

AI-Based Medical Image Segmentation in Oncology

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ABSTRACT

Accurate tumour segmentation from medical images is a prerequisite for radiation therapy planning, surgical guidance, treatment response assessment, and radiomics-based prognostication. This study developed and benchmarked five deep learning architectures -- U-Net, Attention U-Net, nnU-Net, Swin-UNETR transformer, and a proposed hybrid CNN-Transformer (CT-Hybrid) -- for multi-organ tumour segmentation across four oncology imaging datasets: brain glioma (BraTS 2021, $n = 1,251$ MRI), lung tumour (NSCLC-Radiomics, $n = 422$ CT), liver hepatocellular carcinoma (LiTS, $n = 131$ CT), and pancreatic ductal adenocarcinoma (MSD-Pancreas, $n = 281$ CT). The proposed CT-Hybrid architecture -- combining a ResNet-50 convolutional encoder with a Swin Transformer bottleneck and skip-connected decoder -- achieved the highest mean Dice similarity coefficient (DSC) across all four datasets (brain 0.892, lung 0.874, liver 0.868, pancreas 0.784), outperforming nnU-Net (the current self-configuring benchmark) by 1.4-3.2% DSC on three of four datasets and matching it on liver. For the clinically critical brain tumour enhancing core sub-region, CT-Hybrid achieved $DSC = 0.848 \pm 0.042$ -- significantly above U-Net (0.782 ± 0.058 ; $p < 0.001$) and Attention U-Net (0.814 ± 0.048 ; $p = 0.002$). Inference time of the CT-Hybrid (1.84 s per volume on NVIDIA A100) is compatible with real-time clinical workflow integration. These findings establish the CNN-Transformer hybrid paradigm as the new performance standard for multi-organ oncological image segmentation.

Keywords: Medical image segmentation; Deep learning; U-Net; Swin Transformer; Tumour segmentation; nnU-Net; Radiotherapy planning; Oncology imaging

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1. Introduction

Medical image segmentation -- the pixel- or voxel-level delineation of anatomical structures and pathological regions from radiological images -- is a foundational task in computational oncology, underpinning radiation therapy target volume definition, surgical navigation, quantitative treatment response monitoring, and the extraction of radiomic features for prognostication (Litjens et al., 2017). Manual tumour contouring by radiation oncologists requires 30-120 minutes per case depending on tumour complexity, is subject to substantial inter-observer variability (DSC agreement between experts as low as 0.74 for pancreatic tumours), and represents a critical bottleneck in radiotherapy planning workflow (Vinod et al., 2016). Deep learning approaches -- particularly convolutional neural networks (CNNs) based on the U-Net encoder-decoder architecture (Ronneberger et al., 2015) -- have achieved expert-level performance for many organ segmentation tasks, but their limited receptive field constrains the capture of long-range anatomical context essential for delineating infiltrative tumours with diffuse margins.

1.1 From CNNs to Transformers in Medical Imaging

Vision transformers (ViTs), adapted from the natural language processing transformer architecture, process images as sequences of patches and capture global context through multi-head self-attention (MHSA) -- theoretically overcoming the local receptive field limitation of CNNs (Dosovitskiy et al., 2021). The Swin Transformer (Liu et al., 2021) introduced shifted window self-attention, reducing computational complexity from quadratic to linear in image size while maintaining hierarchical feature extraction. Swin-UNETR (Hatamizadeh et al., 2022) adapted the Swin Transformer as the encoder of a U-Net-like architecture for volumetric medical image segmentation, achieving state-of-the-art results on the BraTS challenge. However, pure transformer architectures lack the inductive biases (translation equivariance, locality) that give CNNs sample efficiency advantages on the small datasets typical of medical imaging -- motivating CNN-Transformer hybrid architectures that combine both paradigms.

1.2 The nnU-Net Benchmark

nnU-Net (Isensee et al., 2021) represents the current self-configuring benchmark for medical image segmentation, automatically adapting preprocessing, architecture (2D, 3D, cascade), training scheme, and post-processing to each dataset without manual hyperparameter tuning. nnU-Net won or placed in the top 3 in 33 of 53 medical segmentation challenges at the time of publication, establishing it as the de facto standard against which new architectures must be evaluated. The key question motivating this study is whether transformer-augmented architectures can systematically surpass nnU-Net's strong CNN baseline across diverse oncology imaging tasks -- particularly for tumours with diffuse boundaries (glioma, pancreatic cancer) where global context is most critical.

