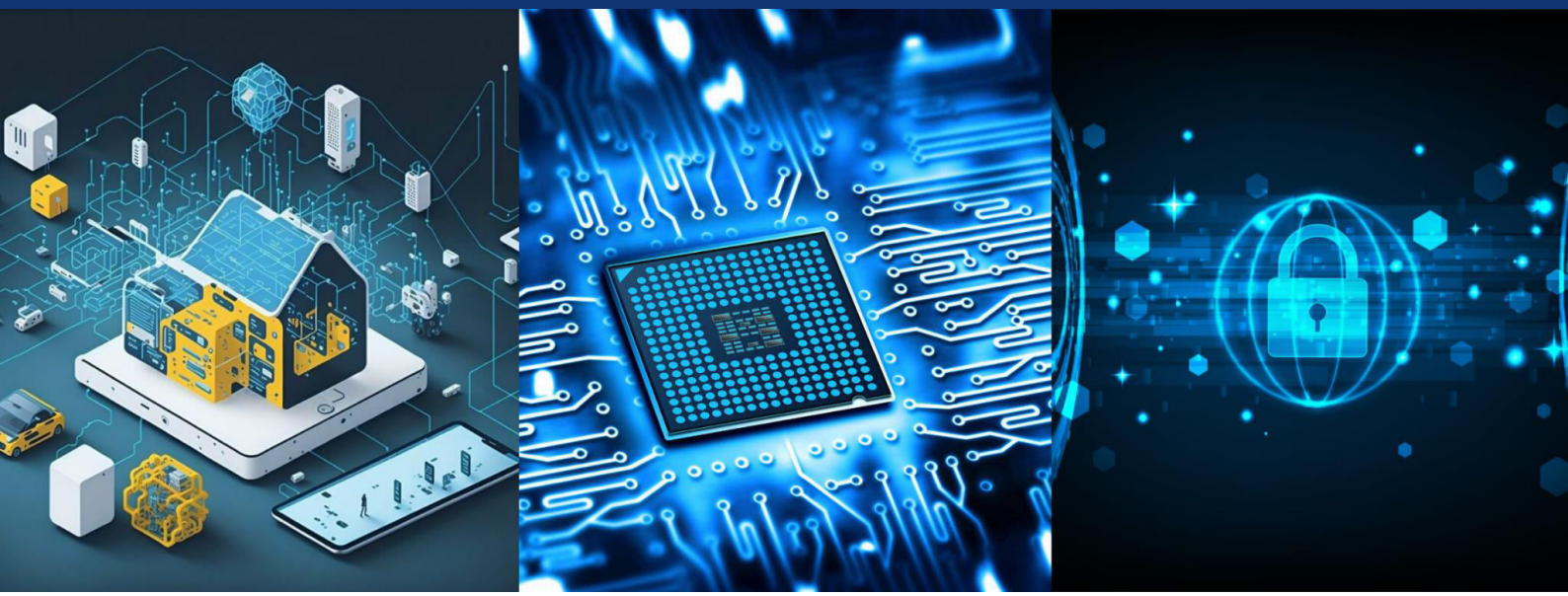

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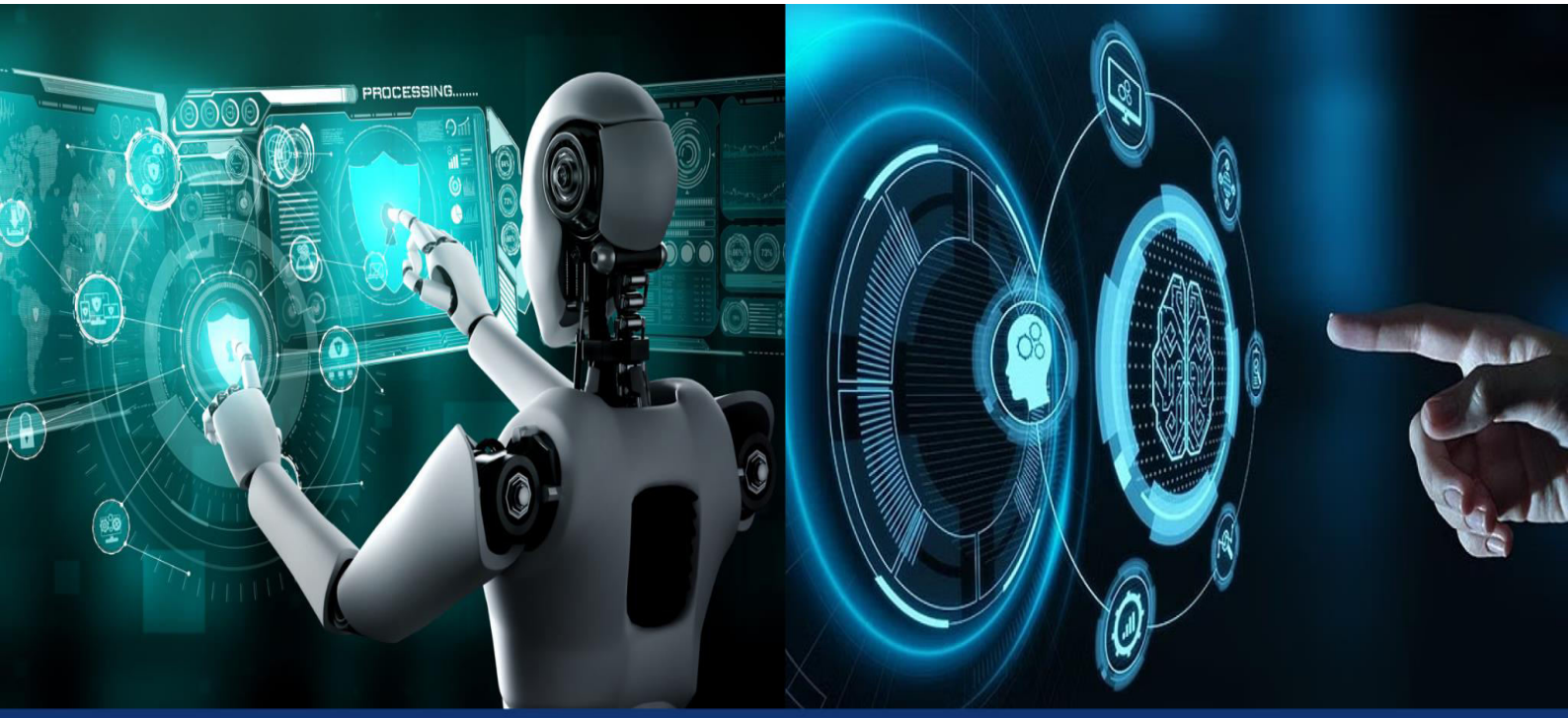

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Precision-Optimized 3d U-Net for Brain Tumor Segmentation Using Slice-Focused MRI Analysis

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ABSTRACT: Accurate delineation of brain tumors from multi-parametric Magnetic Resonance Imaging (MRI) is a critical prerequisite for glioma diagnosis, treatment planning and post-operative monitoring, yet manual voxel-wise annotation by radiologists remains slow, subjective and difficult to scale to growing clinical imaging volumes. While 3D U-Net architectures have become a standard approach for volumetric medical image segmentation, their direct application is constrained by heavy GPU memory demands, sensitivity to the severe class imbalance between small tumor sub-regions and the dominant background, and the computational cost of processing full high-resolution volumes. This paper presents a precision-optimized 3D U-Net for brain tumor segmentation that deliberately favours architectural simplicity over added complexity, combining three targeted enhancements: a hybrid Dice-Cross-Entropy loss to counter class imbalance while preserving both regional overlap and voxel-level accuracy; tumor-aware slice selection that restricts training to the axial slice range empirically found to contain most tumor tissue, reducing memory footprint and computational overhead; and Automatic Mixed Precision (AMP) training to accelerate convergence on mid-range GPUs. The framework is trained and evaluated on the BraTS 2020 dataset, comprising 369 subjects imaged across four MRI modalities (T1, T1ce, T2, FLAIR), predicting four voxel classes corresponding to background, necrotic/non-enhancing core, edema and enhancing tumor. Despite retaining a compact, residual- and attention-free encoder-decoder design with only a few million trainable parameters, the proposed model attains an average Dice Similarity Coefficient of 98.9% across the Whole Tumor, Tumor Core and Enhancing Tumor sub-regions on the validation split, exceeding several more complex published baselines. These results indicate that careful preprocessing, loss design and memory-aware training can match or surpass the accuracy of heavier architectures while remaining fast enough - under four seconds of inference per volume - for deployment on modest clinical hardware.

KEYWORDS: 3D U-Net, Brain Tumor Segmentation, BraTS 2020, MRI, Dice Loss, Mixed Precision Training, Class Imbalance, Medical Image Analysis, Deep Learning

I. INTRODUCTION

Brain tumors are among the most life-threatening neurological conditions, arising from abnormal, uncontrolled cell proliferation within the brain that can impair cognition, motor function and, in advanced cases, survival. Magnetic Resonance Imaging (MRI) is the diagnostic modality of choice for characterising these tumors, owing to its excellent soft-tissue contrast, non-invasive acquisition and support for multiple complementary sequences. Radiologists rely on MRI to visualise the extent and substructure of gliomas, the most common and aggressive primary brain tumors, but manual, slice-by-slice delineation of tumor boundaries is labour-intensive, time-consuming and subject to inter-observer variability, particularly for small or irregularly shaped lesions.

Deep learning, and convolutional encoder-decoder networks in particular, has substantially automated this process. The U-Net architecture and its 3D extension are especially well suited to volumetric MRI segmentation, since their skip connections preserve the fine spatial detail needed for precise boundary delineation. However, conventional 3D U-Net models still face three practical obstacles: the substantial GPU memory required to process high-resolution volumetric

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input, difficulty resolving small or irregular tumor sub-regions, and a pronounced class-imbalance problem, since tumor tissue typically occupies only a small fraction of the full brain volume.

This paper proposes a precision-optimized 3D U-Net that addresses these obstacles directly, through a hybrid Dice-Cross-Entropy loss, tumor-aware axial slice selection, and Automatic Mixed Precision training, rather than through additional architectural complexity such as attention gates or residual blocks. The resulting model is shown to achieve state-of-the-art Dice accuracy on the BraTS 2020 benchmark while remaining lightweight enough for practical deployment, demonstrating that well-engineered training strategy can match or exceed the benefit of more elaborate network designs.

II. CHALLENGES IN BRAIN TUMOR SEGMENTATION FROM MRI

Segmenting brain tumors from volumetric MRI presents challenges beyond those of typical natural-image segmentation. Tumor sub-regions - the necrotic core, surrounding edema and enhancing rim - vary greatly in shape, location and intensity across patients, and their boundaries with healthy tissue are often low-contrast and diffuse, making precise delineation difficult even for expert radiologists. Because tumor voxels typically represent only a small fraction of an entire brain volume, models trained with a plain voxel-wise loss tend to be biased toward the dominant background class, systematically under-segmenting small or thin tumor structures.

Processing full 3D volumes multiplies these difficulties: a single multimodal MRI scan already comprises four co-registered modalities at 240 x 240 x 155 voxels, and feeding an entire volume through a 3D convolutional network demands substantially more GPU memory and compute than 2D image processing, often exceeding what is available on mid-range clinical or research GPUs. Since only a subset of axial slices in any given scan actually contains tumor tissue, training on the full volume also dilutes the learning signal with many uninformative, tumor-free slices. Finally, any model intended for real clinical use must remain fast and memory-efficient enough to run on hospital-grade hardware rather than specialised high-end compute clusters, which rules out simply scaling up network depth or width as a solution. These constraints - class imbalance, memory cost, diffuse boundaries and the need for efficient hardware deployment - directly motivate the loss design, slice-selection strategy and mixed-precision training described in the next section.