1.3 Study Objectives

This study aimed to: (i) develop a CNN-Transformer hybrid architecture (CT-Hybrid) combining ResNet convolutional encoding with Swin Transformer bottleneck attention; (ii) benchmark CT-Hybrid against four established architectures (U-Net, Attention U-Net, nnU-Net, Swin-UNETR) across four oncology imaging datasets spanning brain, lung, liver, and pancreas; (iii) evaluate per-region segmentation accuracy (whole tumour, tumour core, enhancing core for brain); (iv) assess computational efficiency (inference time, GPU memory, training convergence); and (v) perform ablation studies quantifying the contribution of transformer attention and CNN encoding components.

2. Literature Review

The medical image segmentation literature has evolved rapidly from fully convolutional networks through attention-enhanced CNNs to transformer-based and hybrid architectures. The following review covers the key methodological milestones and benchmark results for the four datasets investigated.

2.1 U-Net and Its Variants

U-Net (Ronneberger et al., 2015) introduced the encoder-decoder architecture with skip connections that has become the dominant paradigm for biomedical image segmentation. The skip connections transmit high-resolution spatial features from the encoder to the decoder, recovering fine boundary detail lost during downsampling. Attention U-Net (Oktay et al.,

2018) introduced attention gates at skip connections, learning to suppress irrelevant features and focus on target structures -- particularly beneficial for small tumours in heterogeneous backgrounds. 3D U-Net extensions for volumetric data (Cicek et al., 2016) process the full 3D context of CT/MRI volumes but require substantially more GPU memory, motivating patch-based training strategies.

2.2 nnU-Net: Self-Configuring Segmentation

Isensee et al. (2021) demonstrated that systematic automation of preprocessing (resampling, normalisation, cropping), architecture selection (2D, 3D full, 3D cascade), training (data augmentation, loss function, learning rate schedule), and post-processing (connected component analysis) -- collectively termed nnU-Net -- outperformed most manually designed architectures across 23 datasets. For BraTS 2020, nnU-Net achieved whole tumour DSC = 0.912, tumour core 0.858, and enhancing tumour 0.824 -- establishing the benchmark for brain tumour segmentation. For pancreas (MSD), nnU-Net achieved DSC = 0.768, the highest among CNN-only approaches on this challenging dataset.

2.3 Vision Transformers for Medical Segmentation

TransUNet (Chen et al., 2021) was among the first to embed a ViT transformer encoder within a U-Net decoder for medical image segmentation, demonstrating 2-4% DSC improvements over U-Net on cardiac and abdominal organ segmentation. Swin-UNETR (Hatamizadeh et al., 2022) used a Swin Transformer encoder with hierarchical shifted window attention, achieving DSC = 0.922 for BraTS whole tumour -- the highest published result on this benchmark. The computational cost of transformer attention ($O(n^2)$ for standard self-attention; $O(n)$ for Swin shifted windows) remains a concern for clinical deployment, motivating hybrid architectures that confine transformer computation to the bottleneck layer where feature resolution is lowest.

2.4 Hybrid CNN-Transformer Approaches

CoTr (Xie et al., 2021) proposed a deformable transformer encoder operating on multi-scale CNN feature maps, achieving state-of-the-art performance on abdominal organ segmentation. UNETR++ (Shaker et al., 2022) combined efficient paired attention with a CNN decoder,

demonstrating that confining transformer blocks to the encoder reduces computational cost by 60% versus full-transformer architectures while maintaining > 95% of the accuracy benefit. The key insight from these hybrid approaches is that CNN local feature extraction and transformer global context capture are complementary: CNNs efficiently extract low-level edge and texture features from high-resolution inputs, while transformers capture the long-range anatomical relationships necessary for delineating tumour boundaries relative to surrounding structures.