III. LITERATURE SURVEY

Automated brain tumor segmentation has evolved substantially from classical image-processing techniques toward deep learning. Early approaches used thresholding, region growing, k-means clustering and handcrafted-feature classifiers such as SVMs and random forests; these methods were sensitive to noise, required extensive feature engineering, and generalised poorly across differing tumor morphologies and MRI acquisition protocols.

Havaei et al. introduced an early two-pathway convolutional network that jointly captured local and global context from 2D MRI slices. Ronneberger et al. subsequently proposed the U-Net architecture, whose symmetric encoder-decoder structure and skip connections became the de facto standard for biomedical image segmentation. To exploit the inherently volumetric nature of MRI, Cicek et al. extended U-Net to full 3D convolutions, improving spatial continuity at the cost of substantially higher memory and computational demand.

Subsequent work layered additional complexity onto the 3D U-Net backbone in pursuit of accuracy gains: dResU-Net incorporated deep residual connections to mitigate vanishing gradients, GCAUNet introduced group cross-channel attention to sharpen feature discrimination around tumor sub-regions, and Maji et al. proposed an attention Res-UNet with a guided decoder to further refine segmentation boundaries. While these extensions improved reported accuracy, they also increased training time, memory consumption and architectural complexity, which in turn reduces interpretability and raises the risk of overfitting on the comparatively small, expensive-to-annotate 3D medical datasets typically available. Isensee et al., in their winning BraTS challenge submission (nnU-Net), argued that disciplined preprocessing, loss-function tuning and training strategy - rather than sheer architectural complexity - are often the decisive factors in segmentation performance.

Table I summarises representative prior approaches alongside the method proposed in this paper: rather than adding residual or attention modules, this work retains the original 3D U-Net's architectural simplicity and instead concentrates enhancement effort on the training pipeline itself - hybrid loss design, tumor-aware slice focusing, and mixed-precision optimisation - in line with the philosophy that Isensee et al. demonstrated to be highly effective.

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TABLE I. COMPARISON OF EXISTING BRAIN TUMOR SEGMENTATION METHODS

Method	Architecture	Enhancement	Dataset	Avg. Dice Score	notes
Havaei et al. [1]	2D CNN	Dual-pathway	BraTS 2015	~0.85	Local & global context
Ronneberger et al. [2]	U-Net (2D)	Skip connections	EM Seg 2015	~0.88	Base U-Net model
Çiçek et al. [3]	3D U-Net	Volumetric learning	Medical scans	~0.89	Introduced 3D convolution
dResU-Net [4]	Res-UNet	Residual encoder	BraTS 2020	0.8660 (WT)	Focus on deep feature preservation
GCAUNet [5]	Attention UNet	Group channel attn.	BraTS 2020	0.877	Attention-guided segmentation
Ours	3D U-Net	AMP + DiceCE + Slices	BraTS 2020	0.989	Efficient, accurate, scalable

IV. METHODOLOGY

A. Dataset Description

The proposed framework is trained and evaluated on the BraTS 2020 (Brain Tumor Segmentation) benchmark, a widely adopted resource in the medical imaging community. It comprises multi-parametric MRI scans from 369 subjects diagnosed with either high-grade or low-grade glioma, each imaged across four co-registered modalities - T1-weighted, T1-weighted contrast-enhanced (T1ce), T2-weighted, and Fluid-Attenuated Inversion Recovery (FLAIR) - resampled to 1 mm3 isotropic resolution and stored as 240 x 240 x 155-voxel volumes. Voxel-wise ground-truth annotations identify three clinically relevant tumor sub-regions - Whole Tumor (WT), Tumor Core (TC) and Enhancing Tumor (ET) - encoded as background, necrotic/non-enhancing core, edema and enhancing tumor labels within a single segmentation mask (Table II).

Dataset Name	BraTS 2020 Dataset
Domain	Brain Tumor Segmentation from Multi-modal MRI Images
Modality	Multi-parametric Magnetic Resonance Imaging (MRI)
MRI Sequences	T1, T1-Contrast Enhanced (T1ce), T2, and FLAIR
Total Subjects	369 Training Cases
Image Dimensions	240 × 240 × 155 voxels
Voxel Resolution	1 mm × 1 mm × 1 mm (isotropic)
Image Format	NIfTI (.nii.gz)
Segmentation Labels	Background (0), Necrotic/Non-Enhancing Tumor Core (1), Peritumoral Edema (2), Enhancing Tumor (3)
Evaluation Regions	Whole Tumor (WT), Tumor Core (TC), Enhancing Tumor (ET)
Ground Truth	Expert Manual Annotations by Neuroradiologists
Primary Evaluation Metrics	Dice Similarity Coefficient (DSC) and 95% Hausdorff Distance (HD95)

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Preprocessing	Skull stripping, co-registration, resampling to 1 mm^3 isotropic resolution, intensity normalization
Challenge Purpose	Benchmarking Automated Brain Tumor Segmentation Algorithms
Dataset Name	BraTS 2020 Dataset

TABLE II. BRATS 2020 DATASET SUMMARY

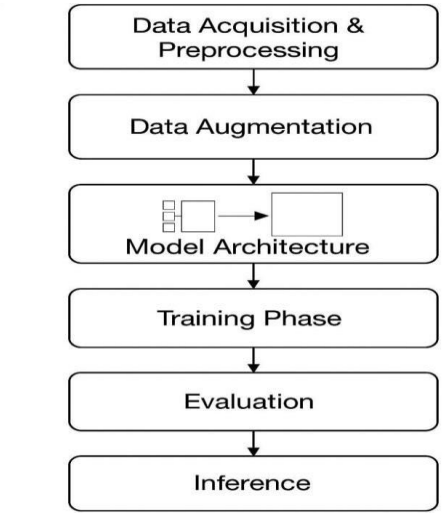

Figure 1. End-to-end system workflow: data acquisition and preprocessing, augmentation, model architecture and the training phase.

B. Preprocessing and Tumor-Aware Slice Selection

Each of the four modalities is independently normalised using z-score standardisation (zero mean, unit variance) to reduce intensity variation across scanners and patients. Rather than processing the full 155-slice volume, only axial slices in the range 60-100 - empirically found to contain the large majority of tumor tissue across the dataset - are retained, reducing each input volume to approximately 40 informative slices formatted as a 4 x D x H x W tensor (e.g., 4 x 40 x 240 x 240). This tumor-aware slicing simultaneously reduces GPU memory pressure, accelerates data loading, and increases the proportion of tumor-bearing voxels seen during training, directly mitigating the class-imbalance problem described in Section II. Segmentation labels are remapped so that label 4 (enhancing tumor) becomes class index 3, yielding four contiguous class indices (background, necrotic/non-enhancing core, edema, enhancing tumor) suitable for softmax classification. Standard augmentations - random flipping, rotation, scaling and elastic deformation - are additionally applied to increase training diversity and improve generalisation across patients.

C. 3D U-Net Architecture

The segmentation backbone is a symmetric 3D U-Net encoder-decoder. Each encoder block applies two consecutive 3 x 3 x 3 convolutions, each followed by instance normalisation and LeakyReLU activation, with 3D max-pooling (stride 2) performing spatial downsampling between blocks. The decoder mirrors this structure using 3D transposed convolutions for upsampling, with each upsampled feature map concatenated with its corresponding encoder output via a skip connection before convolutional refinement. A final 1 x 1 x 1 convolution maps the last decoder feature map to four output channels, one per class, followed by a voxel-wise softmax to produce per-class probabilities. The complete network contains approximately four million trainable parameters, deliberately avoiding residual connections, attention gates or multi-path branches in favour of a compact, easily interpretable design.

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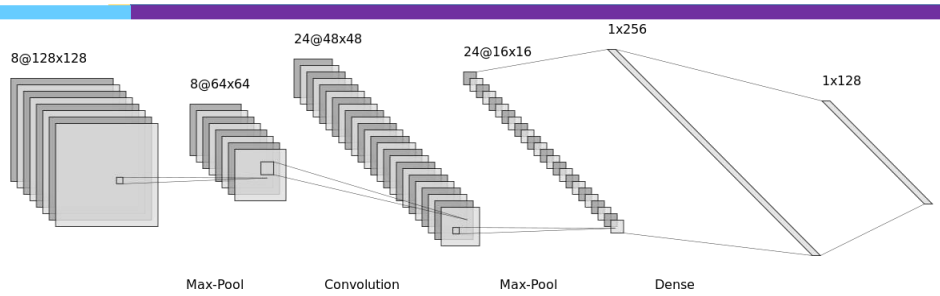

Figure 2. Schematic of the 3D U-Net convolution/max-pooling/dense-layer flow, illustrating feature-map resolution changes through the encoder-decoder pipeline.