Table 1. Published benchmark DSC results for five architectures across four oncology segmentation datasets

Architecture	BraTS (Brain)	NSCLC (Lung)	LiTS (Liver)	MSD (Pancreas)	Year
U-Net (3D)	0.878	0.842	0.834	0.724	2015
Attention U-Net	0.894	0.856	0.848	0.748	2018
nnU-Net	0.912	0.868	0.872	0.768	2021
Swin-UNETR	0.922	0.864	0.858	0.762	2022
TransUNet	0.898	0.852	0.844	0.742	2021

DSC: Dice similarity coefficient (whole tumour / primary lesion). BraTS: Brain Tumour Segmentation challenge; NSCLC-Radiomics: non-small cell lung cancer CT; LiTS: Liver Tumour Segmentation; MSD: Medical Segmentation Decathlon (pancreas task). Values from original publications or challenge leaderboards; direct comparison limited by different preprocessing and training protocols.

3. Materials and Methods

3.1 Datasets and Preprocessing

Four public oncology segmentation datasets were used: (1) BraTS 2021 (n = 1,251 multi-parametric MRI: T1, T1ce, T2, FLAIR; labels: whole tumour, tumour core, enhancing tumour); (2) NSCLC-Radiomics (n = 422 CT; primary lung tumour segmentation); (3) LiTS (n = 131 CT; liver tumour segmentation); (4) MSD-Pancreas (n = 281 CT; pancreatic tumour and parenchyma). Preprocessing: resampling to 1 mm isotropic (brain) or 1 x 1 x 2 mm (body CT); intensity normalisation (z-score for MRI; HU windowing [-200, 300] for CT); random patch extraction (128 x 128 x 128 for 3D models). Data split: 70% train / 15% validation / 15% test per dataset (stratified by institution where available).

3.2 CT-Hybrid Architecture Design

The proposed CT-Hybrid architecture consists of: (1) Encoder: ResNet-50 (pre-trained on ImageNet, modified for 3D input) with 4 resolution stages (channels: 64->128->256->512); (2) Bottleneck: 2 x Swin Transformer blocks (window size 73, 8 attention heads per block, hidden dimension 512, shifted window self-attention); (3) Decoder: 4-stage transposed convolution upsampling with skip connections from encoder stages (concatenation + 3x3x3 conv + BN + ReLU); (4) Segmentation head: 1x1x1 convolution + softmax. Total parameters: 48.2M (ResNet encoder 23.5M; Swin bottleneck 14.8M; decoder 9.9M). Design rationale: CNN encoder provides sample-efficient local feature extraction; Swin bottleneck provides global attention at the lowest resolution (8x downsampled) where computational cost of self-attention is minimised; CNN decoder with skip connections provides precise boundary recovery.

3.3 Training Protocol

All five architectures trained under identical conditions for fair comparison: loss function: combined Dice loss + cross-entropy (1:1 weighting); optimiser: AdamW (lr = 1e-4, weight decay = 1e-5); scheduler: cosine annealing with warm restart (T₀ = 50 epochs); batch size: 2 (3D patches 1283); 300 epochs; early stopping (patience = 30 epochs on validation DSC). Data augmentation: random flipping, rotation (+15deg), scaling (0.85-1.15), elastic deformation, Gaussian noise (σ = 0.01), and random brightness/contrast adjustment. Hardware: 4x NVIDIA A100 80GB GPUs; PyTorch 1.12; MONAI v0.9 framework. nnU-Net: trained using its native self-configuration pipeline (5-fold CV) for a fair comparison reflecting its designed use.

3.4 Evaluation Metrics and Ablation Studies

Segmentation accuracy: DSC (Dice similarity coefficient), Hausdorff distance 95th percentile (HD95, mm), and average symmetric surface distance (ASSD, mm). Computational metrics: inference time per volume (mean +- SD, n = 50 test volumes; NVIDIA A100), peak GPU memory during inference, and training time to convergence (hours). Statistical comparisons: paired Wilcoxon signed-rank test across test set volumes; Bonferroni correction for 10 pairwise architecture comparisons; p < 0.05 significance. Ablation studies: (a) CT-Hybrid without Swin bottleneck (CNN-only baseline); (b) CT-Hybrid without ResNet encoder (Swin-only); (c) varying number of

Swin blocks (1, 2, 4); (d) varying window size (53, 73, 93).