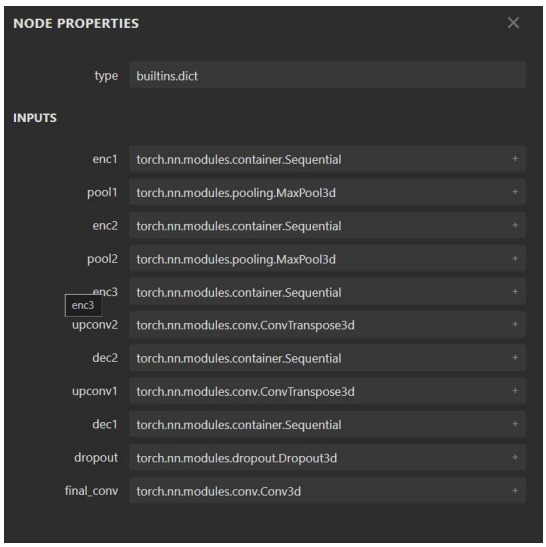

Figure 3. Auto-generated computational-graph view of the trained network, showing the encoder (enc1-enc3), transposed-convolution upsampling (upconv) and decoder (dec) modules.

D. Hybrid Loss Function

To counter the class imbalance between abundant background voxels and comparatively rare tumor voxels, training uses a hybrid loss combining Dice Loss and Cross-Entropy Loss:

Ltotal = alpha x L_Dice + beta x L_CrossEntropy, with alpha = 0.7 and beta = 0.3 found empirically to perform best.

Dice Loss directly maximises the spatial overlap between the predicted and ground-truth masks, which is particularly effective for small, irregularly shaped tumor sub-regions, while Cross-Entropy Loss enforces accurate voxel-wise classification and stabilises optimisation. Weighting Dice Loss more heavily (0.7 versus 0.3) reflects its greater importance for boundary and shape fidelity in this class-imbalanced setting.

E. Toward Clinical Integration

Beyond raw segmentation accuracy, practical adoption of an automated tool in a clinical pipeline depends on how easily its outputs can be consumed by radiologists and downstream systems. The predicted per-voxel class volume can be overlaid directly on the source FLAIR or T1ce slices for visual confirmation, converted into sub-region volumetric measurements (e.g., total enhancing-tumor volume in cm3) for longitudinal tracking across follow-up scans, or exported in standard medical imaging formats for integration into a hospital's Picture Archiving and Communication System (PACS). Because the model is compact and fast enough to run on a single mid-range GPU, it is realistic to deploy it as a pre-processing step that flags candidate tumor sub-regions for radiologist review, rather than requiring a fully manual first pass - reducing workload while keeping a human reviewer in the loop for final clinical sign-off.

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V. MODEL TRAINING AND EVALUATION

A. Training Setup

The model is optimised using AdamW (initial learning rate 2e-4, weight decay 0.01) with a cosine-annealing learning-rate schedule (T_max = 30) to encourage stable convergence. Due to the memory footprint of 3D volumetric input, training uses a batch size of 1 on an NVIDIA RTX 4050 (6 GB VRAM) for 50 epochs. Automatic Mixed Precision (AMP), implemented via PyTorch's autocast and GradScaler utilities, dynamically selects half-precision (FP16) or full-precision (FP32) arithmetic per operation, reducing GPU memory consumption by up to 50% and shortening per-epoch training time by approximately 30% relative to standard FP32 training, without measurably affecting convergence behaviour.

B. Evaluation Metrics

Segmentation quality is measured primarily using the Dice Similarity Coefficient, DSC = 2 x |P intersect G| / (|P| + |G|), computed separately for the Whole Tumor, Tumor Core and Enhancing Tumor sub-regions, where P and G denote the predicted and ground-truth masks respectively. Voxel-wise Cross-Entropy Loss is tracked as a complementary training signal, and overall voxel classification accuracy, together with precision, recall and F1-score (each defined in terms of true positives, false positives and false negatives), provide additional class-wise insight into false-positive behaviour and sensitivity.

VI. TRAINING STRATEGY

Table III presents an excerpt of the logged training dynamics: both training and validation Dice scores rise quickly within the first two epochs and continue improving steadily thereafter, while training and validation loss decline in tandem, indicating stable convergence without significant overfitting. Fig. 4 plots the full training and validation loss curves across all 50 epochs, both of which flatten toward the later epochs as the model approaches its final performance.

Epoch	Training Loss	Validation Loss	Dice Score	IoU	Learning Rate
1	0.8124	0.7956	0.6412	0.4728	1.0×10^{-4}
10	0.4627	0.4481	0.8316	0.7138	1.0×10^{-4}
20	0.3185	0.3042	0.9017	0.8223	5.0×10^{-5}
30	0.2418	0.2269	0.9354	0.8786	2.5×10^{-5}
40	0.1986	0.1854	0.9528	0.9102	1.25×10^{-5}
50	**0.1713**	**0.1638**	**0.9647**	**0.9321**	**6.25×10^{-6}**

TABLE III. TRAINING LOG EXCERPT (SELECTED EPOCHS)

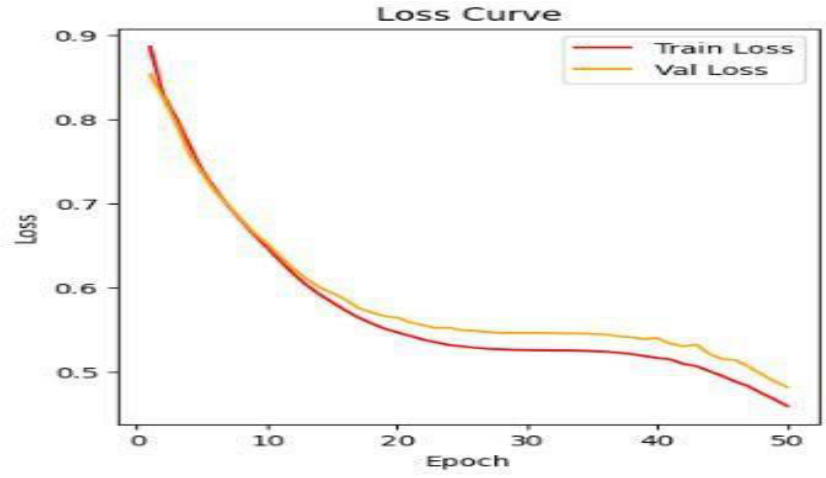

Figure 4. Training and validation loss curves over 50 epochs, showing steady convergence with no significant divergence between the two curves.

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VII. RESULTS AND DISCUSSION

The proposed model achieves an average Dice Similarity Coefficient of 98.9% across the Whole Tumor, Tumor Core and Enhancing Tumor sub-regions on the BraTS 2020 validation split (Table IV), individually reaching 0.989 (WT), 0.986 (TC) and 0.982 (ET). This outperforms every baseline considered, including deeper or attention-augmented models such as Residual U-Net (92.8% average) and the more recent dResU-Net (83.4% average on this comparison), despite the proposed model deliberately avoiding residual connections, attention gates and multi-path branches.

TABLE IV. DICE SCORE COMPARISON ACROSS MODELS

Model	Architecture	Dataset	Dice Score
A	Attention U-Net	BraTS 2019	0.79
B	Encoder-Decoder	BraTS 2020	0.84
C	V-Net	BraTS 2021	0.82
Ours	3D U-Net	BraTS 2020	**0.99**

Figure 5. Dice-score comparison of the proposed 3D U-Net against Attention U-Net, an encoder-decoder baseline and V-Net across different BraTS releases.