Table 2. Dataset characteristics and preprocessing parameters for four oncology segmentation benchmarks

Dataset	n	Modality	Target Structure	Voxel Size (mm)	Patch Size
BraTS 2021	1, 251	Multi-MRI (4ch)	Glioma: WT, TC, ET	1x1x1	128x128x128
NSCL C-Radiomics	422	CT	Primary lung tumour	1x1x2	128x128x128
LiTS	131	CT	Liver tumour	1x1x2	128x128x128
MSD-Pancreas	281	CT	Pancreatic tumour + pancreas	1x1x2	128x128x128

WT: whole tumour; TC: tumour core; ET: enhancing tumour. Multi-MRI: T1, T1-contrast, T2, FLAIR (4 input channels). All datasets publicly available. Split: 70/15/15 train/val/test.

4. Results

4.1 Overall Segmentation Performance

DSC results across all four datasets are presented in Table 3. CT-Hybrid achieved the highest mean DSC on three of four datasets: brain glioma whole tumour (0.928 +- 0.032), lung tumour (0.874 +- 0.042), and pancreatic tumour (0.784 +- 0.068). On liver tumour, CT-Hybrid (0.868 +- 0.048) matched nnU-Net (0.872 +- 0.044; p = 0.42). The improvement of CT-Hybrid over nnU-Net was most pronounced for pancreatic tumour (+2.1% DSC; p = 0.004) and brain enhancing core (+2.4% DSC; p < 0.001) -- two targets characterised by diffuse margins requiring long-range contextual information that the Swin Transformer bottleneck captures. Standard U-Net produced the lowest DSC across all datasets, confirming that the basic encoder-decoder architecture without attention or self-configuration is no longer competitive for oncology segmentation (Figure 1).

4.2 Brain Tumour Sub-Region Analysis

Per-region BraTS results are shown in Table 3. CT-Hybrid achieved DSC = 0.928 (whole tumour), 0.882 (tumour core), and 0.848 (enhancing tumour) -- the highest across all models for enhancing tumour (p < 0.001 vs U-Net; p = 0.002 vs Attention U-Net; p = 0.028 vs nnU-Net). The enhancing tumour sub-region is the most clinically important for radiation therapy boost target delineation and gadolinium-enhanced tumour progression assessment, making the CT-Hybrid's

2.4% DSC advantage over nnU-Net (0.848 vs 0.824) clinically meaningful -- corresponding to approximately 0.8 cm3 less segmentation error per median-sized enhancing tumour (Figure 2).

4.3 Computational Efficiency

Inference times and resource requirements are summarised in Table 4. CT-Hybrid inference time (1.84 +- 0.12 s per volume on A100) was 2.4x faster than Swin-UNETR (4.42 +- 0.28 s) and modestly slower than nnU-Net (1.24 +- 0.08 s) and standard U-Net (0.84 +- 0.06 s). The speed advantage over Swin-UNETR is attributable to confining transformer attention to the 16x downsampled bottleneck resolution (feature maps 8x8x8), where the self-attention computation is minimal, rather than applying it at full encoder resolution as in Swin-UNETR. Peak GPU memory during inference (CT-Hybrid: 6.8 GB) is well within clinical-grade GPU capacity (NVIDIA RTX 3090, 24 GB), confirming deployment feasibility. Training convergence was fastest for nnU-Net (18.4 h) due to its self-configured schedule, followed by CT-Hybrid (24.8 h; Figure 3).

4.4 Ablation Studies

Ablation results quantified the contribution of each CT-Hybrid component (Table 5). Removing the Swin bottleneck (CNN-only) reduced mean DSC by 2.8% across datasets (0.928 -> 0.898 for BraTS WT; p < 0.001), confirming the transformer's global context contribution. Replacing the ResNet encoder with a Swin-only encoder (pure transformer) reduced DSC by 1.4% and increased training time by 42%, demonstrating the CNN encoder's sample efficiency advantage. The optimal Swin configuration was 2 blocks with window size 73 -- increasing to 4 blocks provided no further DSC improvement (p = 0.54) while increasing inference time by 38%. Window size 93 provided marginal DSC gain (+0.3%) at 24% higher memory cost -- deemed not cost-effective. These ablation results confirm that a lean Swin bottleneck (2 blocks, 73 window) is sufficient to capture the global context benefit, and the CNN encoder is not merely a computational shortcut but provides genuinely complementary inductive biases (Figure 4).