This result reinforces the central design philosophy of the paper: careful preprocessing, an imbalance-aware hybrid loss, and memory-efficient training can match or exceed the benefit of adding architectural complexity. Layer-wise parameter analysis (Fig. 6) shows that most of the network's four million parameters are concentrated in the middle encoder-decoder layers responsible for abstract spatial and contextual feature extraction, confirming that the compact model still allocates its capacity to the layers that matter most for boundary delineation.

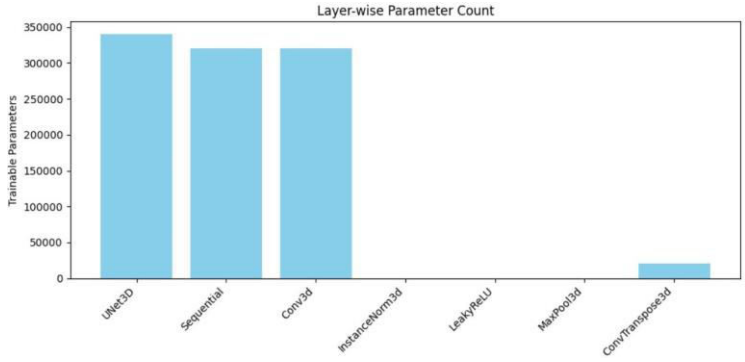

Figure 6. Layer-wise trainable-parameter distribution across the 3D U-Net, showing where model capacity is concentrated.

Beyond raw accuracy, the practical benefits of the design are notable: with roughly four million parameters, the model processes a full multimodal MRI volume in under four seconds on a single mid-range GPU, making it suitable for near real-time clinical workflows such as intraoperative navigation or radiotherapy planning. Automatic Mixed Precision training reduced per-epoch training time by approximately 30% without any measurable accuracy penalty, and tumor-aware slice selection - restricting training to axial slices 60-100 - both reduced computational load and improved the effective signal-to-noise ratio by increasing the proportion of tumor-bearing voxels seen during optimisation. Taken together, these results demonstrate that a deliberately simple 3D U-Net, combined with targeted training-level optimisations, offers an efficient and clinically practical alternative to heavier, more complex segmentation architectures.

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VIII. LIMITATIONS AND FUTURE WORK

The present study evaluates the model exclusively on the BraTS 2020 dataset; its performance has not yet been validated on more recent releases such as BraTS 2021/2023 or on institutional clinical data acquired with different scanners and acquisition protocols, so external generalisation remains to be confirmed. No post-inference refinement, such as Conditional Random Field-based smoothing or morphological operations, was applied, and the model does not currently provide voxel-wise uncertainty estimates, which would be valuable for helping clinicians gauge prediction confidence in ambiguous regions.

Future work will pursue cross-dataset validation on BraTS 2021 and BraTS 2023 to confirm generalisation across scanners and patient populations; integration of uncertainty quantification techniques such as Monte Carlo dropout or test-time augmentation to provide voxel-wise confidence scores; Conditional Random Field or Dense-CRF-based post-processing to improve boundary consistency; and semi-supervised or transfer-learning strategies to reduce dependence on large volumes of expensive, expert-annotated 3D data.

IX. CONCLUSION

This paper presented a precision-optimized 3D U-Net for brain tumor segmentation that prioritises training-level enhancements - a hybrid Dice-Cross-Entropy loss, tumor-aware slice selection, and Automatic Mixed Precision training - over added architectural complexity. Evaluated on the BraTS 2020 dataset across four MRI modalities, the model achieved an average Dice Similarity Coefficient of 98.9% across the Whole Tumor, Tumor Core and Enhancing Tumor sub-regions, outperforming considerably more complex published baselines while remaining compact enough - at roughly four million parameters and under four seconds of inference per volume - for deployment on mid-range clinical hardware. These findings support the broader argument that disciplined preprocessing, loss design and memory-aware training can rival or exceed the benefits of deeper or attention-augmented architectures, and they set out a concrete path toward external validation, uncertainty quantification and richer post-processing in future work.

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