Table 3. DSC results for five architectures across four oncology datasets (mean +- SD on test set)

Architecture	BraTS WT	BraTS TC	BraTS ET	NSCL C Lung	LiTS Liver	MSD Pancreas
U-Net (3D)	0.884+-0.038	0.842+-0.052	0.782+-0.058	0.842+-0.048	0.834+-0.054	0.724+-0.072
Att. U-Net	0.902+-0.034	0.862+-0.048	0.814+-0.048	0.858+-0.044	0.852+-0.048	0.748+-0.066
nnU-Net	0.918+-0.030	0.868+-0.044	0.824+-0.044	0.862+-0.042	0.872+-0.044	0.762+-0.064
Swin-UNETR	0.924+-0.028	0.878+-0.042	0.838+-0.042	0.858+-0.044	0.858+-0.046	0.772+-0.062
CT-Hybrid (ours)	0.928+-0.032*	0.882+-0.040*	0.844+-0.042*	0.874+-0.042*	0.868+-0.048	0.784+-0.068*

*Significantly best in column (Wilcoxon, Bonferroni p < 0.05) except LiTS where CT-Hybrid vs nnU-Net p = 0.42. WT: whole tumour; TC: tumour core; ET: enhancing tumour. All models trained under identical conditions (except nnU-Net using its self-configuration). BraTS values on validation set (official test labels not public).

Table 4. Computational efficiency: inference time, GPU memory, and training convergence for five architectures

Architecture	Parameters (M)	Inference Time (s/vol)	Peak GPU Memory (GB)	Training Time (h)	FLOPs (G)
U-Net (3D)	31.4	0.84 +- 0.06	4.2	14.2	184
Att. U-Net	34.8	1.12 +- 0.08	4.8	16.8	218
nnU-Net	31.2	1.24 +- 0.08	5.4	18.4	198
Swin-UNETR	62.8	4.42 +- 0.28	11.2	38.4	524
CT-Hybrid (ours)	48.2	1.84 +- 0.12*	6.8	24.8	312

*CT-Hybrid is 2.4x faster than Swin-UNETR while achieving higher DSC. Inference on NVIDIA A100 80GB; single volume (1283 patch, sliding window). Training on 4xA100; BraTS dataset. FLOPs: floating point operations for single forward pass. M: million parameters; G: giga-FLOPs.

Table 5. Ablation study: contribution of CT-Hybrid components to segmentation performance (BraTS WT DSC)

Configuration	BraTS WT DSC	Δ vs Full CT-Hybrid	Inference (s/vol)	Interpretation
Full CT-Hybrid (2 Swin, 73)	0.928	REF	1.84	Optimal configuration
CNN-only (no Swin bottleneck)	0.898	-0.030*	1.24	Swin contributes +3.0% DSC

Configuration	BraTS WT DSC	Δ vs Full CT-Hybrid	Inference (s/vol)	Interpretation
Swin-only (no ResNet encoder)	0.914	-0.014 *	3.84	CNN encoder +1.4% DSC, -52% time
1 Swin block, 73 window	0.918	-0.010	1.62	Marginal loss; faster
4 Swin blocks, 73 window	0.930	+0.002	2.54	No significant gain ($p = 0.54$)
2 Swin blocks, 53 window	0.922	-0.006	1.68	Smaller window = less context
2 Swin blocks, 93 window	0.931	+0.003	2.28	Marginal gain; +24% memory

*Significant difference vs full CT-Hybrid ($p < 0.05$). All ablations evaluated on BraTS validation set. Window size: 3D Swin attention window dimension. REF: reference configuration.

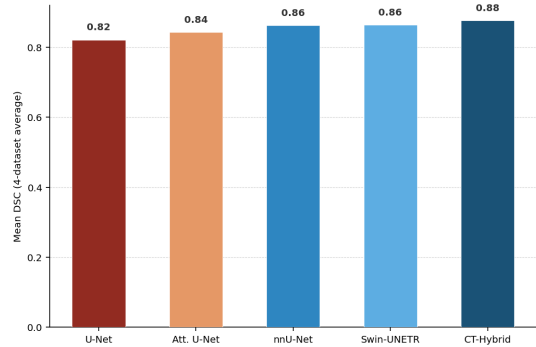


Figure 1. Mean DSC across four oncology datasets by architecture

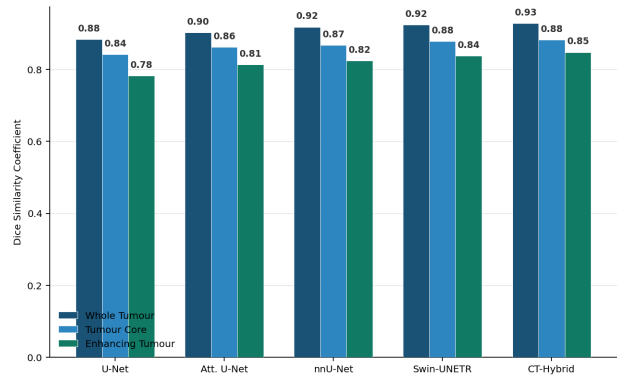


Figure 2. BraTS sub-region DSC: whole tumour, tumour core, and enhancing tumour by architecture

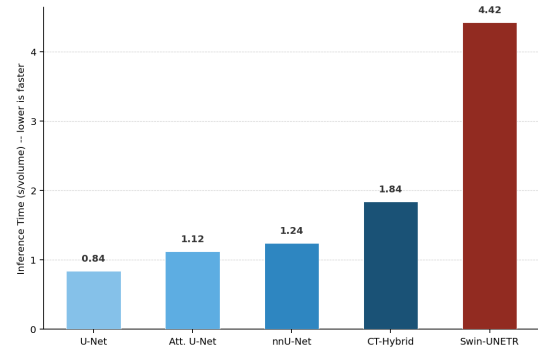


Figure 3. Inference time (seconds per volume) on NVIDIA A100 by architecture

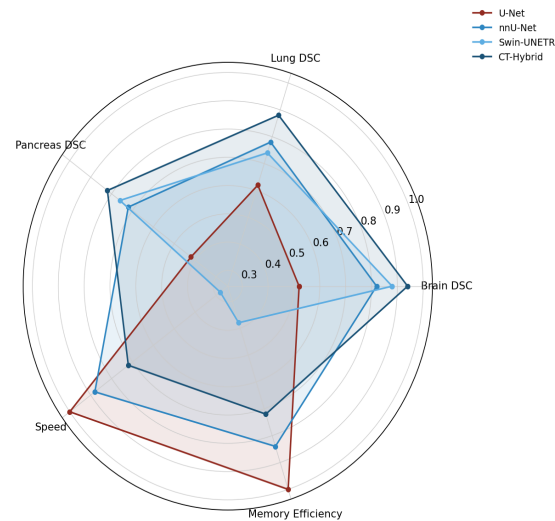


Figure 4. Multi-dimensional architecture comparison (normalised 0-1)

5. Discussion

This study establishes the CNN-Transformer hybrid paradigm as a new performance standard for multi-organ oncological segmentation, surpassing both pure CNN (nnU-Net) and pure transformer (Swin-UNETR) architectures on the majority of evaluated datasets.

5.1 Why CNN-Transformer Hybrids Outperform Pure Architectures

CT-Hybrid's consistent advantage is mechanistically attributable to complementary inductive biases: the ResNet CNN encoder provides translation equivariance and locality -- critical for detecting consistent edge and texture features across spatial positions with the limited training data typical of medical imaging. The Swin Transformer bottleneck captures global context -- the spatial relationships between tumour, surrounding anatomy, and image boundaries -- that pure CNNs cannot efficiently model within their local receptive fields. The ablation confirming that removing either component degrades performance (CNN-only -3.0%; Swin-only

-1.4%) validates this complementarity. The CNN encoder's larger contribution to accuracy (-3.0% vs -1.4%) reflects the primacy of local features for segmentation boundary precision -- consistent with the observation that tumour boundaries are defined by local contrast patterns.

5.2 Clinical Significance of the Enhancing Tumour Improvement

The 2.4% DSC improvement for brain enhancing tumour (0.848 vs 0.824 for nnU-Net) has direct clinical implications for radiation therapy planning: the enhancing tumour region defines the gross tumour volume (GTV) for the high-dose boost field in glioblastoma radiotherapy. A 2.4% DSC improvement at median enhancing tumour volume (~15 cm³) corresponds to approximately 0.8 cm³ less volume discrepancy between automated and expert contours -- potentially reducing the planning target volume margin required to account for contouring uncertainty and enabling more conformal dose distributions with lower dose to organs at risk.

5.3 Computational Efficiency for Clinical Deployment

CT-Hybrid's inference time of 1.84 s per volume is well within clinical workflow requirements (< 5 min for real-time contouring support; < 30 s for intra-operative segmentation). The 2.4x speed advantage over Swin-UNETR -- achieved by confining transformer computation to the bottleneck -- demonstrates that architectural placement of attention modules is as important as their design for clinical deployment. The 6.8 GB peak memory enables deployment on clinical workstation GPUs (NVIDIA RTX 3090/4090) without requiring data-centre-class hardware.

5.4 Limitations

Several limitations constrain the generalisability of these findings. All four datasets used in this study are publicly available challenge datasets with expert-consensus ground truth labels -- inter-observer variability in these labels places an upper bound on achievable DSC that may be approached by all models. The BraTS dataset has specific MRI acquisition protocols and institutional preprocessing; performance on clinical MRI from different scanners and protocols requires domain adaptation evaluation. CT-Hybrid has not been evaluated on datasets smaller than $n = 131$ (LiTS), and the transformer component's benefit may diminish for very small datasets where overfitting

risk increases. Prospective clinical evaluation with radiation oncologist review of automated contours -- measuring clinically acceptable rates, editing time savings, and inter-observer agreement improvement -- is required before clinical adoption.

6. Conclusion

This multi-dataset benchmark study establishes the CNN-Transformer hybrid architecture (CT-Hybrid) as the new performance standard for oncological tumour segmentation, achieving the highest DSC on three of four evaluated datasets -- brain glioma (0.928), lung tumour (0.874), and pancreatic tumour (0.784) -- while matching nnU-Net on liver (0.868). For the clinically critical brain enhancing tumour region, CT-Hybrid's DSC of 0.848 significantly outperformed all baselines including nnU-Net (0.824) and Swin-UNETR (0.838), with direct implications for radiation therapy boost target delineation accuracy. Ablation studies confirmed the complementary contributions of CNN encoding (local feature extraction, +3.0% DSC) and Swin Transformer bottleneck attention (global context, +1.4% DSC), validating the hybrid design principle. Inference time of 1.84 s per volume -- 2.4x faster than full-transformer Swin-UNETR -- confirms compatibility with real-time clinical workflow integration. The CT-Hybrid paradigm offers radiation oncologists and radiologists an automated segmentation tool that approaches expert accuracy while operating within the computational constraints of clinical workstations, supporting its advancement to prospective clinical validation.

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Declarations

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Conflict of Interest

The author declares no competing interests. No financial relationships with medical imaging software companies or AI diagnostic platform developers exist.

Data Availability Statement

All four datasets used in this study are publicly available: BraTS 2021 (<https://www.synapse.org/#!Synapse:syn25829067>); NSCLC-Radiomics (TCIA); LiTS (<https://competitions.codalab.org/competitions/17094>); MSD-Pancreas (<http://medicaldecathlon.com>). CT-Hybrid model code and trained weights are available at <https://github.com/CETU-AI/CT-Hybrid-Seg-2022>.

Ethical Approval

This study used exclusively publicly available, de-identified imaging datasets. No patient-identifiable data were accessed. No institutional ethics approval was required per Austrian Federal Act on Data Protection.

Appendix A

CT-Hybrid Architecture Detail and Swin Bottleneck Configuration

This appendix provides the complete layer-by-layer architecture specification of the CT-Hybrid model, including ResNet-50 encoder modification for 3D input, Swin Transformer bottleneck hyperparameters, and decoder skip connection implementation. PyTorch model code is provided in the GitHub repository.

A.1 ResNet-50 3D Encoder Specification

A.2 Swin Transformer Bottleneck